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Singapore researchers reveal breakthrough approach to tackle antibiotic resistance

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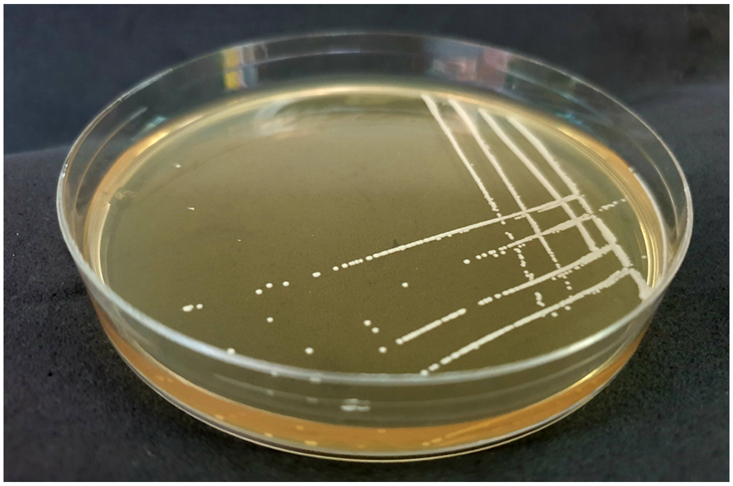
A new high-resolution approach using portable DNA sequencers provides a more complete genomic picture of antibiotic resistance in gut bacteria



A study led by scientists from the Agency for Science, Technology and Research’s (A*STAR) Genome Institute of Singapore (GIS), together with clinicians from Tan Tock Seng Hospital (TTSH) and researchers from the National University of Singapore (NUS), has resulted in a breakthrough approach to studying gut bacteria, and a step forward in the battle against antibiotic resistance.

Their technique leverages portable DNA sequencing technology and sophisticated clustering algorithms to analyse complex bacterial communities in the gut, pulling together their entire genetic code to track the spread of antibiotic resistance and study microbial contributions to human health.

Until now, studies have been limited by the resolution of genetic analysis and the ability to understand microbial function in communities harbouring hundreds of bacterial species. The newly-developed method provides a more complete genomic map allowing scientists to study how individual bacterial strains contribute to overall microbial community function in the human body.

Prof Niranjan Nagarajan, Associate Director and Senior Group Leader at GIS, noted, “The complete genome sequence of an organism is its ultimate fingerprint. We are excited to now be able to extract it directly out of metagenomic data. We need powerful technological capabilities like this to successfully apply clinical metagenomics in the battle against antibiotic resistance.”

Prof Patrick Tan, Executive Director at GIS, said, “It is exciting to see the power of new nanopore sequencing technologies being brought to bear on this important problem. Real-time clinical metagenomics can transform our understanding of how antibiotic-resistant organisms spread and help us curb this growing menace.”