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Fwd: Response to questionnaire - M2/SAGE/01/OP

1 message

solicitors Mailbox <solicitors@covid19.public-inquiry.uk> 15 September 2022 at 13:27
To: Module 02 Sols < Personal Data >

UK
Covid-19
Inquiry

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---------- Forwarded message ---------
From: **Oliver Pybus** <oliver.pybus I&S
Date: Thu, 15 Sept 2022 at 12:35
Subject: Response to questionnaire - M2/SAGE/01/OP
To: solicitors@covid19.public-inquiry.uk <solicitors@covid19.public-inquiry.uk>

Dear Mr Suter

Please find my requested responses to your questions below

Yours sincerely

Oliver Pybus (REF: M2/SAGE/01/OP)

- A brief overview of your qualifications, career history, professional expertise and major publications.

I am Professor of Evolution & Infectious Disease at the University of Oxford and Professor of Infectious Diseases at the Royal Veterinary College London (RVC). Since March 2022 I have been Vice Principal for Research & Innovation at RVC. I have 20 years experience of researching virus evolution, ecology and epidemiology. I was the founder and editor-in-chief of the scientific journal Virus Evolution. I am co-director of the Oxford Martin School Programme on Pandemic Genomics. I was a Principal Investigator of the UK COVID-19 genomics consortium (COG-UK) and I co-devised the lineage nomenclature system for SARS-CoV-2 (Pango). I have researched the evolution and transmission of many virus epidemics, including those caused by HIV-1, pH1N1 influenza, Zika virus, hepatitis C virus, yellow fever virus, and highly pathogenic avian influenza. I have helped to develop several statistical and computational methods used in virus phylogenetics and phylodynamics. A list of my publication is available here: https://scholar.google.co.uk/citations?user=X9jrBKMAAAAJ&hl=en.

- A list of the groups (i.e. SAGE and/or any of its sub-groups) in which you have been a participant, and the relevant time periods.

I was a member of SPI-M-O between approximately Dec 2020 and Feb 2022.

- An overview of your involvement with those groups between January 2020 and February 2022, including:

I attended some but not all SPI-M-O meetings.

- When and how you came to be a participant;

I was invited by the SPI-M-O chair around Dec 2020/Jan 2021

- The number of meetings you attended, and your contributions to those meetings;

I don't have a record of which dates I attended. The SPI-M-O secretariat will provide that information.

- Your role in providing research, information and advice.

On SPI-M-O, my role was primarily to provide expertise and advice on virus genome sequencing and COG-UK to the mathematical and computation modelling groups. Virus genome data became more relevant to the work of SPI-M-O after the discovery and spread of the first variant of concern (B.1.1.7 / alpha), which is when I joined the committee.

- A summary of any documents to which you contributed for the purpose of advising SAGE and/or its related subgroups on the Covid-19 pandemic. Please include links to those documents where possible.

I co-authored some papers that were submitted to SAGE by NERVTAG or COG-UK, which are listed below.
- Co-author of paper: "NERVTAG: Is there evidence for genetic change in SARS-CoV-2? - 30 September 2020"
- Lead author of research on international introductions of SARS-CoV-2 in 2020, reported in "COG-UK: Use of SARS-CoV-2 genomics to understand transmission, 28 June 2020".
- Co-author of paper: "COVID-19 Genomics UK (COG-UK) Consortium: weekly report 1, 23 March 2020"
- Co author of paper "SARS-CoV-2 variants that have been selected in mink"

- A summary of any articles you have written, interviews and/or evidence you have given regarding the work of the above-mentioned groups and/or the UK's response to the Covid-19 pandemic. Please include links to those documents where possible.

I have co-authored approximately 45 scientific papers on SARS-CoV-2. They are listed below. They span a range of topics, including patterns of national and international virus spread and introduction, analyses of virus evolution, virus lineage structure and nomenclature, virus genomics and genomic epidemiology, the evolution and emergence of variants of concern etc.

- Your views as to whether the work of the above-mentioned groups in responding to the Covid-19 pandemic (or the UK's response more generally) succeeded in its aims.

This is outside my area of expertise.

- Your views as to any lessons that can be learned from the UK's response to the Covid-19 pandemic, in particular relating to the work of the above-mentioned groups. Please describe any changes that have already been made, and set out any recommendations for further changes that you think the Inquiry should consider making.

I provided my scientific expertise to SPI-M-O but have not considered how it and other committees should operate. I am not confident that I have the knowledge and expertise to answer this question usefully.

Phylogenetic and phylodynamic approaches to understanding and combating the early SARS-CoV-2 pandemic.
Nat Rev Genet. 2022 Sep;23(9):547-562. doi: 10.1038/s41576-022-00483-8. Epub 2022 Apr 22.

Context-specific emergence and growth of the SARS-CoV-2 Delta variant.
Nature. 2022 Aug 11. doi: 10.1038/s41586-022-05200-3.

Emergence and widespread circulation of a recombinant SARS-CoV-2 lineage in North America.
Cell Host Microbe. 2022 Aug 10;30(8):1112-1123.e3. doi: 10.1016/j.chom.2022.06.010. Epub 2022 Jun 20.

Emergence of SARS-CoV-2 Omicron lineages BA.4 and BA.5 in South Africa.
Nat Med. 2022 Jun 27. doi: 10.1038/s41591-022-01911-2.

Genomic Epidemiology of Early SARS-CoV-2 Transmission Dynamics, Gujarat, India.
Emerg Infect Dis. 2022 Apr;28(4):751-758. doi: 10.3201/eid2804.212053.

Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa.
Nature. 2022 Mar;603(7902):679-686. doi: 10.1038/s41586-022-04411-y.

Pango lineage designation and assignment using SARS-CoV-2 spike gene nucleotide sequences.
BMC Genomics. 2022 Feb 11;23(1):121. doi: 10.1186/s12864-022-08358-2.

Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission.
Nat Commun. 2022 Feb 8;13(1):751. doi: 10.1038/s41467-021-27942-w.

Purifying Selection Determines the Short-Term Time Dependency of Evolutionary Rates in SARS-CoV-2 and pH1N1 Influenza.
Mol Biol Evol. 2022 Feb 3;39(2):msac009. doi: 10.1093/molbev/msac009.

Viral infection and transmission in a large, well-traced outbreak caused by the SARS-CoV-2 Delta variant.
Nat Commun. 2022 Jan 24;13(1):460. doi: 10.1038/s41467-022-28089-y.

Track Omicron's spread with molecular data.
Science. 2021 Dec 17;374(6574):1454-1455. doi: 10.1126/science.abn4543.

Global disparities in SARS-CoV-2 genomic surveillance.
medRxiv. 2021 Dec 9:2021.08.21.21262393. doi: 10.1101/2021.08.21.21262393.

Monitoring key epidemiological parameters of SARS-CoV-2 transmission.
Nat Med. 2021 Nov;27(11):1854-1855. doi: 10.1038/s41591-021-01545-w.

Neutralisation of SARS-CoV-2 lineage P.1 by antibodies elicited through natural SARS-CoV-2 infection or vaccination with an inactivated SARS-CoV-2 vaccine: an immunological study.
Lancet Microbe. 2021 Oct;2(10):e527-e535. doi: 10.1016/S2666-5247(21)00129-4.

Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic.
Cell. 2021 Sep 30;184(20):5179-5188.e8. doi: 10.1016/j.cell.2021.08.014.

Vaccine nationalism and the dynamics and control of SARS-CoV-2.
Science. 2021 Sep 24;373(6562):eabj7364. doi: 10.1126/science.abj7364.

Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2 with grinch.
Wellcome Open Res. 2021 Sep 17;6:121. doi: 10.12688/wellcomeopenres.16661.2.

Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence.
Science. 2021 Aug 20;373(6557):889-895. doi: 10.1126/science.abj0113.

Assignment of epidemiological lineages in an emerging pandemic using the pangolin tool.
Virus Evol. 2021 Jul 30;7(2):veab064. doi: 10.1093/ve/veab064.

SARS-CoV-2 Variants of Interest and Concern naming scheme conducive for global discourse.
Nat Microbiol. 2021 Jul;6(7):821-823. doi: 10.1038/s41564-021-00932-w.

Genomic epidemiology of SARS-CoV-2 transmission lineages in Ecuador.
Virus Evol. 2021 Jun 4;7(2):veab051. doi: 10.1093/ve/veab051.

Identification of site-specific evolutionary trajectories shared across human betacoronaviruses.
bioRxiv. 2021 May 25:2021.05.24.445313. doi: 10.1101/2021.05.24.445313.

Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil.
Science. 2021 May 21;372(6544):815-821. doi: 10.1126/science.abh2644.

Epidemiological and evolutionary considerations of SARS-CoV-2 vaccine dosing regimes.
Science. 2021 Apr 23;372(6540):363-370. doi: 10.1126/science.abg8663.

Local Transmission of SARS-CoV-2 Lineage B.1.1.7, Brazil, December 2020.
Emerg Infect Dis. 2021 Mar;27(3):970-972. doi: 10.3201/eid2703.210038.

Serial interval distribution of SARS-CoV-2 infection in Brazil.
J Travel Med. 2021 Feb 23;28(2):taaa115. doi: 10.1093/jtm/taaa115.

Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK.
Science. 2021 Feb 12;371(6530):708-712. doi: 10.1126/science.abf2946.

Resurgence of COVID-19 in Manaus, Brazil, despite high seroprevalence.
Lancet. 2021 Feb 6;397(10273):452-455. doi: 10.1016/S0140-6736(21)00183-5.

Three-quarters attack rate of SARS-CoV-2 in the Brazilian Amazon during a largely unmitigated epidemic.
Science. 2021 Jan 15;371(6526):288-292. doi: 10.1126/science.abe9728.

Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity.
Cell. 2021 Jan 7;184(1):64-75.e11. doi: 10.1016/j.cell.2020.11.020.

Total infectomes of 162 SARS-CoV-2 cases using meta-transcriptomic sequencing.
J Infect. 2021 Jan;82(1):e44-e48. doi: 10.1016/j.jinf.2020.12.004.

Crowding and the shape of COVID-19 epidemics.
Nat Med. 2020 Dec;26(12):1829-1834. doi: 10.1038/s41591-020-1104-0.

A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology.
Nat Microbiol. 2020 Nov;5(11):1403-1407. doi: 10.1038/s41564-020-0770-5.

Evolution and epidemic spread of SARS-CoV-2 in Brazil.
Science. 2020 Sep 4;369(6508):1255-1260. doi: 10.1126/science.abd2161.

Clinical, immunological and virological characterization of COVID-19 patients that test re-positive for SARS-CoV-2 by RT-PCR.
EBioMedicine. 2020 Sep;59:102960. doi: 10.1016/j.ebiom.2020.102960.

Identification of Common Deletions in the Spike Protein of Severe Acute Respiratory Syndrome Coronavirus 2.
J Virol. 2020 Aug 17;94(17):e00790-20. doi: 10.1128/JVI.00790-20.

Epidemiological and clinical characteristics of the COVID-19 epidemic in Brazil.
Nat Hum Behav. 2020 Aug;4(8):856-865. doi: 10.1038/s41562-020-0928-4.

Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California.
Science. 2020 Jul 31;369(6503):582-587. doi: 10.1126/science.abb9263.

Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China.
Cell. 2020 May 28;181(5):997-1003.e9. doi: 10.1016/j.cell.2020.04.023.

Routes for COVID-19 importation in Brazil.
J Travel Med. 2020 May 18;27(3):taaa042. doi: 10.1093/jtm/taaa042.

An investigation of transmission control measures during the first 50 days of the COVID-19 epidemic in China.
Science. 2020 May 8;368(6491):638-642. doi: 10.1126/science.abb6105.

The effect of human mobility and control measures on the COVID-19 epidemic in China.
Science. 2020 May 1;368(6490):493-497. doi: 10.1126/science.abb4218.

Epidemiological data from the COVID-19 outbreak, real-time case information.
Sci Data. 2020 Mar 24;7(1):106. doi: 10.1038/s41597-020-0448-0.

Importation and early local transmission of COVID-19 in Brazil, 2020.
Rev Inst Med Trop Sao Paulo. 2020;62:e30. doi: 10.1590/s1678-9946202062030.

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