



Singapore-MIT Alliance for Research and Technology

News Release

SMART and MIT Researchers Uncover Genetic Differences between 2009 H1N1 Strain and Previously Circulating H1N1 Strain

2009 strain would only require one key mutation or change to become resistant to viral inhibitors like Tamiflu®

Singapore, 10 June 2009 – Researchers at the Singapore-MIT Alliance for Research and Technology (SMART) and the Massachusetts Institute of Technology (MIT) have uncovered genetic differences between 2009 H1N1 flu strain and previously circulating H1N1 strain. In their research, Professor Ram Sasisekharan and his colleagues found the 2009 H1N1 strains distinct from existing strains. This means that individuals are likely not protected from infection due to the presence of any existing *cross-reactive antibodies* – proteins that protect humans from infections. The 2009 H1N1 is presently vulnerable to antivirals but would only require one key mutation or change to become resistant to viral inhibitors like Tamiflu®.

SMART and MIT reported their full sequence analysis of the 2009 H1N1 virus in the current issue of *Nature Biotechnology*. The study comes from the laboratory of Professor Sasisekharan and details a structural and functional context for some of the noted genetic differences between the recent and previously circulating strain.

Other important findings of this study include the fact that for 2009 H1N1, a key viral protein, the *polymerase complex* that plays a role in copying the viral genome and is critical for influenza to transmit from person-to-person, is not fully human-adapted.

According to this study, if the 2009 H1N1 acquires a “humanised” polymerase complex, its ability to transmit human-to-human would likely greatly increase. Analysis of a particular cell surface viral protein (*hemagglutinin* which is responsible for binding to human receptors) indicates that it is likely to bind to a wide variety of host receptors, or glycans, and therefore move between birds, pigs, and humans fairly easily. This finding confirms the previous ground-breaking work of the Sasisekharan laboratory at MIT which examined virus specifically based on these particular binding characteristics.

Professor Sasisekharan is a principal investigator in the Infectious Diseases Interdisciplinary Research Group of the SMART Centre in Singapore. He is also the Director of the Harvard-MIT Division of Health Sciences and Technology and the Edward Hood Taplin Professor of Health Sciences and Technology and Biological Engineering at MIT.

“The foundation provided by SMART was key to moving this research forward. The cross-disciplinary interaction amongst researchers within SMART has led and will continue to lead to cutting-edge research in infectious disease. Through collaborative efforts, such as those made possible by SMART, it has proven feasible to develop a detailed framework for many

infectious diseases including influenza. This type of framework continues to permit highly pertinent research, which has a real impact on the public health, to be conducted. I am happy to be part of SMART," stated Professor Sasisekharan.

Rohan Abeyaratne, Director of SMART Centre said, "The Sasisekharan group at SMART has long been at the leading edge of research on influenza. The distinction between the new 2009 H1N1 flu strain and the previously known H1N1 strain is a very significant finding. This latest result is typical of the kinds of breakthroughs they are making."

In addition to the scientific discoveries presented in Nature Biotechnology, this paper also provides an outline for the design of novel vaccines and/or therapeutics to combat influenza broadly and the 2009 H1N1 strain in particular.

About SMART

SMART Centre is a major new research enterprise established by the Massachusetts Institute of Technology (MIT) in partnership with the National Research Foundation of Singapore (NRF) in 2007. It is the first entity in the Campus for Research Excellence and Technological Enterprise (CREATE) being developed by NRF.

SMART Centre serves as an intellectual hub for research interactions between MIT and Singapore. Cutting-edge research projects in areas of interest to both Singapore and MIT are undertaken at the SMART Centre. Interdisciplinary, experimental, computational and translational research will also be conducted. Three interdisciplinary research groups (IRG) have been established to date: they are BioSystems and Micromechanics (BioSym), Centre for Environmental Sensing and Modelling (CENSAM) and Infectious Disease (ID). Two more IRGs, as well as an Innovation Centre will be established at [SMART](#) Centre in the near future.

About SMART's Infectious Disease Interdisciplinary Research Group

SMART Infectious Disease IRG (ID-IRG) seeks fundamental understanding of host-pathogen interactions as well as direct impact on human health through translational research. The ID-IRG focuses on infectious diseases that have major impact on human health, including influenza, RSV, dengue fever, malaria and tuberculosis. The strategy of the IRG is to develop enabling technologies, including humanized mouse model, high throughput single cell assay, high resolution proteomics, glycomics, metabolomics and cellular mechanics platforms, to study infectious diseases using novel approaches and from new angles. The ID-IRG has developed an integrated, cutting-edge research program with participation of both MIT faculty and investigators from Singapore universities and research institutes.

About Sasisekharan Laboratory

The Sasisekharan group employs a multidisciplinary strategy to develop tools to study glycans such as the glycosaminoglycans with an ultimate goal towards the development of novel pharmacological approaches to alleviate glycan-mediated disease processes.

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