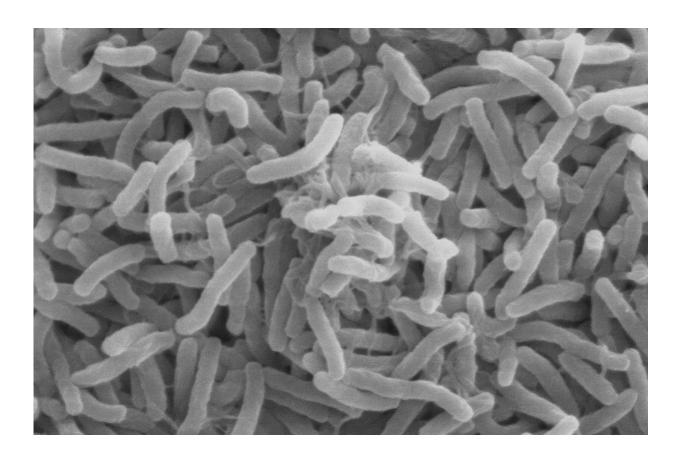


Genetic code of WWI soldier's cholera mapped

April 9 2019



Scanning electron microscope image of Vibrio cholerae. Credit: Wikipedia

The oldest publicly-available strain of the cholera-causing bacterial species, *Vibrio cholerae*, has had its genetic code read for the first time by researchers at the Wellcome Sanger Institute and their collaborators.



The bacterium was isolated from a British soldier during World War One (WWI) and stored for over 100 years before being revived and sequenced.

The results, published today in *Proceedings of the Royal Society B*, show that this strain is a unique, non-toxigenic strain of *V. cholerae* that is distantly related to the <u>strains</u> of bacteria causing cholera pandemics today and in the past.

Cholera is a severe diarrhoeal disease caused by ingesting food or water that is contaminated with toxigenic *V. cholerae*. The disease can spread rapidly in epidemics and in global pandemics.

WWI coincided with an historical global cholera pandemic, known as the sixth pandemic, which was caused by 'classical' *V. cholerae*. Surprisingly, very few soldiers in the British Expeditionary Forces contracted cholera during the war, despite the disease being considered as a threat.

In 1916, a strain of *V. cholerae* was extracted from the stool of a British soldier who was convalescing in Egypt. Reports indicate that the isolate was taken from 'choleraic diarrhoea'. The bacterium was stored and subsequently deposited in the National Collection of Type Cultures (NCTC) in 1920.

Researchers at the Sanger Institute revived the WWI soldier's bacteria—thought to be the oldest publicly-available *V. cholerae* sample—and sequenced its <u>entire genome</u>.

The team found this particular strain of *V. cholerae* was not the type capable of causing epidemic cholera, and was unrelated to the classical *V. cholerae* that caused the sixth pandemic at the time of WWI.



Professor Nick Thomson, lead author from the Wellcome Sanger Institute, said: "We have decoded the genome of what we believe to be the oldest archived 'live' sample of *V. cholerae*. It is a privilege to be able to look at the genome of this isolate. Studying strains from different points in time can give deep insights into the evolution of this species of bacteria and link that to historical reports of human disease. Even though this isolate did not cause an outbreak it is important to study those that do not cause disease as well as those that do. Hence this isolate represents a significant piece of the history of cholera, a disease that remains as important today as it was in past centuries."

Matthew Dorman, first author from the Wellcome Sanger Institute, said: "Reports in the literature indicated that there was something unusual about the strain of bacteria from the WWI soldier. It's promising to see that our genomic information aligns with those historical records. We also made other observations—under the microscope, the <u>bacterium</u> looks broken; it lacks a flagellum—a thin tail that enables bacteria to swim. We discovered a mutation in a gene that's critical for growing flagella, which may be the reason for this characteristic."

The soldier was reported to have cholera-like diarrhoea, but researchers now know he was infected with a non-toxigenic strain of *V. cholerae*. The team discovered genes that may have been responsible for producing a toxin that caused diarrhoea, but are unsure whether such diarrhoea would be classified as choleraic.

Researchers also found that this strain of *V. cholerae* possessed a gene for ampicillin resistance. This adds to increasing evidence that genes for <u>antibiotic resistance</u> in bacteria existed before the introduction of antibiotic treatments, possibly because the bacteria needed them to protect against naturally-occurring antibiotics.

Julie Russell, Head of Culture Collections at NCTC, said: "The National



Collection of Type Cultures grows and maintains over 5,000 strains of bacteria from the last hundred years or so. Studying these bacteria offers a window into the past and helps scientists to understand how <u>bacteria</u> evolve over time, and the roles they played in history."

More information: The history, genome, and biology of NCTC 30, a non-pandemic Vibrio cholerae isolate from World War One, *Proceedings of the Royal Society B*, <u>rspb.royalsocietypublishing.or</u>1098/rspb.2018.2025

Provided by Wellcome Trust Sanger Institute

Citation: Genetic code of WWI soldier's cholera mapped (2019, April 9) retrieved 11 May 2024 from <u>https://phys.org/news/2019-04-genetic-code-wwi-soldier-cholera.html</u>

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