

Wellcome Sanger Institute sequences reference genomes of 3,000 dangerous bacteria

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New Delhi: The genomes of more than 3,000 bacteria, including some of the world's most dangerous, have been sequenced by researchers at the Wellcome Sanger Institute in collaboration with Pacific Biosciences (PacBio). Infecting tens of millions of people worldwide every year, these bacteria have been collected by the National Collection of Type Cultures (NCTC) and include deadly strains of plague, dysentery and cholera.

By decoding the DNA, researchers will be able to better understand these diseases and how they become resistant to antibiotics. The publicly available genomic maps could also lead to the development of new diagnostic tests, vaccines or treatments.

Set up in 1920, the NCTC is the longest established collection of bacteria in the world. With more than 5,500 species of bacteria so far, the NCTC is also one of the world's largest collections of clinically relevant bacteria. It is used extensively by researchers who are comparing historical and modern strains to advance global knowledge about the epidemiology, virulence, prevention and treatment of infectious diseases.

Antibiotic resistance is a significant problem globally and the collection includes some of the

most important known drug-resistant bacteria. These include tuberculosis, one of the top ten causes of death worldwide, infecting 10.4 million and killing 1.7 million people in 2016 alone*, and gonorrhoea, the sexually transmitted disease that infects 78 million people a year** and is now becoming extremely difficult to treat. The NCTC also contains samples of methicillin resistant *Staphylococcus aureus* (MRSA), which is resistant to multiple antibiotics and which can cause life-threatening infections in hospitals.

The genetic study of these strains will help researchers to understand the mechanisms of antibiotic resistance, and to look for any cracks in their armour to enable treatment.

All ‘type strains’ of bacteria in the collection, the first strains that describe the species and are used to classify them, were sequenced as part of this initiative. The genome sequences of these highly valuable strains are fundamental for developing ways to identify specific infections in people, including tests diagnosing bacterial infections in the field to rapidly identify the source of an outbreak and help contain infections.

Amongst the many historically important strains in the collection are 16 deposited by penicillin discoverer Alexander Fleming, including a sample taken from his own nose. Also notable is the first bacteria to be deposited in the NCTC: A strain of dysentery-causing *Shigella flexneri* that was isolated in 1915 from a soldier in the trenches of World War 1.

Dr Julian Parkhill from the Wellcome Sanger Institute said: “Historical collections such as the NCTC are of enormous value in understanding current pathogens. Knowing very accurately what bacteria looked like before and during the introduction of antibiotics and vaccines, and comparing them to current strains from the same collection, shows us how they have responded to these treatments. This in turn helps us develop new antibiotics and vaccines. PacBio’s comprehensive DNA sequencing enables deep genomic analyses, and we are happy to be partnering with them for this important project.”

Jonas Korch, Ph.D., Chief Scientific Officer of PacBio, said: “The high-quality genomic maps enabled by SMRT® Sequencing allow an unprecedented understanding of these bacteria. We are delighted to be chosen by institutions like Wellcome Sanger to help create such essential resources for the scientific and public health communities.”

Dr Julie Russell, Head of Culture Collections, which is operated by the National Infection Service of Public Health England, said: “This resource is a vital tool for public health and by sequencing the bacteria, we have made the NCTC collection ready for the 21st century so that the research community can track and understand the bacteria. With this collection, we are providing tools for tracing infections, and identifying outbreaks of resistant bacteria, transforming public health in the UK.”

Going forward, all the bacterial species in the NCTC collection will be sequenced as they are collected. Researchers can order bacterial strains from the [NCTC website](#). Full information about each strain, including the DNA sequences, are available at [EMBL-EBI](#).