

**MEDIA RELEASE
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**A*STAR SCIENTISTS SEQUENCE STREPTOCOCCUS BACTERIA STRAIN
CAUSING SEVERE INFECTIONS**

Sequencing of GBS strain by Genome Institute of Singapore aims to determine the reason for the recent increase in infection and to help combat the disease

SINGAPORE – Scientists from 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 year¹.

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”.

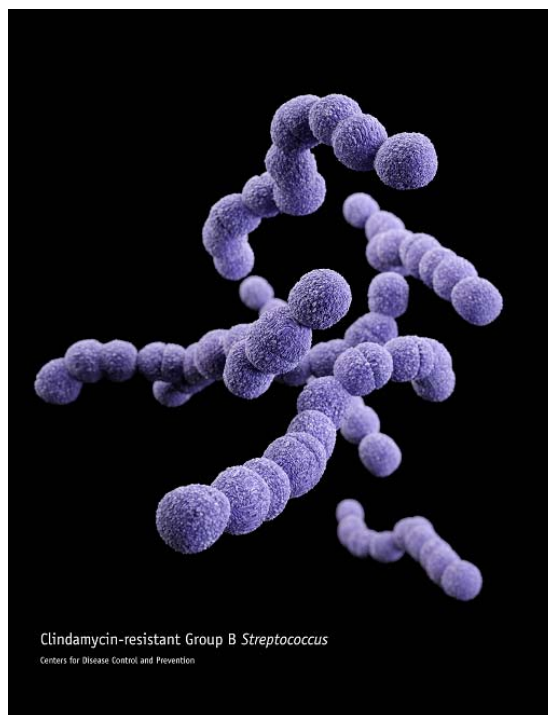
^{1&2} Update on Investigation into Group B Streptococcus Cases, Ministry of Health, 24 July 2015, www.moh.gov.sg/content/moh_web/home/pressRoom/pressRoomItemRelease/2015/update-on-investigation-into-group-b-streptococcus-cases.html

“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.”

The project, a collaborative effort organised by SIDI to study the recent increase in GBS infections, involves GIS, local hospitals and universities. SIDI is funded by the Ministry of Health (MOH).



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.

(Image source: Centers for Disease Control and Prevention, Office of the Associate Director for Communications, Division of Public Affairs)

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About the A*STAR's Genome Institute of Singapore (GIS)

The Genome Institute of Singapore (GIS) is an institute of the Agency for Science, Technology and Research (A*STAR). It has a global vision that seeks to use genomic sciences to achieve extraordinary improvements in human health and public prosperity. Established in 2000 as a centre for genomic discovery, the GIS will pursue the integration of technology, genetics and biology towards academic, economic and societal impact.

The key research areas at the GIS include Human Genetics, Infectious Diseases, Cancer Therapeutics and Stratified Oncology, Stem Cell and Regenerative Biology, Cancer Stem Cell Biology, Computational and Systems Biology, and Translational Research.

The genomics infrastructure at the GIS is utilised to train new scientific talent, to function as a bridge for academic and industrial research, and to explore scientific questions of high impact.

For more information about GIS, please visit www.gis.a-star.edu.sg.

About the Agency for Science, Technology and Research (A*STAR)

The Agency for Science, Technology and Research (A*STAR) is Singapore's lead public sector agency that spearheads economic oriented research to advance scientific discovery and develop innovative technology. Through open

innovation, we collaborate with our partners in both the public and private sectors to benefit society.

As a Science and Technology Organisation, A*STAR bridges the gap between academia and industry. Our research creates economic growth and jobs for Singapore, and enhances lives by contributing to societal benefits such as improving outcomes in healthcare, urban living, and sustainability.

We play a key role in nurturing and developing a diversity of talent and leaders in our Agency and Research Institutes, the wider research community and industry. A*STAR oversees 18 biomedical sciences and physical sciences and engineering research entities primarily located in Biopolis and Fusionopolis.

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