Whole genome sequence analysis of early community transmission SARS-CoV-2 samples in the Philippines

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Background

The Philippines has recorded over 1.2 million COVID-19 cases and more than 20,000 deaths. The first three cases of COVID-19 were reported in January 2020 (1 lineage A and 2 lineage B, all Chinese tourists), with the first death outside China occurring among these cases. No cases were reported in February 2020, and the first Filipino cases were reported March 2020. With over one million overseas Filipinos repatriated, the introduction of subsequent waves of variants is of interest in tracking the evolution of COVID-19 in this country, including the emergence P.3, a local variant under investigation.

Methodology

We analyzed 35 biobanked samples collected from March to September 2020. RNA of the SARS-CoV2-positive samples screened via RT PCR with Ct values ranging from 15 to 25 were sequenced using the Illumina HiSeq and analyzed using an in-house bioinformatics pipeline. Lineages were assigned using PANGOLIN. Out of the 35 samples, 14 whole genome sequences were generated with sufficient coverage. These were analyzed together with 439 whole genome sequences from February to September 2020 that were publicly available on ViruSurf and GISAID to generate transmission maps (Figure 1).

Results

The earliest community transmission of COVID-19 in the Philippines was caused by lineage B.6 from India as early as March 2020. There is no evidence of onward transmission of the January 2020 infections (lineage A and B) from the China and this initial introduction was contained by stringent testing and tracing protocols and strict border control. Around June 2020, the predominant lineage switched to B.1 (and the D614G mutation appeared, coincident with a surge in cases).

Conclusion

Early community transmission in the Philippines in March 2020 was driven by lineage B.6 and was eventually replaced by B.1 and its sublineages. The first 3 reported cases from Chinese nationals in January 2020 was contained, but subsequent introductions from other Asian and European countries drove community transmission. This finding suggests that stringent control measures work, but border control measures need to anticipate rapid spread to other countries which may serve as sources of infection.
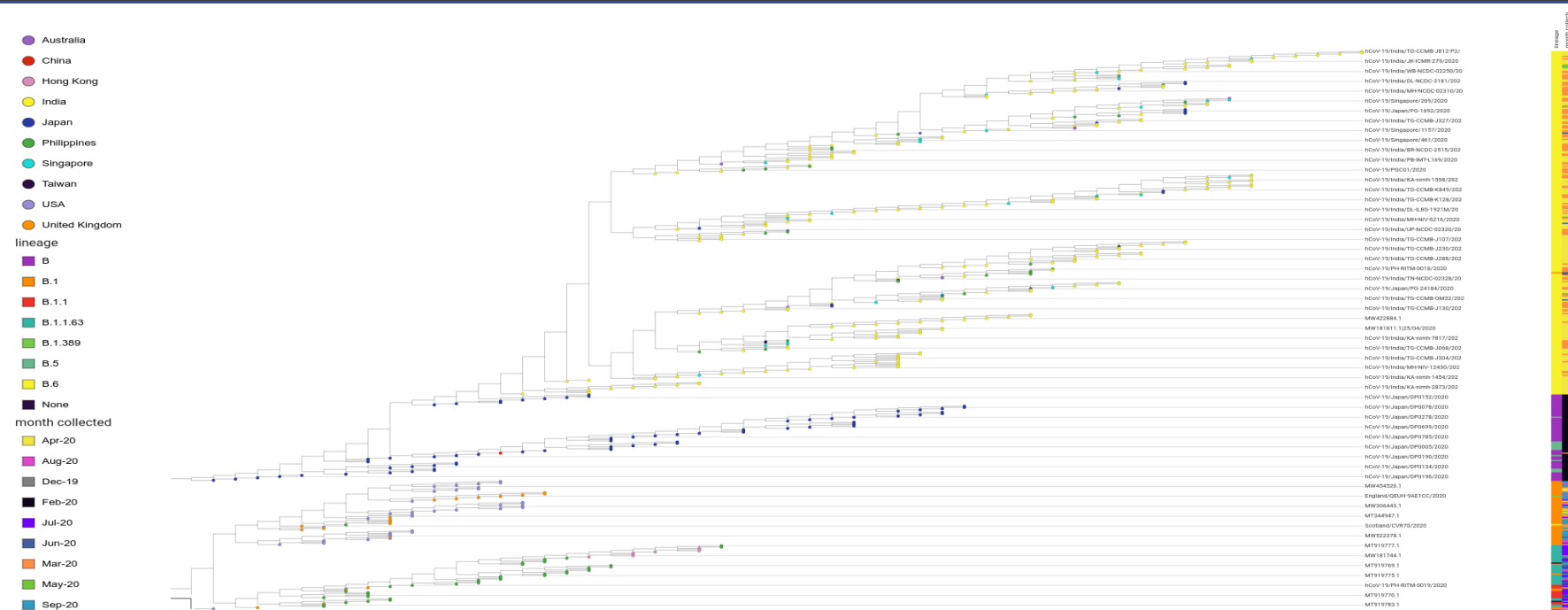

Figure 1. Alignment of the whole genome sequences along with other SARS-COV2 whole genome sequences downloaded from ViruSurf and GISAID using the criteria: collection date- February 1 to September 30, 2020; location- Asia, Europe, North America; lineage- B, B.1, B.1.1, B.1.1.63, B.1.389, B.5 and B.6. was performed using MAFFTv.7 The phylogenetic tree rooted on the first SARS-CoV2 whole genome sequence from Wuhan, China (MN908947.30) was constructed using RAxML with 1000 bootstrap replicates and visualized using Microreact (http://microreact.org/). The initial phase of the B.6 lineage (yellow block) appears to have been related to a lineage from the Diamond Princess Cruise Ship and community transmission appears to have started by March 2020. It is likely the Philippine B.6 lineage had an ancestor in common with the Diamond Princess rather than being introduced by repatriated passengers as the timeline of community transmission preceded repatriation. Lineages related to B.1 (B.1.1, B.1.1.63) accounted for most of the cases starting in June 2020 and it appears to be community transmission.