Correspondence

First isolation of SARS-CoV-2 from clinical samples in India

Sir,

The outbreak of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has, as on March 31, 2020, spread to over 207 countries around the world, with a total of 896,475 confirmed cases and 45,525 deaths. The number of reported SARS-CoV-2 cases in India is also on an increase with 1,636 cases and 38 deaths. In the current pandemic situation, the isolation of SARS-CoV-2 is important for developing and evaluating diagnostic reagents, for antiviral studies and for screening of vaccine candidates. Earlier studies showed that SARS-CoV-2 could not replicate in several cell lines, which are routinely used for isolation of respiratory viruses. Human and animal cell lines that were found to support SARS-CoV-1 replication during the first outbreak of SARS in China, 2002, are currently being studied. The virus was first isolated in the human airway epithelial cells from clinical specimens as part of early attempts to identify the aetiological agent of infection. We describe here the successful isolation and characterization of SARS-CoV-2 from clinical samples in India using Vero CCL-81 cells by observing cytopathic effects (CPEs) and cycle threshold (Ct) values in real-time reverse transcription-polymerase chain reaction (RT-PCR), electron microscopy and next-generation sequencing (NGS).

The first three SARS-CoV-2 cases were reported from Kerala during January 27-31, 2020. Later during March 2020, cases were also reported from a group of Italian tourists (n=15) and their contacts in New Delhi, India. Simultaneously, cases were reported in Agra, Uttar Pradesh, which was the outcome of close contact of an infected Delhi-based individual who returned from Italy. The designated COVID-19 testing laboratories of Virus Research Diagnostic Laboratory network (All India Institute of Medical Sciences, New Delhi; Sawai Man Singh Medical College, Jaipur; and King George’s Medical University, Lucknow) referred the specimens (throat swab/nasal swab, oropharyngeal swab/sputum) to the Indian Council of Medical Research-National Institute of Virology (ICMR-NIV), Pune, after screening for envelope (E) gene by real-time RT-PCR was done. A total of 12 SARS-CoV-2 positive specimens having a Ct <30 for the E gene were included in the study. Of these, eight samples were from positive cases of Italian tourists and their contacts in New Delhi. The rest of the specimens were from four positive cases at Agra, Uttar Pradesh, and the close contact cases of an infected Delhi-based individual who returned from Italy.

The clinical specimens of the 12 cases were used for infecting Vero CCL-81 which was maintained in Eagle’s minimum essential medium (MEM; Gibco, UK) supplemented with 10 per cent foetal bovine serum (FBS) (HiMedia, Mumbai), penicillin (100 U/ml) and streptomycin (100 mg/ml). Likewise, 100 µl was inoculated onto 24-well cell culture monolayers of Vero CCL-81, before growth medium was decanted. The cells were incubated for one hour at 37°C to allow virus adsorption, with rocking every 10 min for uniform virus distribution. After the incubation, the inoculum specimen was removed and the cells were washed with 1X phosphate-buffered saline (PBS). The MEM supplemented with two per cent FBS was added to each well. The cultures were incubated further in five per cent CO₂ incubator at 37°C and observed daily for CPEs under an inverted microscope (Nikon, Eclipse Ti, Japan). Cellular morphological changes were recorded using a camera (Nikon, Japan). From each well of cell culture plate, on the third post-infection day (PID-3) of passage-1 (P-1), 50 µl of supernatant was taken and tested for SARS-CoV-2 using real-time RT-PCR for E and RNA-dependent RNA polymerase (RdRp) (2) genes

Supplementary material available from http://www.ijmr.org.in/article.asp?issn=0971-5916;year=2020;volume=151;issue=2;spage=244;epage=250;aulast=Sarkale
as described earlier\textsuperscript{7,8}. Similar testing was repeated on the cell supernatant of passage-2 (P-2) at PID-4 for observing viral copy number. Cultures that showed CPE on PID-4 were centrifuged at 4815 × g for 10 min at 4°C; the supernatants were processed immediately or stored at −86°C. Further, those that showed CPE were grown in T-25 cm\textsuperscript{2} flasks at P-2 and titration was done after serial dilution. Tissue culture infective dose 50 per cent (TCID\textsubscript{50}) values were calculated by the Reed and Muench method\textsuperscript{9}. CPEs were observed in 9 of 12 cultures in the P-1. The TCID\textsubscript{50} values ranged from 10\textsuperscript{5.5} to 10\textsuperscript{6.4} /ml for the different clinical specimens passaged in Vero CCL-81 at P-2. The cells were examined microscopically for cellular morphological changes following inoculation.

Vero CCL-81 cells infected with SARS-CoV-2 strain NIV-2020-770 and uninfected cells (CC) were transferred onto microcavity slides and fixed with acetone. Serum samples (1:25 dilution) from the confirmed COVID-19 cases (POD nCOV-S11, nCOV-S13 and nCOV-S7) and negative serum samples were added followed by incubation at 37°C for 1.5 h\textsuperscript{10}. Antibody reactivity was visualized using anti-human immunoglobulin fluorescein-isothiocyanate. In immunofluorescence assay of COVID-19 positive patients, three serum samples exhibited specific reactivity against SARS-CoV-2 virus isolate (Fig. 1).

Vero CCL-81 cells that were inoculated with the samples showed evidence of cell rounding and detachment from 9 of 12 clinical samples in P-1 at PID-4. Syncytial cells formed large cell masses that increased in size and number as the infection progressed. Enhanced CPE was noted in P-2 at PID-2. The cells were detached from the tissue culture plate surfaces by PID-3. Similar cellular morphological changes were observed after passing of the above nine samples up to P-2. No cellular changes were observed in the cell control during both passages. Figure 2 depicts the day-wise changes during the passage of a representative clinical isolate (NIV-2020-770). Virus replication was confirmed using real-time RT-PCR with RNA extracted from the cell culture medium on PID-3. The Ct values ranged from 9.79 to 15.41 (in Vero CCL-81 cells) for the isolates at P-2, which were lower than the Ct values of 16-25.1 in the clinical samples (Table I). The number of virus copies in the isolates at P-1 in Vero CCL-81 cells ranged from 5.18×10\textsuperscript{7} to 8.12×10\textsuperscript{8} copy/ml and increased 1-26 fold to a range of 1.69×10\textsuperscript{8} to 6.77×10\textsuperscript{9} in the cell culture supernatants at P-2 (Table I).

On PID-4, enhanced CPE was observed. The P-1 material was reinoculated in a new batch of cells, and it showed progressive enhancement of CPE as observed day-wise. Further, an aliquot of cell culture supernatant was harvested from infected Vero CCL-81 showing CPE and the supernatant used for negative staining as described elsewhere\textsuperscript{11,12}. Distinct CoV particles with an average size of 95±10 nm having a distinct envelope fringe could be detected in the fields scanned (Fig. 3), as observed earlier\textsuperscript{13}.

Fig. 1. Immunofluorescence images (red panel) showing uninfected Vero CCL-81 cells probed by positive patient serum samples after post infection day of 13th (left), 11th (middle) and seventh (right) and with SARS-CoV-2 strain NIV-2020-770 infected Vero CCL-81 cells probed by positive patients serum (green panel) showing the reactivity of virus and antibody.
Table I. Cycle threshold (Ct) of SARS-CoV-2 positive clinical specimens and respective viral copy number in isolates in different passages for two different cell culture types using real-time reverse transcription-polymerase chain reaction (RT-PCR). E gene was targeted in all.

| Serial number | Sample ID   | Isolate ID | Ct (copy number) of viral RNA in real-time RT-PCR |
|---------------|-------------|------------|--------------------------------------------------|
|               |             |            | Original (clinical) samples by qRT-PCR (Ct)       |
|               |             |            | Vero CCL-81 passage-1 Ct (copy number)           |
|               |             |            | Vero CCL-81 passage-2 Ct (copy number)           |
| 1             | nCoV-763    | NIV-2020-763 | 18.07 (4.08×10⁹)  |
| 2             | nCoV-770    | NIV-2020-770 | 18  |
| 3             | nCoV-772    | NIV-2020-772 | 20.2 (1.96×10⁸)  |
| 4             | nCoV-773    | NIV-2020-773 | 25.1 (5.18×10⁸)  |
| 5             | nCoV-781    | NIV-2020-781 | 22.1 (4.18×10⁸)  |
| 6             | nCoV-C132   | NIV-2020-C132 | 16  |
| 7             | nCoV-777    | NIV-2020-777 | 23.3 (5.12×10⁹)  |
| 8             | nCoV-C31    | NIV-2020-C31 | 25  |
| 9             | nCoV-C32    | NIV-2020-C32 | 16  |

Serial numbers 1-7: Italian tourists who arrived in Delhi, India and an Indian contact of the cohort; Serial numbers 8-9: Close contacts in Agra, Uttar Pradesh, of an infected Delhi-based person who returned from Italy. qRT-PCR, quantitative RT-PCR

Fig. 2. Cytopathic effect of the SARS-CoV-2 isolate (NIV-2020-770) demonstrated in Vero CCL-81 cells on different post-infection days (PID).
Next-generation sequencing was performed on SARS-CoV-2 positive clinical samples (100 µl) included in the study and the tissue culture fluid (50 µl) of virus isolates at PID-3 as described earlier. Reference-based mapping as implemented in the CLC genomics workbench 11.0 (CLC, Qiagen) was used to retrieve the sequence of the SARS-CoV-2. BLAST identification of the viral genome sequences retrieved from the clinical samples and their isolates had 99.98 per cent identity with the SARS-CoV-2 isolate Wuhan-Hu-1 (Accession No. NC_045512). Details of the sequences obtained including the per cent of the reads mapped, total reads and the per cent of genome coverage recovered for the clinical samples and the isolates are provided in Table II. Partial sequences were retrieved from the clinical samples (nCoV-C 132 and nCoV-C 31) and were not included in the analysis.

MEGA software version 7.0.11 was used for the multiple alignments of the sequences retrieved in this study and the sequences from the Global Initiative on Sharing All Influenza Data (GISAID) database (https://www.gisaid.org/) (Supplementary Table (available from http://www.ijmr.org.in/articles/2020/151/2/images/IndianJMedRes_2020_151_2_244_282559_sm7.pdf)). A neighbour-joining tree was generated using the best substitution model (Kimura 2-parameter model) with a bootstrap of 1000 replicates. As per Tang et al, the circulating SARS-CoV-2 can be grouped into two types (S and L type) based on the two different single-nucleotide polymorphisms (SNPs) at positions 8782 and 28144 in the genome. The S type possesses TC SNPs while the L type possesses CT SNPs at positions 8782 and 28144, respectively. In the present study, it was observed that two sequences from clinical samples (nCoV-763 and nCoV-770) had TT SNPs, while the other sequences

| Sample type | Sample/isolate details | Total reads | Per cent of reads mapped | Per cent of genome recovered | Position of nucleotide in genome |
|-------------|------------------------|-------------|--------------------------|-----------------------------|---------------------------------|
| Isolate     | NIV-2020-763           | 10,054,258  | 94.8                     | 100                         | C                              |
|             | NIV-2020-770           | 4,384,130   | 99.0                     | 100                         | C                              |
|             | NIV-2020-772           | 3,482,648   | 98.4                     | 99.9                        | C                              |
|             | NIV-2020-773           | 5,952,758   | 94.2                     | 99.9                        | C                              |
|             | NIV-2020-777           | 3,949,748   | 98.7                     | 100                         | C                              |
|             | NIV-2020-781           | 2,226,464   | 91.6                     | 99.9                        | C                              |
|             | NIV-2020-C32           | 4,159,878   | 99.0                     | 100                         | C                              |
| Clinical sample | nCoV-763       | 8,721,610   | 84.9                     | 99.9                        | T                              |
|             | nCoV-770              | 5,197,614   | 93.1                     | 99.9                        | T                              |
|             | nCoV-772              | 4,222,912   | 81.7                     | 99.8                        | C                              |
|             | nCoV-773              | 9,951,190   | 19.9                     | 99.8                        | C                              |
|             | nCoV-777              | 8,808,756   | 26.9                     | 99.8                        | C                              |
|             | nCoV-781              | 15,688,460  | 35.5                     | 99.9                        | C                              |
|             | nCoV-C32              | 2,772,158   | 88.5                     | 100                         | C                              |

Fig. 3. Transmission electron microscopy imaging of SARS-CoV-2. A negative-stained SARS-CoV-2 viral particle, demonstrating spike morphology of glycoprotein along with peplomeric projections, a feature typical to the family Coronaviridae, is seen.
had CT as the SNP (L type) (Table II). The TT SNPs have been observed in few of the GISAID sequences, including one of the Kerala genome sequences (nCoV-19/India/31 January 2020) submitted by us earlier. All the isolates of the clinical samples were of L type. Specific amino acid mutations in the nsp3 region, spike protein and ORF8, in general, lead to the formation of V, G and S genetic variants/clades, respectively, as per the recent classification followed by GISAID. It was observed that the clinical samples, as well as the isolates, had the mutation D614G in the spike protein, classifying the study samples and isolates into the G clade (Table II and Fig. 4). No specific substitutions were observed in any of the isolate sequences with respect to the corresponding clinical sample sequences, as these were sequences from a low passage. The sequences of the clinical samples and the isolate from the contact of the infected Delhi-based individual, who returned from Italy, further showed two mutations, R203K and G204R in the nucleocapsid protein (N). Although all strains demonstrated 99.6 per cent identity with the original Wuhan Hu-1 sequence, the role of unique SNPs and mutations in identifying the source of infection needs to be explored.

After the first isolation of the virus in the human airway epithelial cells reported by China, countries such as Australia, Korea, Germany and the USA have also isolated the SARS-CoV-2 strain. In India, initial attempts to isolate the virus from the first three cases did not succeed due to low titres in the clinical specimens. This is the first successful virus isolation of SARS-CoV-2 in the Vero CCL-81 cells in India from nasal and throat swabs of persons with a travel
history from Italy and their contacts. Isolation of SARS-CoV-2 from clinical samples will be helpful to address key questions of correlating the differential cell line susceptibility and viral replication efficiency, especially important for clinical samples with low viral titres. Isolation of the virus in such a pandemic situation would help to develop indigenously designed reagents such as positive controls, virus antigen and antibodies, which could lead to the indigenous development of sero-diagnostic assays. These assays would be critical for conducting population-based serosurveys. Propagation in culture will also facilitate antiviral susceptibility studies and vaccine efforts in India.

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Prasad Sarkale¹, Savita Patil¹, Pragya D. Yadav¹, Dimpal A. Nyayaniti², Gajanan Sapkal³, Shrikant Baradkar⁴, Rajen Lakra⁴, Anita Shete-Aich⁵, Sharda Prasad⁶, Atanu Basu⁶, Lalit Dar⁶, Veena Vipat⁶, Siddhartha Girį⁶, Varsha Potdar⁶, Manohar Lal Choudhary⁶, Ira Praharaj⁷, Amita Jain⁷, Bharati Malhotra⁷, Pranita Gawande⁷, Kaumudi Kalele⁷, Nivedita Gupta⁷, Sarah S. Cherian⁷ & Priya Abraham⁷  

¹Maximum Containment Laboratory, ²Diagnostic Virology Group, ³Electron Microscopy & Histopathology Group, ⁴Influenza Group, ⁵Bioinformatics & Data Management Group, ⁶ICMR-National Institute of Virology, Pune 411 001, Maharashtra, ⁷Department of Microbiology, All India Institute of Medical Sciences, New Delhi 110 029, ⁸Division of Epidemiology & Communicable Diseases, Indian Council of Medical Research, New Delhi 110 029, ⁹King George’s Medical University, Lucknow 226 003, Uttar Pradesh & ¹⁰Department of Microbiology, SMS Medical College, Jaipur 302 004, Rajasthan, India  

*For correspondence:* hellopragya22@gmail.com

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| EPI_ISL_406862 | hCoV-19/Germany/ BavPat1/2020 | Europe/Germany/ Bavaria/Munich | 2020-01-28 | Charité Universitätsmedizin Berlin, Institute of Virology; Institut für Mikrobiologie der Bundeswehr, Munich | Charité Universitätsmedizin Berlin, Institute of Virology | Victor M Corman, Julia Schneider, Talitha Veith, Barbara Mühlemann, Markus Antwerpen, Christian Drosten, Roman Wölfl |
| EPI_ISL_413520 | hCoV-19/Beijing/233/2020 | Asia/China/Beijing | 2020-01-28 | unknown | Infectious Disease Control Center | Li, J., Li, L., Li, Z., Qiu, S., Song, H., Li, P. and Li, P. |
| EPI_ISL_413521 | hCoV-19/Beijing/235/2020 | Asia/China/Beijing | 2020-01-28 | unknown | Infectious Disease Control Center | Li, J., Li, L., Li, Z., Qiu, S., Song, H., Li, P. and Li, P. |
| EPI_ISL_413522 | hCoV-19/India/1-27/2020 | Asia/India/Kerala | 2020-01-27 | Indian Council of Medical Research - National Institute of Virology | National Influenza Center, Indian Council of Medical Research - National Institute of Virology | Potdar V, Yadav PD, Choudhary ML, Shete-Aich A |
| Accession ID | Virus name | Location | Collection date | Originating laboratory | Submitting laboratory | Authors |
|-------------|------------|----------|-----------------|------------------------|-----------------------|---------|
| EPI_ISL_413523 | hCoV-19/India/1-31/2020 | Asia/India/Kerala | 2020-01-31 | Indian Council of Medical Research-National Institute of Virology | National Influenza Center, Indian Council of Medical Research-National Institute of Virology | Potdar V, Yadav PD, Choudhary ML, Shete-Aich A |
| EPI_ISL_413518 | hCoV-19/Beijing/105/2020 | Asia/China/Beijing | 2020-01-26 | unknown | Infectious Disease Control Center | Li, J., Li, L., Li, Z., Qiu, S., Song, H., Li, P. and Li, P. |
| EPI_ISL_413519 | hCoV-19/Beijing/231/2020 | Asia/China/Beijing | 2020-01-28 | unknown | Infectious Disease Control Center | Li, J., Li, L., Li, Z., Qiu, S., Song, H., Li, P. and Li, P. |
| EPI_ISL_413562 | hCoV-19/USA/WA11-UW7/2020 | North America/USA/Washington | 2020-03-02 | UW Virology Lab | UW Virology Lab | Pavitra Roychoudhury, Hong Xie, Keith Jerome, Alexander Greninger |
| EPI_ISL_411951 | hCoV-19/Sweden/01/2020 | Europe/Sweden | 2020-02-07 | unknown | Unit for Laboratory Development and Technology Transfer, Public Health Agency of Sweden | Bengner, M., Palmerus, M., Lindsjö, O., Lind Karlfberg, M., Monteil, V., Appelberg, S., Brave, A., Muradrasoli, S. and Tegmark-Wisell, K. |
| EPI_ISL_412872 | hCoV-19/South Korea/KCDC12/2020 | Asia/South Korea/Gyeonggi-do | 2020-02-01 | Division of Viral Diseases, Center for Laboratory Control of Infectious Diseases, Korea Centers for Diseases Control and Prevention | Division of Viral Diseases, Center for Laboratory Control of Infectious Diseases, Korea Centers for Diseases Control and Prevention | Jeong-Min Kim, Yoon-Seok Chung, Namjoo Lee, Mi-Seon Kim, Sang Hee Woo, Hye-Jun Jo, Sehee Park, Heui Man Kim, Myung Guk Han |
| EPI_ISL_411915 | hCoV-19/Taiwan/CGMH-CGU-01/2020 | Asia/Taiwan/Taoyuan | 2020-01-25 | Laboratory Medicine | Department of Laboratory Medicine, Lin-Kou Chang Gung Memorial Hospital, Taoyuan, Taiwan. | Kuo-Chien Tsoa, Yu-Nong Gong, Shu-Li Yang, Yi-Chun Li, Chung-Guei Huang, Yhu-Chering Huang, Shin-Ru Shih |
| EPI_ISL_407893 | hCoV-19/Australia/NSW01/2020 | Oceania/Australia/New South Wales/Sydney | 2020-01-24 | Centre for Infectious Diseases and Microbiology Laboratory Services | NSW Health Pathology - Institute of Clinical Pathology and Medical Research; Westmead Hospital; University of Sydney | Eden J-S, Carter I, Rahman H, Holmes EC, Rockett R, O’Sullivan MV, Sintchenko V, Chen SC, Maddocks S, Kok J and Dwyer DE for the 2019-nCoV Study Group |
| Accession ID | Virus name | Location | Collection date | Originating laboratory | Submitting laboratory | Authors |
|--------------|------------|----------|----------------|------------------------|-----------------------|---------|
| EPI_ISL_407896 | hCoV-19/Australia/QLD02/2020 | Oceania/Australia/Queensland/Gold Coast | 2020-01-30 | Pathology Queensland | Public Health Virology Laboratory | Ben Huang, Alyssa Pyke, Amanda De Jong, Andrew Van Den Hurk, Carmel Taylor, David Warrilow, Doris Genge, Elisabeth Gamez, Glen Hewitson, Ian Maxwell Mackay, Inga Sultana, Jamie McMahon, Jean Barcelona, Judy Northill, Mitchell Finger, Natalie Simpson, Neelima Nair, Peter Burtonclay, Peter Moore, Sarah Wheatley, Sean Moody, Sonja Hall-Mendelin, Timothy Gardam, and Frederick Moore. |
| EPI_ISL_406597 | hCoV-19/France/IDF0373/2020 | Europe/France/Ile-de-France/Paris | 2020-01-23 | Department of Infectious and Tropical Diseases, Bichat Claude Bernard Hospital, Paris | National Reference Center for Viruses of Respiratory Infections, Institut Pasteur, Paris | Mélanie Albert, Marion Barbet, Sylvie Béhifil, Méline Bizard, Angela Brisebarre, Flora Donati, Vincent Enouf, Maud Vanpeene, Sylvie van der Werf, Yazdan Yazdanpanah, Xavier Lescure. |
| EPI_ISL_413692 | hCoV-19/China/WF0002/2020 | Asia/China | 2020-01 | Weifang Center for Disease Control and Prevention | Weifang Center for Disease Control and Prevention & BGI-Shenzhen | Qing Nie, Xingguang Li, Erik M Volz, Han Fu, Haowei Wang, Xiaoyue Xi, Wei Chen, Dehui Liu, Yingying Chen, Mengmeng Tian, Wei Tan, Junjie Zai, Wanying Sun, Jiandong Li, Junhua Li |
| EPI_ISL_413694 | hCoV-19/China/WF0004/2020 | Asia/China | 2020-01 | Weifang Center for Disease Control and Prevention | Weifang Center for Disease Control and Prevention & BGI-Shenzhen | Qing Nie, Xingguang Li, Erik M Volz, Han Fu, Haowei Wang, Xiaoyue Xi, Wei Chen, Dehui Liu, Yingying Chen, Mengmeng Tian, Wei Tan, Junjie Zai, Wanying Sun, Jiandong Li, Junhua Li |
| EPI_ISL_413623 | hCoV-19/USA/CruiseA-18/2020 | North America/USA | 2020-02-24 | unknown | Pathogen Discovery, Respiratory Viruses Branch, Division of Viral Diseases, Centers for Diseases Control and Prevention | Clinton R. Paden, Ying Tao, Krista Queen, Anna Uehara, Jing Zhang, Yan Li, Haibin Wang, Shifaq Kamili, Xiaoyan Lu, Brian Lynch, Senthil Kumar K. Sakhivel, Brett L. Whitaker, Lijuan Wang, Janna’ R. Murray, Jasmine Padilla, Justin Lee, Susan I. Gerber, Stephen Lindstrom, Suxiang Tong |
| Accession ID | Virus name | Location | Collection date | Originating laboratory | Submitting laboratory | Authors |
|--------------|------------|----------|-----------------|------------------------|-----------------------|---------|
| EPI_ISL_413603 | hCoV-19/Finland/ FIN03032020B/2020 | Europe/Finland/ Helsinki | 2020-03-03 | Department of Virology and Immunology, University of Helsinki and Helsinki University Hospital, HUSlab Finland | Department of Virology, Faculty of Medicine, University of Helsinki, Helsinki, Finland | Teemu Smura, Hannimari Kallio-Kokko, Olli Vapalahti |
| EPI_ISL_412912 | hCoV-19/Germany/ Baden-Wuerttemberg-1/2020 | Europe/Germany/ Baden-Wuerttemberg | 2020-02-25 | State Health Office Baden-Wuerttemberg | Charité Universitätsmedizin Berlin, Institute of Virology | Victor M Corman, Julia Schneider, Barbara Mühlmann, Talitha Veith, Jörn Beheim-Schwarzbach, Terry Jones, Rainer Oehme, Silke Fischer, Christian Drosten |
| EPI_ISL_412972 | hCoV-19/Mexico/ CDMX-InDRE_01/2020 | North America/ Mexico/Mexico City | 2020-02-27 | Instituto Nacional de Enfermedades Respiratorias | Instituto de Diagnostico y Referencia Epidemiologicos (INDRE) | Ramirez-Gonzalez Ernesto, Gareces-Ayala Fabiola, Araiza-Rodriguez Adnan, Mendizeta-Condado Edgar, Rodriguez-Maldonado Abril, Wong-Arambula Claudia, Vazquez-Perez Joel, Martinez Arturo, Boukadiida Celia, Munoz-Medina Esteban, Sanchez Alejandro, Isa Pavel, Taboada Blanca, Lopez Susana, Arias Carlos, Barrera-Badiillo Gisela, Hernandez-Rivas Lucia, Lopez-Martinez Irma |
| EPI_ISL_412964 | hCoV-19/Brazil/ SPBR-01/2020 | South America/ Brazil/Sao Paulo/Sao Paulo | 2020-02-25 | Hospital Israelita Albert Einstein | Instituto Adolfo Lutz Interdisciplinary Procedures Center Strategic Laboratory | Jaqueline Goes de Jesus, Claudio Tavares Sacchi, Daniela Bernardes Borges da Silva, Ingra Morales Claro, Flávia Cristina da Silva Sales, Claudia Regina Gonçalves, Joshua Quick, Maria do Carmo, Sampaio Tavares Timenetsky, Nicholas James Loman, Andrew Rambaut, Ester Cerdeira Sabino, Nuno Rodrigues Faria |
| EPI_ISL_410301 | hCoV-19/Nepal/61/2020 | Asia/Nepal/ Kathmandu | 2020-01-13 | National Influenza Centre, National Public Health Laboratory, Kathmandu, Nepal | The University of Hong Kong | Ranjit Sah, Runa Jha, Daniel Chu, Haogao Gu, Malik Peiris, Anup Bastola, Alfonso J. Rodriguez-Morales, Bibek Kumar Lal, Basu Dev Pandey, Leo Poon |
| Accession ID | Virus name | Location | Collection date | Originating laboratory | Submitting laboratory | Authors |
|-------------|------------|----------|-----------------|------------------------|-----------------------|---------|
| EPI_ISL_412980 | hCoV-19/Wuhan/ HBCDC-HB-04/2020 | Asia/China/Hubei/Wuhan | 2020-01-18 | Union Hospital of Tongji Medical College, Huazhong University of Science and Technology | Hubei Provincial Center for Disease Control and Prevention | Bin Fang, Xiang Li, Xiao Yu, Linlin Liu, Bo Yang, Faxian Zhan, Guojun Ye, Xixiang Huo, Junqiang Xu, Bo Yu, Kun Cai, Jing Li, Yongzhong Jiang. |
| EPI_ISL_407976 | hCoV-19/Belgium/ GHB-03021/2020 | Europe/Belgium/Leuven | 2020-02-03 | KU Leuven, Clinical and Epidemiological Virology | KU Leuven, Clinical and Epidemiological Virology | Bert Vanmechelen, Elke Wollants, Annabel Rector, Els Keyaerts, Lies Laenen, Marc Van Ranst, and Piet Maes |
| EPI_ISL_410720 | hCoV-19/France/ IDF0372-isl/2020 | Europe/France/Ile-de-France/Paris | 2020-01-23 | Department of Infectious and Tropical Diseases, Bichat Claude Bernard Hospital, Paris | National Reference Center for Viruses of Respiratory Infections, Institut Pasteur, Paris | Mélanie Albert, Marion Barbet, Sylvie Behillil, Mélène Bizard, Angela Brisebarre, Flora Donati, Vincent Enouf, Maud Vanpeene, Sylvie van der Werf, Yazdan Yazdanpanah, Xavier Lescure. |
| EPI_ISL_410716 | hCoV-19/ | Singapore/10/2020 | 2020-02-04 | National Public Health Laboratory, National Centre for Infectious Diseases | National Centre for Infectious Diseases, National Centre for Infectious Diseases | Octavia S, Mak TM, Cui L, Lin RTP |
| EPI_ISL_410715 | hCoV-19/ | Singapore/9/2020 | 2020-02-04 | National Public Health Laboratory, National Centre for Infectious Diseases | National Public Health Laboratory, National Centre for Infectious Diseases | Octavia S, Mak TM, Cui L, Lin RTP |
| EPI_ISL_410713 | hCoV-19/ | Singapore/7/2020 | 2020-01-27 | National Public Health Laboratory, National Centre for Infectious Diseases | National Public Health Laboratory, National Centre for Infectious Diseases | Octavia S, Mak TM, Cui L, Lin RTP |
| EPI_ISL_413647 | hCoV-19/Portugal/ CV62/2020 | Europe/Portugal | 2020-03-01 | Centro Hospital do Porto, E.P.E. - H. Geral de Santo Antonio | Instituto Nacional de Saude (INSA) | Raquel Guiomar, Inês Costa, Pedro Pechира, Joana Mendonça, Luís Vieira, Helena Ramos, Joana Isidro, Vitor Borges, João Paulo Gomes |
| EPI_ISL_412046 | hCoV-19/Shenzhen/ HKU-SZ-005/2020 | Asia/China/Shenzhen | 2020-01-01 | unknown | University of Hong Kong-Shenzhen Hospital | Chan, J.F.-W., Yuan, S., Kok, K.H., To, K.K.-W., Chu, H., Yang, J., Xing, F., Liu, J., Yip, C.C.-Y., Poon, R.W.-S., Tsai, H.W., Lo, S.K.-F., Chan, K.H., Poon, V.K.-M., Chan, W.M., Ip, J.D., Cai, J.P., Cheng, V.C.-C., Chen, H., Hui, C.K.-M. and Yuen, K.Y. |

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| Accession ID | Virus name | Location | Collection date | Originating laboratory | Submitting laboratory | Authors |
|-------------|------------|----------|-----------------|------------------------|------------------------|---------|
| EPI_ISL_403935 | hCoV-19/ Guangdong/20SF025/2020 | Asia/China/ Guangdong/ Shenzhen | 20-01-15 | Guangdong Provincial Center for Diseases Control and Prevention; Guangdong Provincial Public Health | Department of Microbiology, Guangdong Provincial Center for Diseases Control and Prevention | Min Kang, Jie Wu, Jing Lu, Tao Liu, Baisheng Li, Shujiang Mei, Feng Ruan, Lifeng Lin, Changwen Ke, Haojie Zhong, Yingtao Zhang, Lirong Zou, Xuguang Chen, Qi Zhu, Jianpeng Xiao, Jianxiang Geng, Zhe Liu, Jianxiong Hu, Weilin Zeng, Xing Li, Yuhuang Liao, Xiujuan Tang, Songjian Xiao, Ying Wang, Yingchao Song, Xue Zhuang, Lijun Liang, Guanhao He, Huihong Deng, Tie Song, Jianfeng He, Wenjun Ma |
| EPI_ISL_403934 | hCoV-19/ Guangdong/20SF014/2020 | Asia/China/ Guangdong/Shenzhen | 20-01-15 | Guangdong Provincial Center for Diseases Control and Prevention; Guangdong Provincial Public Health | Department of Microbiology, Guangdong Provincial Center for Diseases Control and Prevention | Min Kang, Jie Wu, Jing Lu, Tao Liu, Baisheng Li, Shujiang Mei, Feng Ruan, Lifeng Lin, Changwen Ke, Haojie Zhong, Yingtao Zhang, Lirong Zou, Xuguang Chen, Qi Zhu, Jianpeng Xiao, Jianxiang Geng, Zhe Liu, Jianxiong Hu, Weilin Zeng, Xing Li, Yuhuang Liao, Xiujuan Tang, Songjian Xiao, Ying Wang, Yingchao Song, Xue Zhuang, Lijun Liang, Guanhao He, Huihong Deng, Tie Song, Jianfeng He, Wenjun Ma |
| EPI_ISL_407084 | hCoV-19/Japan/Al/ I-004/2020 | Asia/Japan/Aichi | 20-01-25 | Department of Virology III, National Institute of Infectious Diseases | Pathogen Genomics Center, National Institute of Infectious Diseases | Tsuyoshi Sekizuka, Shutoku Matsuyama, Nagano Nao, Kazuya Shirato, Shinji Watanabe, Makoto Takeda, Makoto Kuroda |
| EPI_ISL_413488 | hCoV-19/Germany/ NRW-01/2020 | Europe/Germany/ North Rhine Westphalia/ Heinsberg District | 2002-28 | Center of Medical Microbiology, Virology, and Hospital Hygiene, University of Duesseldorf | Center of Medical Microbiology, Virology, and Hospital Hygiene, University of Duesseldorf | Ortwin Adams, Marcel Andree, Alexander Dilthey, Torsten Feldt, Sandra Hauka, Torsten Houwaart, Björn-Erik Jensen, Detlef Kindgen-Milles, Malte Kohns Vasconcelos, Klaus Pfeffer, Tina Senff, Daniel Strelow, Jörg Timm, Andreas Walker, Tobias Wiemann |
| Accession ID | Virus name | Location | Collection date | Originating laboratory | Submitting laboratory | Authors |
|--------------|------------|----------|-----------------|------------------------|------------------------|---------|
| EPI_ISL_412116 | hCoV-19/England/09c/2020 | Europe/United Kingdom/England | 2020-02-09 | Respiratory Virus Unit, Microbiology Services Colindale, Public Health England | Respiratory Virus Unit, Microbiology Services Colindale, Public Health England | Monica Galiano, Shahjahan Miah, Angie Lackenby, Omolola Akinbami, Tiina Talts, Leena Bhaw, Richard Myers, Steven Platt, Kirstin Edwards, Jonathan Hubb, Joanna Ellis, Maria Zambon |
| EPI_ISL_405839 | hCoV-19/Shenzhen/HKU-SZ-005/2020 | Asia/China/Guangdong/Shenzhen | 2020-01-11 | The University of Hong Kong - Shenzhen Hospital | Li Ka Shing Faculty of Medicine, The University of Hong Kong | Chan, J.F.-W., Yuan, S., Kok, K.H., To, K.K.-W., Chu, H., Yang, J., Xing, F., Liu, J., Yip, C.C.-Y., Poon, R.W.-S., Tsai, H.W., Lo, S.K.-F., Chan, K.H., Poon, V.K.-M., Chan, W.M., Ip, J.D., Cai, J.P., Cheng, V.C.-C., Chen, H., Hui, C.K.-M. and Yuen, K.Y. |