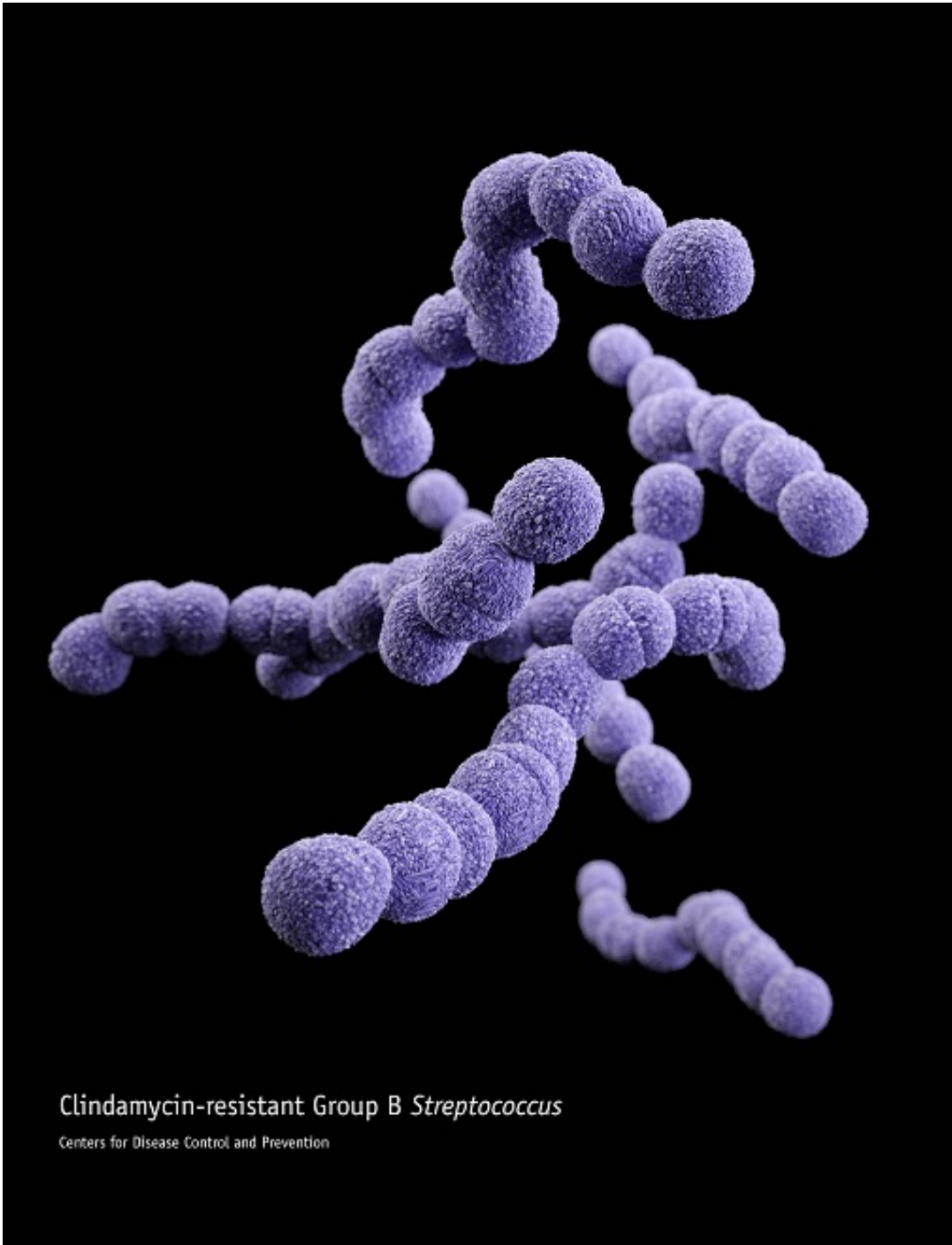


# Scientists sequence streptococcus bacteria strain causing severe infections

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A strain of Group B Streptococcus, also known as *Streptococcus agalactiae*, caused an increased number of cases of severe disease in Singapore. Scientists at the Genome Institute of Singapore have sequenced the genome of this strain to better understand it. Credit: Centers for Disease Control and Prevention, Office of the Associate Director for Communications, Division of Public Affairs

Scientists from Agency for Science, Technology and Research (A\*STAR)'s Genome Institute of Singapore (GIS), together with Tan Tock Seng Hospital (TTSH) and the MOH-supported Singapore Infectious Diseases Initiative (SIDI) have successfully sequenced the genome of a strain of Group B Streptococcus (GBS) responsible for the increase in severe infections observed in Singapore this year.

Most strains of GBS bacteria, found in the gut and urinary tract of about 15 to 30 per cent of adult humans, pose little danger of disease to healthy people. The recent outbreak of GBS is unusual as it is associated with the consumption of raw Song (Asian bighead carp) and Toman (snakehead fish).

Applying the latest sequencing technology, the team was able to arrive quickly at the [complete genome sequence](#) of a GBS isolate that caused meningitis in a local patient. The availability of this genome sequence is a crucial starting point for further studies to understand factors responsible for the strain's ability to cause serious disease and to develop tests to rapidly detect its presence in food and for clinical testing. The team is racing ahead to develop new tests for detection of this bacteria strain.

Dr Swaine Chen, Senior Research Scientist in the GIS Infectious Diseases Group and Assistant Professor in the Department of Medicine at National University of Singapore Yong Loo Lin School of Medicine who led the project said, "Sequencing is a key first step in modern infectious disease outbreak investigation. Having the sequence will help with ongoing studies to understand how and why this strain can cause serious disease. We are making this data publicly available immediately to accelerate progress as much as possible".

"We have had to use rather labourious and expensive methods to identify the exact strain causing the outbreak. This initial [genome sequence](#) will

be a great help in the development of a simpler test that will enable us to detect the bacteria faster and more cost effectively," said Prof Timothy Barkham, Senior Consultant in Laboratory Medicine, TTSH and Adjunct Associate Professor, Department of Microbiology, National University of Singapore Yong Loo Lin School of Medicine, whose team first noticed the rise in infections. "If a simpler test can be developed, it will contribute to testing patients, food products and surveillance. While we are gratified to see the reduction in cases recently, the GIS sequence can now be studied to look for clues as to why this strain causes serious disease and where it may have come from."

Dr Hsu Li Yang, Director of SIDI added, "This rapid result is a testimony to both GIS' technological capability, as well as the ability of our clinical, public health and research communities to quickly work together in the event of an [infectious disease outbreak](#)."

Prof Ng Huck Hui, Executive Director, GIS said, "GIS and the participating hospitals and universities have pooled our respective resources and expertise to study the GBS [disease](#) as quickly as we can."

Provided by Agency for Science, Technology and Research (A\*STAR), Singapore

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