MEDIA 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 Consortium[1].

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 2050[2]. Antimicrobial resistance will exact a heavy healthcare burden in both developed and developing countries[3].

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

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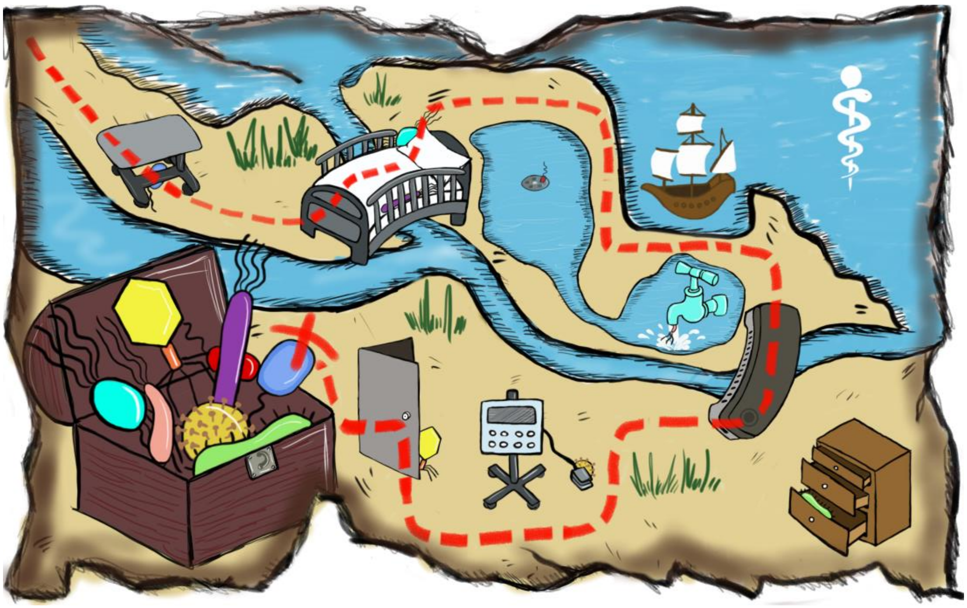
[1] MetaSUB Consortium: The Metagenomics and Metadesign of the Subways and Urban Biomes (MetaSUB) International consortium is a novel, interdisciplinary initiative made up of experts across many fields, including genomics, data analysis, engineering, public health, and design.

[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).

establish the feasibility of systematic genomic surveys to help target resources more efficiently for preventing hospital-acquired infections."

Ongoing work by the team will explore how RNA viruses might be distributed and persist in the hospital environment, the impact of various cleaning measures on their distribution, and how this may improve care for hospitalised patients.



*Charting out a map of opportunistic pathogens in the hospital environment (Copyright: A*STAR's Genome Institute of Singapore)*

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Enclosed:
ANNEX A – Notes to Editor

For media queries and clarifications, please contact:

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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.

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

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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 entities, the wider research community and industry. A*STAR’s R&D activities span biomedical sciences and physical sciences and engineering, with research entities primarily located in Biopolis and Fusionopolis. For ongoing news, visit www.a-star.edu.sg.

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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 Ng[1], Junmei Samantha Kwah[1], Hwee Meng Low[1], Chengxuan Tong[1], Maanasa Natrajan[1], Michael Hongjie Zhang[1], Licheng Xu[2], Karrie Kwan Ki Ko[3,4,5], Eliza Xin Pei Ho[1], Tamar V. Av-Shalom[1], Jeanette Woon Pei Teo[6], Chiea Chuen Khor[1], MetaSUB Consortium, Swaine L. Chen[1] , Christopher E. Mason[7], Oon Tek N[8], Kalisvar Marimuthu[8], Brenda Ang[8], Niranjan Nagarajan[1,9,#].

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