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Singapore researchers develop RNA tool to advance cancer and infectious disease therapies

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SMART researchers develop first-of-its-kind automated tool for identifying disease markers and developing targeted therapies and personalised treatments for diseases such as cancer and antibiotic-resistant infections.

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Researchers at the Antimicrobial Resistance (AMR) interdisciplinary research group of the Singapore-MIT Alliance for Research and Technology (SMART), Massachusetts Institute of Technology's (MIT) research enterprise in Singapore, have developed a powerful tool capable of scanning thousands of biological samples to detect transfer ribonucleic acid (tRNA) modifications — tiny chemical changes to RNA molecules that help control how cells grow, adapt to stress and respond to diseases such as cancer and antibiotic?resistant infections.

The tool opens up new possibilities for science, healthcare and industry — from accelerating disease research and enabling more precise diagnostics, to guiding the development of more effective medical treatments for diseases such as cancer and antibiotic-resistant infections.

The research was led by SMART AMR, in collaboration with Nanyang Technological University (NTU Singapore), University of Florida, University at Albany, Lodz University of Technology and MIT.

Current molecular methods used to study the expansive epitranscriptome and all of the thousands of different types of modified RNA, are often slow, labour-intensive, costly and involve hazardous chemicals, which limits research capacity and speed.

To solve this problem, the SMART team developed a new tool that enables fast, automated profiling of tRNA modifications —

molecular changes that regulate how cells survive, adapt to stress and respond to disease. This capability allows scientists to map cell regulatory networks, discover novel enzymes and link molecular patterns to disease mechanisms, paving the way for better drug discovery and development, and more accurate disease diagnostics.

The tool has already enabled the discovery of previously unknown RNA-modifying enzymes and the mapping of complex gene regulatory networks. These networks are crucial for cellular adaptation to stress and disease, providing important insights into how RNA modifications control bacterial survival mechanisms.

SMART’s automated system was specially designed to profile tRNA modifications across thousands of samples rapidly and safely. Unlike traditional methods — which are costly, labour-intensive and use toxic solvents such as phenol and chloroform — this tool integrates robotics to automate sample preparation and analysis, eliminating the need for hazardous chemical handling and reducing costs. This advancement increases safety, throughput and affordability, enabling routine large-scale use in research and clinical labs.

As the first system capable of quantitative, system?wide profiling of tRNA modifications at this scale, the tool provides a unique and comprehensive view of the epitranscriptome — the complete set of RNA chemical modifications within cells. This capability allows researchers to validate hypotheses about RNA modifications, uncover novel biology and identify promising molecular targets for developing new therapies.