


Changing predominant SARS-CoV-2 lineages drives successive COVID-19 waves in Malaysia, February 2020 to March 2021

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Abstract

Malaysia has experienced three waves of coronavirus disease 2019 (COVID-19) as of March 31, 2021. We studied the associated molecular epidemiology and SARS-CoV-2 seroprevalence during the third wave. We obtained 60 whole-genome SARS-CoV-2 sequences between October 2020 and January 2021 in Kuala Lumpur/Selangor and analyzed 989 available Malaysian sequences. We tested 653 residual serum samples collected between December 2020 to April 2021 for anti-SARS-CoV-2 total antibodies, as a proxy for population immunity. The first wave (January 2020) comprised sporadic imported cases from China of early Pango lineages A and B. The second wave (March–June 2020) was associated with lineage B.6. The ongoing third wave (from September 2020) was propagated by a state election in Sabah. It is due to lineage B.1.524 viruses containing spike mutations D614G and A701V. Lineages B.1.459, B.1.470, and B.1.466.2 were likely imported from the region and confined to Sarawak state. Direct age-standardized seroprevalence in Kuala Lumpur/Selangor was 3.0%. The second and third waves were driven by super-spreading events and different circulating lineages. Malaysia is highly susceptible to further waves, especially as alpha (B.1.1.7) and beta (B.1.351) variants of concern were first detected in December 2020/January 2021. Increased genomic surveillance is critical.

KEYWORDS

COVID-19, Malaysia, phylogenetic analysis, SARS-CoV-2, seroprevalence, whole genome sequencing