

SYNOPSIS

08/26/2020

Review of “COVID-19 re-infection by a phylogenetically distinct SARS-coronavirus-2 strain confirmed by whole genome sequencing”

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One-Minute Summary

- This study documents **Coronavirus Disease 2019 (COVID-19) reinfection in a 33-year-old male resident of Hong Kong**, 142 days after initial infection.
- **Using whole genome sequencing (WGS), there were 24 nucleotide differences in viral samples sequenced from each episode.** Phylogenetic analysis indicated that the viral sample from the **first episode was closely related to strains identified from the United States and England in March and April**, and the viral sample from the **second episode was closely related to strains identified from England and Switzerland in July and August.**
- **Further evidence for a true reinfection in the second episode are:**
 - The high viral load and high C-reactive protein (CRP) gradually declined, with evidence of seroconversion
 - A 142 day delay between the two episodes
 - The presence of a summer time European lineage matching the case’s epidemiology
- **Implications of this research, as suggested by the authors:**
 - Herd-immunity from vaccination or natural infection is unlikely to stop COVID-19 transmission.
 - The second episode was milder than the first, potentially due to primed adaptive immunity.
 - Mutations in the spike protein of the virus are potentially responsible for reinfection.
 - Patients who have recovered from COVID-19 should be included in vaccine studies and should still comply with public health measures.

Additional Information

- In the first episode, the patient tested positive for COVID-19 by RT-PCR from posterior oropharyngeal saliva (POPS) on March 26 after a three-day history of productive cough, sore throat, fever and headache (assumed symptom-onset date of March 23). His symptoms had resolved on hospital admission on March 29, and on April 14 he was discharged after two negative RT-PCR taken 24 hours apart. He tested negative for IgG against SARS-CoV-2 10 days after symptom onset (assuming March 23 was symptom-onset date).

- In the second episode, the patient tested positive by RT-PCR on POPS upon returning to Hong Kong from travel in Spain and the United Kingdom on August 15. Despite being asymptomatic throughout hospitalization, he had a slightly elevated level of CRP that decreased during the first five days after admission. Daily real-time RT-PCR cycle threshold (Ct) values increased during the first five days after admission, indicating decreasing viral loads (day 1 Ct value = 26.7; day 5 Ct value ≈ 32). Serum samples tested for IgG against SARS-CoV-2 were negative on days 1, 2 and 3, and positive on day 5 of admission.
- The first episode viral genome belongs to GISAID (Global Initiative on Sharing All Influenza Data) clade V, Nextstrain clade 19A and Pangolin lineage B.2. The second viral genome belongs to GISAID clade G, Nextstrain clade 20A and Pangolin lineage B.1.79.
- In the first episode sample there was a stop codon inserted into genome at orf8, leading to a truncation of 58 amino acids. The other 23 nucleotide differences led to additional amino acid changes in the spike protein, membrane protein, nucleoprotein, non-structural proteins and accessory proteins.
- **Limitations acknowledged by authors:**
 - Only one sera sample was available for the first episode, collected on day 10 after admission (which was negative). It is likely that the patient developed an antibody response after this date.
 - Since virus culture attempts on respiratory samples from both episodes are still ongoing, the authors could not compare the neutralizing antibody titer against viral samples from each episode.

PHO Reviewer's Comments

- This study of COVID-19 reinfection is based on a single patient and, to date, appears to be a rare event. However, further research on recovered patients is needed to determine the population-wide incidence of reinfection.
- There are [media reports](#) indicating additional cases of reinfection, confirmed through WGS, in Belgium and the Netherlands.

Citation

Ontario Agency for Health Protection and Promotion (Public Health Ontario). Review of “COVID-19 re-infection by a phylogenetically distinct SARS-coronavirus-2 strain confirmed by whole genome sequencing”. Toronto, ON: Queen’s Printer for Ontario; 2020.

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