

Whole genome sequencing of SARS-CoV-2: clinical applications and experience

Jamal I Ching Sam

Department of Microbiology, Universiti Malaya, Malaysia

ABSTRACT

Summary: SARS-CoV-2, cause of the COVID-19 pandemic, is a RNA virus with genome size of 29.9 kbases. The importance of genome sequences of SARS-CoV-2 is clear in epidemiological surveillance, tracking of variants, development of therapies and diagnostics, pathogenesis studies, and others. This has driven global expansion of sequencing facilities and sharing of sequences, such that over 11.5 million sequences were available, as of June 2022. Our research laboratory started whole genome sequencing (WGS) of SARS-CoV-2 in April 2020, and have since completed and shared over 800 sequences using Illumina and Nanopore technologies. In this talk, I will share how we used the generated SARS-CoV-2 sequences in conjunction with a clinical diagnostic microbiology service in our associated teaching hospital: (1) to contribute to surveillance of SARS-CoV-2 lineages both nationally and within our hospital; (2) to investigate clusters within our hospital, and how this impacted clinical protocols; (3) to determine suspected individual cases of reinfection or persistent infection; and (4) to evaluate reduced performance in a commercial diagnostic PCR assay, leading to modified primers and probes. WGS has become increasingly accessible and affordable, with numerous publicly available databases, protocols, training and bioinformatics tools, to help overcome technical and analytical challenges. Sequencing data has a variety of clinical and epidemiological uses.