




OIA: re Isolation of SARS-COV-2

1 message

 Tue, Sep 8, 2020 at 11:53 AM

To: mc@otago.ac.nz

This is an Official Information Act Request to The University of Otago.

Description of Requested Records:

All records in the possession, custody or control of The University of Otago describing the isolation of a SARS-COV-2 virus, directly from a sample taken from a diseased patient, where the patient sample was not first combined with any other source of genetic material (i.e. monkey kidney cells aka vero cells; lung cells from a lung cancer patient).

Please note that I am using "isolation" in the every-day sense of the word: *the act of separating a thing(s) from everything else*. I am not requesting records where "isolation of SARS-COV-2" refers instead to:

- the culturing of something, or
- the performance of an amplification test (i.e. a PCR test), or
- the sequencing of something.

Please also note that my request is not limited to records that were authored by The University of Otago or that pertain to work done by The University of Otago. My request includes any sort of record, for example (but not limited to) any published peer-reviewed study that The University of Otago has downloaded or printed.

If any records match the above description of requested records and are currently available to the public elsewhere, please provide enough information about each record so that I may identify and access each record with certainty (i.e. title, author(s), date, journal, where the public may access it).

I will accept PDFs or links to PDFs.





6 October 2020



I write in response to your Official Information Act request of 8 September 2020, which sought: "All records in the possession, custody or control of The University of Otago describing the isolation of a SARS-COV-2 virus, directly from a sample taken from a diseased patient, where the patient sample was not first combined with any other source of genetic material (i.e. monkey kidney cells aka vero cells; lung cells from a lung cancer patient)".

I can confirm that the University holds no records which fall within the scope of your request, as SARS-CoV-2 is not isolated in the way you describe. However, I attach a letter from one of our research staff, Professor Miguel E. Quiñones-Mateu, which may be of interest to you. This explains how SARS-CoV-2 is detected and isolated from patient-derived specimens in a laboratory environment.

I trust this information is helpful.

Kind regards

Chris Stoddart
Registrar and Secretary to the Council
University of Otago

October 5, 2020

Professor Richard Blaikie
Deputy Vice-Chancellor
Research & Enterprise
University of Otago

Miguel E. Quiñones-Mateu, Ph.D.
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RE: Information Act Request – Isolation of SARS-CoV-2

Dear Prof Blaikie,

I am writing to briefly describe - on lay terms - the process that we, and basically all virology laboratories across the world, have used to detect and isolate SARS-CoV-2 from patient-derived specimens. As you know, this is a relatively simple and standard procedure used for numerous virology groups to isolate viruses, starting with the first virus to be identified (tobacco mosaic virus, Olitsky & Northrop 1925 *Science* 61:544) as well as the first human virus (Yellow fever virus, Reed et al 1901 *JAMA* 36:431). In the case of SARS-CoV-2, we followed protocols described in the literature to originally isolate the virus in China (Zhu et al 2020 *NEJM* 382:727) and Australia (Caly et al 2020 *Med J Aust* 212:459). Briefly,

- Patient-derived nasopharyngeal (NSP) swabs were collected and stored in universal transport medium (UTM) at 4°C
- UTM aliquots were transported to our laboratory where we (i) used 140 microliters to isolate total RNA and (ii) added 500 microliters to a tissue culture flask containing Vero (*Cercopithecus aethiops*, kidney epithelial) cells
- RNA samples were used to (i) detect SARS-CoV-2 by RT-PCR amplification and (ii) identify all the microorganisms present in the sample using metagenomics sequencing
- Vero cells were closely monitored for cytopathic effects (CPE), usually a sign of viral infection
- Once CPE was observed, the cell-free supernatant from the “positive” culture was collected and total RNA isolated (cell-free supernatant from Vero cells not exposed to UTM aliquots were also collected, as negative control)
- As described above, the cell culture-derived RNA samples were used to (i) detect SARS-CoV-2 by RT-PCR amplification and (ii) identify all the microorganisms present in the sample using metagenomics sequencing

As expected, RT-PCR results showed that the NSP samples were positive for SARS-CoV-2, as well as the cell-free supernatant samples obtained from the Vero cell cultures. None of the negative controls were positive by RT-PCR. In addition, metagenomics analysis of the patient-derived NSP samples identified SARS-CoV-2 as the only sequences from eukaryotic viruses present in the samples. Similar analysis of the viral isolates (cell-free supernatant) produced an average of 1.3 million sequences corresponding to SARS-CoV-2. More importantly, whole genome sequences (close to 30,000 nucleotides) from the virus isolates matched exactly those found in the patient-derived samples (obtained without cultivation in Vero cells), indicating that the SARS-CoV-2 isolates obtained in our laboratory came directly from the patient NSP samples.

In summary, we have no doubt that the SARS-CoV-2 isolates cultured in our laboratory were obtained from patients infected with this new coronavirus in New Zealand. Please do not hesitate to contact me if you need any further information.

Sincerely,



Miguel E. Quiñones-Mateu, Ph.D.
Professor, Webster Family Chair in Viral Pathogenesis
Associate Dean Research
Department of Microbiology & Immunology
University of Otago