

# Parallel Session 3: Preparedness for the Next Pandemic

## T3b - Molecular Epidemiological Study of COVID-19 Cases in Hong Kong

Prof Leo POON Kit-man

*School of Public Health, The University of Hong Kong, Hong Kong SAR, China*

**Introduction/Objectives:** Molecular epidemiology can track the spread of epidemics. As a WHO COVID-19 Reference Laboratory, we attempted to use next generation sequence (NGS) technology to understand the viral dynamic of SARS-CoV-2 in Hong Kong. Findings from our analyses were reported to the Hong Kong Government on a weekly basis to inform field investigations, epidemiological studies and public health response.

**Methods:** We obtained SARS-CoV-2 positive respiratory samples from Centre for Health Protection and deduced full-length viral genomes using various NGS platforms (Illumina and Nanopore).

**Results and Discussion:** Hong Kong has experienced 4 major waves of COVID-19. Thus far, we have sequenced about 25% of all COVID-19 cases in Hong Kong. Although there were numerous importations of SARS-CoV-2 variants, including variants of concern (VOC), only three variant introductions were responsible for 90% of locally acquired cases. We also demonstrated that SARS-CoV-2 transmission patterns in these waves were very different from each others. In addition, we observed that non-adherence to prolonged preventative measures may lead to sustained local transmission in Hong Kong. We will discuss a few representative super-spreading events as examples.

We provided genetic evidence to demonstrate the world's first reverse zoonotic transmission (humans to pets), SARS-CoV-2 reinfection, and in-flight transmission. We also identified certain settings (e.g., hotels and airport) and environmental conditions (e.g., poor ventilation) are potential hotspots for SARS-CoV-2 transmission. Our investigations also revealed possible virus sources, previously unknown transmission chains and misdiagnosed cases. These findings helped to develop or refine evidence-based control policy against COVID-19.

We also studied a substantial number of imported cases, thereby identifying countries seriously affected by VOC. Such information is critical to policy makers for revising travel restriction policy on incoming travellers. We also reasoned that travel hubs like Hong Kong can be used as surveillance sites to monitor SARS-CoV-2 sequence diversity at regional level.

In addition to local impacts, we used our experiences to draft WHO guidelines for genomic surveillance of SARS-CoV-2 and use our sequencing pipelines to analysis cases for overseas countries.

**Conclusion:** Hong Kong uses an elimination strategy to control COVID-19 and a close monitoring of SARS-CoV-2 sequence dynamic within Hong Kong is one of the essential components to achieve this. Our work has provided scientific underpinning to develop COVID-19 control strategies.

*Project Number: COVID190205*