

NCID MONTHLY RESEARCH MEETING

*BRINGING PEOPLE TOGETHER,
BRIDGING SCIENCE AND MEDICINE*

19 Apr 2024 | Friday | 11.00am – 12.00pm

About the Meeting

Our research meetings are held every 3rd Friday of the month, with the aim to:

- Inspire research ideas and participation
- Provide guidance on research studies
- Foster research collaborations

Who Should Attend

All who are interested in research are welcome to attend.

Programme

11:00 AM **Breaking the Chain: Decoding Coronavirus Evolution for Next-Generation Therapeutics**

Dr Matthew Zirui Tay

Principal Investigator

A*STAR Infectious Diseases Labs (ID Labs)



11:30 AM **Human Indel Variant as a Predictor of Antibody Responses to mRNA Vaccines**

Dr Chen Hsiu Yi

Senior Scientist

A*STAR Infectious Diseases Labs (ID Labs)



5 to 10 mins Q&A will follow after each talk

To Register

This will be a Zoom meeting.

Click <https://for.sg/apr2024researchmeeting> or scan QR code.

*CME/CNE/CPE points will be awarded



Breaking the Chain: Decoding Coronavirus Evolution for Next-Generation Therapeutics

by **Dr Matthew Zirui Tay**

Principal Investigator

A*STAR Infectious Diseases Labs (ID Labs)

The past two decades have witnessed the emergence of three novel human coronaviruses, two of which have now become endemic. Coronaviruses evolve rapidly in the face of immune pressure. Identifying the degree of mutability in coronaviruses is key toward defining the space that must be covered by next-generation escape-resistant vaccines and therapeutics. These efforts include the identification and targeting of conserved epitopes that are not necessarily immunodominant. Such strategies enable us to better combat endemic coronaviruses, as well as prepare for emergent coronaviruses.

Learning Points

1. The ladder-like evolution of coronaviruses highlights immune escape as a major factor contributing to viral fitness; such escape can be predicted in advance as a basis for development of future-resistant vaccines and therapeutics.
2. The ongoing levels of zoonotic coronavirus exposure coupled with low immune cross-protection indicate that the threat of new emergent coronaviruses remains high.
3. Conserved epitopes against diverse coronavirus strains are a basis for development of broadly-neutralizing therapeutics, including monoclonal antibodies and receptor-based decoys.

Human Indel Variant as a Predictor of Antibody Responses to mRNA Vaccines

by **Dr Chen Hsiu Yi**

Senior Scientist

A*STAR Infectious Diseases Labs (ID Labs)

Vaccination is a powerful tool to fight infectious diseases. However, its effectiveness varies among individuals, which is why the one-size-fits-all vaccination plan falls short in providing protection for everyone. To solve this problem, I develop a tool that predicts an individual's antibody response to vaccines, based on age, gender, and 12 insertion and deletion (indel) variants in the genome. This tool has the potential to prepare Singapore for future pandemics by strategically distributing vaccines to ensure timely and optimal protection.

Learning Points

1. Age and gender are not sufficient to predict antibody responses to COVID-19 mRNA vaccines.
2. An individual's antibody response to vaccines could be predicted by a new tool, based on age, gender, and 12 indel variants.
3. The tool has the capacity to equip Singapore for future pandemics by strategically distributing vaccines to better protect people.