

CELEBRATING A CENTURY OF HKU'S RESEARCH EXCELLENCE AND BEYOND

AN INTERVIEW WITH PROFESSOR YUEN, KWOK YUNG

Widely known among specialists in infectious diseases, Professor Yuen made his mark in 2003 when the outbreak of Severe Acute Respiratory Syndrome, or SARS, gripped the globe. He played a key role in leading his team to the discovery of the agent causing SARS, the SARS coronavirus, thus allowing the development of measures that were crucial to containing the outbreak of this disease. He has published more than 500 papers on microbial discovery and emerging infections such as influenza and novel viruses in peer reviewed journals including the Lancet, New England Journal of Medicine, Science, Journal of Virology and PNAS, with over 16,000 citations. He is now chair in the Department of Microbiology at the University of Hong Kong, and has the rare distinction of being a microbiologist, surgeon and physician. Professor Yuen is elected to the Chinese Academy of Engineering (basic medicine section), is also the awardee of the Silver Bauhinia Star of HKSAR and winner of the HKU Distinguished Research Achievement Award (DRAA), 2003-2004 and HKU Outstanding Research Award (ORA) Winner.



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1. Could you please share with us briefly about your key research areas?

My field of expertise is in emerging infectious diseases which are caused by microbes jumping from animals to human. I led my team in the discovery of human and bat SARS coronavirus, human coronavirus HKU1, bat coronavirus HKU2 to 10, avian coronavirus HKU11 to 13, bat tuhokovirus (a paramyxovirus), bat picornavirus, feline picornavirus, avian turdivirus (a picornavirus), bovine and porcine hokovirus (a partetravirus) and a novel virus genus called the canine picodicitrovirus. We have also discovered more than 10 novel genus and species of bacteria and fungi from human specimens. Our research often starts with a patient with an unknown infectious disorder; which then leads to finding the microbe that causes the problem and subsequently the microbial source in the environment or other animal hosts.

2. How did you become involved in this research, were there any challenges encountered along the way and what motivates you to continue in these areas of research?

I started on developing laboratory diagnostics on cytomegalovirus and tuberculosis in the 1990s. In 1997, we devised the first RT-PCR test for the influenza A H5N1 which caused an outbreak in Hong Kong killing 6 patients. Since then, my department has prepared well in this area of research on novel microbial discovery and diagnosis. We therefore won the battle of SARS in 2003. Looking back, there are many diseases in human that have no known etiology. I am a clinician scientist who sees and manages patient on a daily basis. We find that many respiratory or diarrheal illnesses have no known microbial etiology. If we can find out a microbial etiology, it can impact on their management because microbial infections are highly treatable and can be prevented by vaccination. This is especially important as such novel agent may one day cause a major disease outbreak. It is the prospect for the control of major epidemics with direct help to patients that motivates me to stay in this fruitful area for research.

3. Why do you think your research papers have been highly cited?

Because emerging infectious diseases directly affect the well-being and livelihood of many people and the topic is a favorite one for funding and research after SARS in 2003. Many researchers are publishing in this area while referring to our work, therefore our citation is very high and now exceeds 10,000.

4. Do they usually describe a new discovery, methodology, or synthesis of knowledge? Could you summarize the significance of your papers in layman's terms?

Using molecular and metagenomic technology, we found new viruses, bacteria and fungi. With the sequencing of their genomes, we are able to find useful microbial targets to make rapid diagnostics by RT-PCR, recombinant antigen and monoclonal antibodies for serodiagnosis, find new antivirals and develop effective and safe vaccines. We can also study their pathogenesis in animal models such as in the case of SARS coronavirus, pandemic influenza A H1N1 and influenza A H5N1 so that timely intervention by drugs or infection control can improve the outcome of patients or stop or slow down further disease transmission. For example, we have identified the natural animal reservoirs of SARS in Chinese horseshoe bat so that such animals are no longer allowed to be mixed with other wild game food animals for sale. This will minimize the risk of further interspecies jumping of SARS like coronavirus between different animal species.

5. What outcomes or impact on society do you hope to see as a result of your research? Where do you see your research heading in the future?

Our scientific findings have helped to improve the outcome of patients suffering from human pandemic swine flu of 2009, halt the outbreak of SARS in 2003 and control the poultry H5N1 outbreak. Due to our timely and novel diagnostic tests for the control and monitoring of such infections, panic of the public was curbed significantly even when these outbreaks reached their peaks. We are now trying to find the final common pathway of disease pathogenesis for these agents.