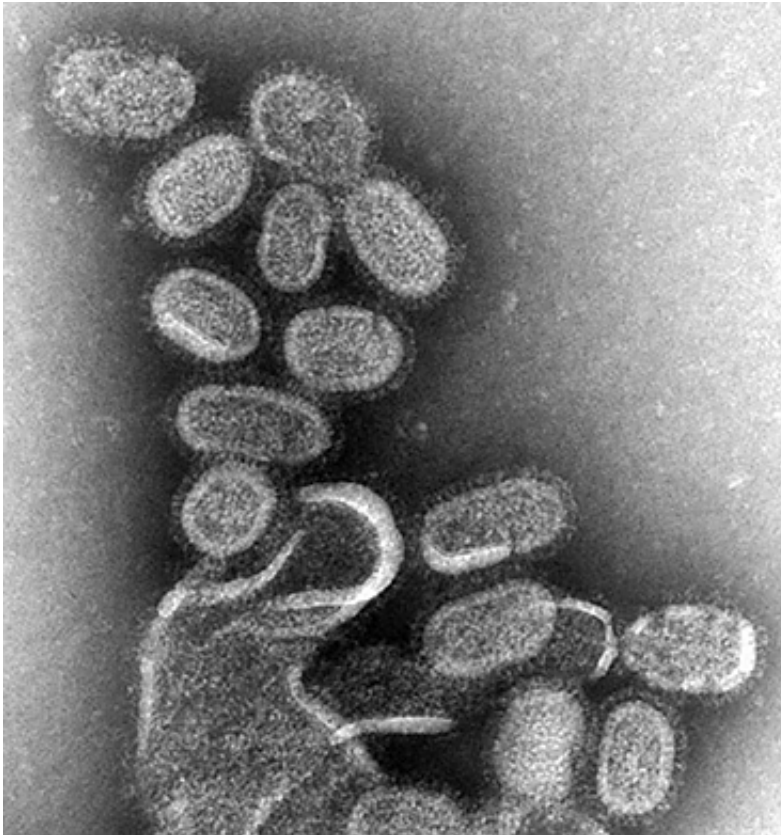


Breakthrough may impact flu vaccination

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Electron microscopy of influenza virus. Credit: CDC

An analysis of 10 years' worth of data on human influenza B viruses has shed new light on the pathogen which can cause the seasonal flu. Findings from this study could help make flu immunization programs more effective; by better targeting vaccines or by eventually eliminating one of the flu lineages completely.

What are Influenza B viruses?

Influenza epidemics seriously affect populations worldwide, with an estimated three to five million cases of severe illness and 250,000 to 500,000 deaths, yearly. Four [influenza](#) virus lineages co-circulate in the human population to cause seasonal epidemics. Of the four, two are influenza A and two are influenza B virus lineages, named Victoria and Yamagata. To date, most studies have focused on the influenza A virus lineages because they are the more commonly circulating lineages in humans which have also caused occasional pandemics.

A new study, led by Assistant Professor Vijay Dhanasekaran and Associate Professor Gavin Smith from Duke-NUS Graduate Medical School (Duke-NUS), has presented the largest comparative analysis of [human influenza](#) B viruses undertaken to date. Results were achieved using advanced computational methodologies to analyze genomic data of the pathogen taken from human hosts. Significantly, this study is also the first to integrate demographic information such as the host's age.

Findings offer new insight into the evolution and epidemiology of this highly infectious virus, and reveal how the two influenza B virus lineages fundamentally differ from each other and from the influenza A virus lineages.

Flu Vaccine Implications

"Our research shows that school aged children are more susceptible than adults to influenza B virus lineages, especially the Victoria lineage," explained first author Asst Prof Dhanasekaran from the Emerging Infectious Diseases Program at Duke-NUS. "This younger population should be targeted for the use of the quadrivalent influenza vaccines."

Commonly administered influenza vaccines are generally composed of two influenza A lineage viruses - but only one influenza B lineage virus. Recently, quadrivalent influenza vaccines, which target all four lineages, have been approved for use. However, they are significantly more difficult to prepare, more expensive and have limited availability. This new study shows that it may be important to use these vaccines for a specific population.

Virus Eradication through Vaccination

The research team also ventures that a re-evaluation of influenza B vaccination strategies may have long term benefits in controlling the flu in the human population. Influenza B Yamagata viruses evolve at a much slower than influenza B Victoria viruses.

If the administration of the quadrivalent [influenza vaccine](#) was expanded sufficiently - it may be possible to eradicate the slower Yamagata lineage from humans. This would signify a major step towards triumph in influenza control and allow the return to an effective trivalent influenza vaccine, sometime in the future, which would target the remaining three flu virus lineages.

The study was authored by a group of international scientists from Australia, New Zealand, the United States, Switzerland and Singapore and marked a major collaboration between Duke-NUS and the Bioinformatics Institute (BII), Agency for Science, Technology and Research (A*STAR). The next step for this team is to better understand the underlying cause of differences in patient age, using laboratory experiments.

Provided by Duke University

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