

Richard Yu Lecture – Lessons from Past Outbreaks: Preparation for Next Pandemic

Biography



Professor Yuen Kwok Yung is the Chair in the Department of Microbiology and Henry Fok Professor of Infectious Diseases at the University of Hong Kong, and the co-director of the State Key Laboratory of Emerging Infectious Diseases since 2005. He is a physician and microbiologist, and holds an MBBS and MD from the University of Hong Kong.

Professor Yuen has discovered over 100 novel species of virus, bacteria, fungi and parasites from patients and animals. Several of these novel animal viruses or their close relatives cause emerging infectious diseases by jumping from animals to human. In 2003, he led his team in the discovery of human SARS coronavirus, and the bat SARS related coronavirus. Professor Yuen has published extensively in the areas of coronaviruses, influenza and other emerging virus infections, and was named by Clarivate, in its list of Highly Cited Researchers, among the top 1% of scholars worldwide, for three consecutive years from 2020 to 2022.

During the COVID-19 outbreak, Professor Yuen was the first in the world to provide evidence that SARS-CoV-2 could be easily transmitted from person-to-person in a family cluster presenting to the hospital, and that patients could be re-infected with the virus. His discoveries and expertise have been referenced by governments and healthcare policy makers internationally as they responded to the spread of the global pandemic.

Professor Yuen is a qualified specialist in clinical microbiology, internal medicine and surgery in the Hong Kong SAR and the United Kingdom. He is also academician of the Chinese

Academy of Engineering (Basic Medicine) and the American Academy of Microbiology. He was awarded the Future Science Prize in 2021. The HKSAR government has awarded him a Silver and Gold Bauhinia Star for his work on microbial hunting and emerging infections.

Abstract

Animal surveillance in Hong Kong SAR between 1997 to 2019 has identified many animal influenza viruses and over 30 novel coronaviruses (CoV). Some of these viruses or their close relatives have subsequently jump into humans several years later. This is best exemplified by the bat SARS related CoV found in 2005 which turns out to be the ancestral virus of 2003 SARS-CoV-1 and 2019 SARS-CoV-2. The bat CoV -HKU4 and -HKU5 are closely related to the human and camel MERS-CoV of the 2012 outbreak in Middle East. The relative of porcine DeltaCoV-HKU15 found in 2012 was reported to infect Haitian children in 2021. However, often only the full genome sequences of these 30 novel animal CoVs are available because the majority of them cannot be cultured in vitro. Since most of these animal CoVs are found in enteric specimens while human CoVs are more often found in respiratory specimens, we use adult stem cells harvested from bat intestinal tissue and human lung tissue for setting up three dimensional (3D) organoids for the isolation and characterization of some CoVs known to have health or public health significance. Multiplexed rapid diagnostic assay, broad spectrum antiviral, versatile vaccine platform, efficient electronic contact tracing system and surge capacity for rapid isolation and contact quarantine, and reusable personal protective equipment are also important in preparedness against future pandemics.