Will a new clade of SARS-CoV-2 imported into the community spark a fourth wave of the COVID-19 outbreak in Hong Kong?

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Hong Kong has already been hit by three waves of the coronavirus disease 2019 (COVID-19) as of October 2020. More than 120 people were infected in the first round, which was triggered mainly by tourists arriving from Mainland China. Our team analysed the SARS-CoV-2 genomes of 50 cases up to 28 February 2020, and identified that the majority of the locally acquired cases belonged to GISAID clade V, which is characterized by the mutation Orf3a G251V [1]. The second wave was attributed to imported cases of students and working people returning from Europe and North America. Over 640 people had contracted the virus between March and April 2020. Multiple GISAID clades of SARS-CoV-2 were involved, including clade S, clade L, and most importantly clade G which harboured the hallmark mutation D614G in the spike (S) protein gene [2].

The third wave started in early July when infections surged abruptly. The virus swept through the city, affecting care homes for the elderly and the disabled, public hospitals, detention facilities, wet markets, and a container terminal. The total number of cases had expanded five-fold from just over 1000 in early July to over 5000 as of 31 August 2020 [3]. To et al. conducted whole-genome sequencing for 50 cases, and identified that the majority of genomes from locally acquired cases belonged to two novel lineages within the GISAID clade GR. Both lineages were phylogenetically related to the cases from marine crew and aircrew who were exempted from quarantine [2].

Zero local case was finally recorded on 15 September 2020 [3]. The city then relaxed social-distancing measures, including doubling the maximum number of people who could gather in the public to four, and reopening venues such as bars, cinemas and karaoke lounges. After a few days of relative quiescence, a series of untraceable locally acquired cases reappeared since 30 September 2020 cases [3]. From 30 September to 11 October (data cut-off), there were 51 locally acquired cases, in which 13 had unknown source(s) and 38 were epidemiologically linked to these 13 [3,4]. While the relapse of local cases was believed to be due to untraceable infections leftover in the community from the third wave after the recent easing of restrictions, an influx of 170 infected travellers had been reported between 1 September and 11 October, 2020 (Supplementary Figure 1 and Supplementary Table 1) [3].

This study aimed to determine viral genomic characteristics of locally acquired infections reported in October 2020 and to investigate their phylogenetic relationship with the cases in the previous three waves of local outbreak and the recent imported cases.

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reported between September and October 2020. Whole-genome sequencing (WGS) of SARS-CoV-2 was conducted on respiratory specimens using Nanopore MinION (Oxford Nanopore Technologies, Oxford, UK) coupled with Artic Network nCoV-2019 novel coronavirus bioinformatics protocol [5]. Phylogenetic analysis was performed using PhyML v3.0 with maximum likelihood algorithm [6]. Detailed methodologies are provided in Supplemental Materials.

This study was approved by the Institutional Review Boards of The Hong Kong Polytechnic University (RSA20021) and the public hospitals involved (HKECREC-20200014;KCC/KEC-20200070;KWC-20200040;NTWC-20200038).

A total of 64 SARS-CoV-2-positive specimens collected from four public hospitals were selected for WGS in this study as they had higher SARS-CoV-2 viral load (PCR Ct values <20). These included 15 cases collected in the second wave of local outbreak (March–April), 25 in the third wave (July–August), eight locally acquired infections reported in October 2020, and 16 imported cases reported in September and October 2020. The sequences were submitted to the NCBI GenBank with accession numbers MW181702 – MW181765.

For phylogenetic analysis, we included an additional of 18 genomes which were reported by us in the first wave of local outbreak (January–February) (Supplementary Table 2) [1]. Epidemiological information of these cases was retrieved from the Centre for Health Protection (CHP) of the Department of Health [3]. We adopted the CHP case numbering system, which was based on the date of case confirmation.

Here we showed that the eight locally acquired cases in October shared highly similar genome and belonged to GISAID clade GH, which is characterized by 241c > t, 3037c > t, 14408c > t (to GISAID clade GH, which is characterized by 241c > t, 14408c > t (Supplementary Table 2) [1]. Epidemiological information of these cases was retrieved from the Centre for Health Protection (CHP) of the Department of Health [3]. We adopted the CHP case numbering system, which was based on the date of case confirmation.

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especially when they combine with untraceable cases that still circulating in the city.

**Disclosure statement**

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