

**MEDIA RELEASE
FOR IMMEDIATE RELEASE**

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**INNOVATIVE METAGENOMICS STUDY MAPS OUT ANTIBIOTIC RESISTANCE
GENES FROM HOSPITAL ENVIRONMENT MICROBIOMES**

*Findings were made by A*STAR's Genome Institute of Singapore (GIS), through its analysis of genetic sequences of microbes and multi-drug resistant organisms found in hospital environments*



*Virtual-reality visualisation of metagenomic data for infection control in smart hospitals
(Copyright: A*STAR's Genome Institute of Singapore)*

SINGAPORE – Nature Medicine published a [study](#) by the Agency for Science, Technology and Research's (A*STAR) Genome Institute of Singapore (GIS), on 8 June 2020, providing the first extensive genomic mapping of microbiomes and antibiotic resistance genes in a tertiary hospital in Singapore.

This paper is a potentially ground-breaking analysis, enlisting the emerging technology of metagenomics to provide a detailed survey useful in the increasingly important worldwide battle against antimicrobial resistance, and represents a collaboration between GIS, Tan Tock Seng Hospital (TTSH), National Centre for Infectious Diseases (NCID), National

University Hospital (NUH), Singapore General Hospital (SGH), Weill Cornell Medicine, and the MetaSUB Consortium¹.

This study maps out for the first time the diversity and range of bacteria and antibiotic resistant genes found in hospitals. In this study, environmental samples were collected from different sites in a hospital, cultures were enriched to find antibiotic resistant bacteria, and the sequences were compared to databases of previously published sequences from bacteria found in hospital environments as well as patients.

While all-out efforts have been focused on the COVID-19 pandemic, the global epidemic of antibiotic resistance is a looming danger, projected to cause millions of deaths worldwide over the next three decades, with an economic impact estimated at 100 trillion dollars by 2050². Antimicrobial resistance will exact a heavy healthcare burden in both developed and developing countries³.

This study shows that modern gene sequencing technologies and metagenomic analyses can systematically characterise the distribution of bacteria, along with antibiotic resistance genes. Such detailed data could provide potential information to identify microbial reservoirs in hospital environments, including organisms that form biofilms or are potential risks for human infection.

Dr Niranjan Nagarajan, Associate Director and Group Leader at GIS, said, “Our analysis highlights that hospital environments may harbour significant uncharacterised genetic diversity. A large baseline survey such as this study provides a reference map that can be updated based on periodic scans.”

Associate Prof Christopher E Mason, from Weill Cornell Medicine, commented, “We are now merging these data with the global catalogue of other viruses, antibiotic markers, fungi, and bacteria found in the global MetaSUB Consortium to give us a genetic ranking for antibiotic resistance that we can use for tracing in hospitals around the world.”

“This study leverages cutting-edge metagenomics to understand the distribution of multidrug-resistant organisms. The current findings support the possibility of precision infection control where we can apply targeted infection control interventions to control MDROs in the healthcare setting,” said Dr Kalisvar Marimuthu and Associate Professor Ng Oon Tek, Senior Consultants at NCID.

Prof Patrick Tan, Executive Director of GIS, said, “These findings highlight the importance of characterising antibiotic resistance reservoirs in the hospital environment. They

¹ [MetaSUB Consortium](#): The Metagenomics and Metadesign of the Subways and Urban Biomes (MetaSUB) International consortium is a novel, interdisciplinary initiative made up of experts across many fields, including genomics, data analysis, engineering, public health, and design.

² O’Neill, J. Tackling drug-resistant infections globally: final report and recommendations, <<https://amr-review.org/Publications.html>> (2016).

³ Allegranzi, B. et al. Burden of endemic health-care-associated infection in developing countries: systematic review and meta-analysis. *Lancet* 377, 228-241, doi:10.1016/S0140-6736(10)61458-4 (2011).

About 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.a-star.edu.sg/gis.

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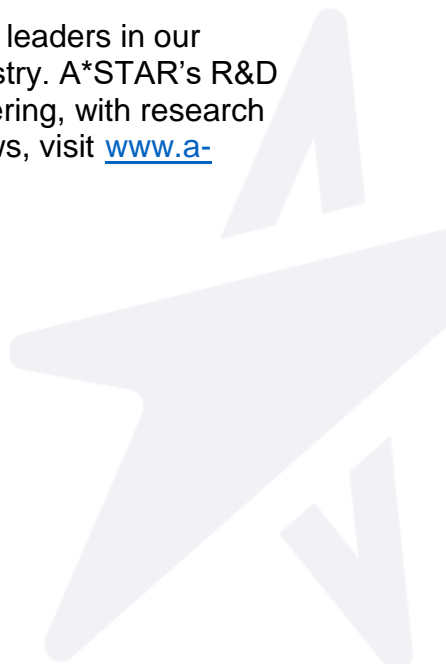
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ANNEX A – NOTES TO EDITOR

The research findings described in this media release can be found in the scientific journal Nature Medicine, under the title, “[Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment](#)” by Kern Rei Chng^{1,*}, Chenhao Li^{1,*}, Denis Bertrand^{1,*}, Amanda Hui Qi Ng¹, Junmei Samantha Kwah¹, Hwee Meng Low¹, Chengxuan Tong¹, Maanasa Natrajan¹, Michael Hongjie Zhang¹, Licheng Xu², Karrie Kwan Ki Ko^{3,4,5}, Eliza Xin Pei Ho¹, Tamar V. Av-Shalom¹, Jeanette Woon Pei Teo⁶, Chiea Chuen Khor¹, MetaSUB Consortium, Swaine L. Chen¹, Christopher E. Mason⁷, Oon Tek N⁸, Kalisvar Marimuthu⁸, Brenda Ang⁸, Niranjana Nagarajan^{1,9,#}.

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