

Rapid approach to identify influenza A virus mutations and drug resistance developed

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Genome Institute of Singapore scientists, led by Christopher Wong, Ph.D., have developed a novel approach to uncover the complete sequence of any influenza A virus, including H1NI, with just a quick nasal swab or nasal pharyngeal wash from patients.

The new method, which enables scientists to amplify full genomes of influenza A viruses and sequence them within a day, was developed at the <u>Genome</u> Institute of Singapore (GIS), one of the research institutes sponsored by Singapore's A*STAR (Agency for Science, Development and Research), in collaboration with Roche NimbleGen.

The system, which combines a novel generic polymerase chain reaction (PCR) with NimbleGen's unique microarray-based platform, makes use of the same RNA (ribonucleic acid) material that is left over from traditional PCR-based diagnostics and is able to recognize any novel strain of influenza A in the first pass.

This enables a faster development of diagnostics for any possible new variant; it can also rapidly determine whether the strain has developed drug resistance. (Details of NimbleGen's microarray-based platform are provided below.)

"This new approach takes advantage of our novel PCR technology, developed for detecting a wide range of pathogens," said Dr. Wong, GIS Chief Scientific Officer for Biomarker Development. "This should greatly simplify the process of sequencing novel viruses."



The scientists' approach is also able to trace the mutations in the <u>influenza A virus</u> that may cause its resistance to drugs.

"The significance of this tracking process can be better appreciated in that it provides for vital information that can be used to prevent or combat a pandemic," said Edison Liu, M.D., GIS Executive Director.

This is especially important given the rapid spread of the new strain of the influenza A (nH1N1) virus. Experts have been concerned that the evolutionary track of this new strain might lead to mutation or reassortment with other influenza <u>strains</u> with the potential to produce a more deadly strain, as the world experienced with the 1918 strain.

"With the development of this new system, the entire project team hopes to better and more quickly track this new flu variant and keep the world informed of how the virus is evolving," said Gerd Maass, Ph.D., CEO of Roche NimbleGen.

GIS scientists used NimbleGen arrays in a similar way during the SARS outbreak in 2003, to understand the infectious source and to globally monitor the SARS virus.

Roche NimbleGen's custom-developed microarrays:

The first arrays developed by Roche NimbleGen were designed, manufactured and shipped to Singapore just four days after the project was started. As the custom-developed high-density microarray contains probes which can reveal the complete sequence of the flu virus from patient samples, it enables the detection of any single base mutations in the regions of the genome, which is important for drug susceptibility. Where virus re-assortment has occurred, it will be able to identify which strain of influenza A it has recombined with, as well as the genomic location of the re-assortment to better understand and track the



evolutionary path and variants of the virus.

NimbleGen's microarray-based customised platform is able to sequence as many as 36 genomes per day per chip reader device.

Source: Agency for Science, Technology and Research (A*STAR)

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