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Case report: A previously well 34-year-old man with mild COVID-19 symptoms tested positive by SARS-CoV-2 RT-PCR on 14/08/2020 (Ct 17.6). He was epidemiologically and genomically linked to the Auckland August 2020 cluster. He represented with acute breathlessness 150 days later on 11/01/2021, and tested positive on two different SARS-CoV-2 RT-PCR assays (Ct 36.9/38.4). At this time, excluding two discrete community clusters, COVID-19 transmission had been eliminated in New Zealand since May 2020.

The patient denied infective symptoms and could not be linked to any imported COVID-19 cases or high risk exposures. His breathlessness was due to bronchial obstruction from sarcoidosis mediastinal lymphadenopathy. Genome sequencing of the 11/01/2021 result failed to yield analysable sequence, but re-infection was unlikely, and with an alternative diagnosis for his breathlessness the result was attributed to prolonged upper respiratory tract viral shedding. He was discharged without further isolation. He had tested negative twice in the interim since his initial positive result.

In individuals with previous COVID-19, sporadic positive RT-PCR results may be obtained many months after initial infection, even with multiple negative results in the interim. This represents one of the longest shedding durations reported, and has important implications for interpretation of RT-PCR results in previously infected individuals.

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SARS-COV-2 VIRAL LOAD DYNAMICS AND REAL-TIME RT-PCR CYCLE THRESHOLD INTERPRETATION IN SYMPTOMATIC NON-HOSPITALISED INDIVIDUALS IN NEW ZEALAND: A MULTICENTRE CROSS-SECTIONAL OBSERVATIONAL STUDY

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Aims: To describe population-level SARS-CoV-2 upper respiratory tract (URT) viral load dynamics by stratifying PCR positivity rates and Ct values by days since symptom onset (DSSO), and to explore utility of Ct values in determining infectivity.

Methods: Multicentre cross-sectional observational study of laboratory, public health and hospitalisation data for PCR-confirmed COVID-19 cases, New Zealand 12/02/2020–08/06/2020.

Results: Of 123,124 SARS-CoV-2 PCR tests, 579 tests from 368 symptomatic non-hospitalised COVID-19 cases were included. Positivity rate was 93.2% (317/340) for symptomatic infectious period (SIP=0-10 DSSO) samples, and 36.3% (82/226) for post-infectious period samples. URT viral load peaked shortly after symptom onset. Of positive samples with Ct <20.00, 96.1% were collected during the SIP. However, of positive samples with Ct ≥30.00 and ≥35.00, 46.9% and 18.5% respectively were also collected during the SIP.

Conclusion: At or soon after symptom onset represents the optimum time to test for SARS-CoV-2 in the URT. In asymptomatic individuals or those with unknown symptom onset, Ct values <20.00 imply recent onset/potential infectivity, but Ct values ≥30.00/≥35.00 do not exclude recent onset/potential infectivity. Individual sample Ct values should not be used as a marker of time post-infection or to exclude infectivity where date of symptom onset is unavailable.

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CAN MASS SPECTROMETRY BE USED TO IDENTIFY BURKHOLDERIA PSEUDOMALLEI DIRECTLY FROM SPIKED BLOOD CULTURES?

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Background: Melioidosis, caused by *B. pseudomallei*, frequently presents with bacteraemia. This study assessed the safety and sensitivity of the Vitek® mass spectrometer (MS) for identification of *B. pseudomallei* from spiked positive blood cultures.

Methods: MS target spots were scraped into an enrichment broth to assess organism inactivation. Direct from blood culture experiments included both a manufacturer and in-house method. MS analysis after incubation on Chocolate agar for 4-, 6-, and 8-hours was performed.

Results: Standard α-cyano-4-hydroxycinnamic acid (CHCA) matrix inactivated all 70 MS spots. The manufacturer's blood culture extraction method identified 0/26 (0%) *B. pseudomallei* samples compared with 38/38 (100%) using an in-house method. MS analysis of a blood culture broth drop on Chocolate agar following a 6-hour incubation identified 30/32 (94%) samples.

Conclusion: Early diagnosis of melioidosis bacteraemia is likely to improve patient outcomes. This study demonstrates the utility of MALDI-TOF MS identification of *B. pseudomallei* both directly from positive blood culture broth and an abbreviated plate incubation. Finally, the use of a standard MS matrix solution inactivates the organism and therefore additional safety precautions are not required.