

Parallel Session 3: Preparedness for the Next Pandemic

T3c - Whole-genome Sequencing of COVID-19 Cases in Hong Kong: Development of a Geophylogenetic Database and Characterisation of SARS-CoV-2 Variants Circulating in the Community

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Background: In spite of stringent public health measures, Hong Kong experienced four epidemic waves of COVID-19, resulting in 12,348 infected cases and 213 deaths as of October 2021. Our team established Nanopore GridION and Illumina Miseq platform for whole-genome sequencing of SARS-CoV-2 at the early stage of the pandemic (in February 2020).

Objective: We aim to develop a phylogenomic database coupled with geospatial information system to unveil the transmission linkage of COVID-19 cases in Hong Kong.

Result: Phylogenomic analysis enabled us to identify an asymptomatic patient as the source of the first superspreading event of COVID-19 (Buddhist worship hall cluster) happened in late February 2020. After months of relative quiescence, a large COVID-19 outbreak (third wave) occurred in Hong Kong in July 2020. The phylogeny of some early cases indicated that the outbreak was attributed to a single lineage B.1.1.63, which was identical to viral genomes isolated from marine crew and aircrew who were exempted from mandatory quarantine.

In early October 2020, before the onset of the fourth wave, we identified a novel viral genome (lineage B.1.36.27) among local cases, which was most closely related to imported cases from Nepal. We highlighted flaws in hotel quarantine arrangements, under which travellers could still receive visitors. The Government later implemented the policy that inbound travellers should be quarantined at designated hotels and not be allowed visitors.

In December 2020, the United Christian Hospital experienced a large outbreak of SARS-CoV-2 in a palliative care and medicine ward. Later in January 2021, two healthcare workers from North District Hospital tested positive after taking care of COVID-19 patients. In both cases, we conducted phylogenomic analysis, enabling the hospitals to trace the transmission chain and prevent further cases.

In April 2021, we used rapid phylogenomic analysis to identify the transmission link between Filipino domestic helpers and an Indian businessman who had travelled from Dubai and tested positive for a SARS-CoV-2 VOC Beta. The genomic data enabled us to trace the entire transmission chain and their close contacts. Eventually, we identified an inbound traveller, who had stayed in the adjacent hotel room to the Indian businessman during quarantine, was the source of the transmission.

Recently we developed a phylogeographical information system which integrated the genomic, epidemiological, spatial and temporal information of COVID-19 cases in Hong Kong. Data visualizations are combined with the cartographic display to yield a clear view of the genomic diversity of SARS-CoV-2 variants and their distributions across Hong Kong districts, with a focus on the clustering of cases based on phylogenetic proximity.

Conclusion: Continued genomic surveillance of the imported cases is pivotal in detecting novel lineages that enters Hong Kong.

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