A Case of Early Re-infection with SARS-CoV-2

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Dear Editor,

It is with great interest that we read the first report of re-infection from SARS-CoV-2, which represented an important data point in the ongoing COVID-19 pandemic [1-3]. Questions have arisen regarding the timing and severity of re-infections, for which we offer a case report of symptomatic re-infection within 90 days.

42-year-old healthy male military healthcare provider presented with cough, subjective fever, and myalgias on 21 March following a workplace COVID-19 exposure and tested positive by SARS-CoV-2 RT-PCR (Figure 1). Physical examination was unrevealing and supportive outpatient management was pursued [4]. Clinical resolution of illness occurred by day 10, and he returned to baseline excellent health for the following 51 days.

On 24 May he presented with fevers, cough, shortness of breath and gastrointestinal symptoms, following a confirmed new household exposure to COVID-19. The physical examination revealed a temperature of 100.2 Fahrenheit, pulse of 119 beats per minute with a blood pressure of 124/87 mmHg, respirations of 24 breaths per minute with oxygen saturation of 92-94% on ambient air. A chest X-ray demonstrated a pulmonary infiltrate. Multiplex respiratory RT-PCR testing was negative but SARS-CoV-2 RT-PCR was again positive. Notably, symptoms were significantly worse when compared with the initial syndrome. Serum collected on 1 June demonstrated presence of SARS-CoV-2 spike IgG antibodies.

Samples were collected as part of the IRB-approved protocol IDCRP-085. Viral culture was attempted but was unsuccessful. RNA sequencing was performed via the ARTIC nCoV-2019 Sequencing protocol [12], the YouSeq SARS-CoV-2 Coronavirus NGS Library prep kit, and SuperScript IV (ThermoFisher Scientific). The consensus genome was generated and Single Nucleotide Variants

(SNVs) were determined [5]. Global lineage was determined using a subset of SARS- CoV-2 genomes available from the Global Initiative on Sharing All Influenza Data repository (GISAID accessed, June 24, 2020). Alignments were performed [6] and a Maximum Likelihood tree was generated [7]. The SARS-CoV-2 genome from the re-infection sample was deposited in NCBI GenBank under Accession MT840184.

A partial genome sequence was obtained from the initial clinical infection, consisting of sequence fragments totaling 4,126 bp and distributed across the genome. Sequencing of the sample from the patient's second illness yielded a nearly coding complete genome of 27,268 bp. One discrete 50 bp region of zero coverage was observed. Phylogenetic analysis placed this virus in lineage B.1.26 and the genome encoded the D614G variation in the spike protein [8]. Comparison of the partial sequence obtained from the initial infection with the nearly complete sequence obtained from the re-infection identified several potential variations, including one high confidence variation.

The clinical, epidemiological, and sequencing data of this case suggest early re-infection with SARS-CoV-2, only 51 days after resolution of initial infection. Importantly, this was observed in a young immunocompetent patient. In contrast to the case reported by To et al., this second infection was more severe, potentially due to immune enhancement, acquisition of a more pathogenic strain, or perhaps a greater inoculum of infection as the second exposure was from within the household.

NOTES

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Conflicts of Interest

The authors of this study report no financial conflicts of interest.

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Figure 1. Timeline of symptoms and testing.