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14 March, 2023

Charlotte Whitaker
2B Module Lead Solicitor
The Inquiry Team
UK Covid-19 Inquiry

Module 2B of the UK Covid-19 Public Inquiry
Request for Evidence under Rule 9 of the Inquiry Rules 2006
Reference for Request - M2B/JM/01

Dear Charlotte,

Thank you for your letter of 18 January. Please find below my response to the questionnaire. If you would like any further information, then please let me know.

Yours sincerely,

Personal Data

Dr Jonathan Mullins
Associate Professor, Swansea University Medical School

Questionnaire

UK COVID-19 Inquiry: Module 2B - Rule 9 Request to Dr Jonathan Mullins - Reference: M2B/JM/01

Please provide the following information:

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

I am an Associate Professor at Swansea University Medical School. I received a Ph.D. in Molecular Biochemistry from the University of Wales, Aberystwyth in 1993. I have been a medical teacher and researcher for over 20 years. I am an expert in the field of protein structural bioinformatics and have led the Genome and Structural Bioinformatics Group at Swansea University Medical School since 2003.

We work at the nexus of biomolecular sciences, chemistry, machine learning (AI) and supercomputing. I work on elucidating the structural and functional mechanisms of proteins across many different organisms. This work has resulted in the co-authoring of over 80 papers. The R&D work of the teams I have led has delivered molecular discovery platforms to government and industry. These include an antibacterial screening platform with the UK Ministry of Defence, toxicity screening tools with Unilever plc, a cross-species comparative *in silico* platform with the NC3Rs, and a machine learning platform with Air Liquide that identifies new therapeutic targets for noble gases.

Work with viral proteomes includes the development of the Generic Rapid Antiviral Screening Platform with Innovate UK.

2. A list of the groups (i.e. TAG and/or any of its subgroups) in which you have been a participant, and the relevant time periods. Please also confirm if you are or have been a participant in SAGE or other relevant groups.

I have been a member of the Welsh Government COVID-19 Technical Advisory Group and VT-TAG (the viral testing and detection subgroup) since March 2021.

I participated in three meetings of the UK Government Variant Technical Group, on 29 April, 2021; 13 May, 2021; and 16 June, 2021.

3. An overview of your involvement with those groups between January 2020 and May 2022, including:
a. When and how you came to be a participant;

TAG and VT-TAG

On 08/03/2021, I received an email from the lead of the Welsh Government Technical Advisory Group Environmental Science subgroup requesting a meeting to discuss the Covid-19 situation, which was arranged for 10/03/2021. Following a productive meeting, I was asked to present to TAG, which happened on 23/03/2021.

I presented on the work of the previous 9 months that had extended from developing computational technologies for antiviral drug discovery to working on approaches for predicting impacts of viral mutations on infectiousness and vaccine efficacy.

We developed the Generic Rapid Antiviral Screening Platform (GRASP), work funded by Innovate UK. The platform screens the key SARS-CoV-2 virus proteins, such as the spike protein, against libraries of approved drugs (repurposing) and wider chemical libraries (future antiviral drugs).

We started with computing the protein structures of the Wuhan strain and generated hundreds of hypothetical variants that provided a framework for assessing the extent of change in molecular shape brought about by particular mutations. At that stage, we had also modelled the notable globally circulating variants - VOCs : B.1.1.7 ; B.1.351; P2. We can assess the extent of structural changes and can associate these with potential for reduced vaccine efficacy by analysis of impacts on the spike protein receptor binding domain (RBD).

On the host side, we had also modelled the five known human receptors for SARS-CoV-2 and the interactions with the spike protein RBD. We can screen for differences in virus/receptor interactions between the different variants. This has consequences for prediction of relative infectiousness through host-to-host transmission by analysis of the specific interactions with human receptors at the molecular level and the affinity of the interactions.

We subsequently expanded our analysis to include analysis of simulated interactions with immune system proteins (antibodies), which was relevant to prediction of the relative immune escape capabilities of emerging variants and vaccine efficacy, as well as predictive capabilities for severity of disease by assessment of differential tissue invasion and consequent viral load.

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

I routinely attended all the scheduled TAG and VT-TAG meetings. I may have missed two or three at most due to teaching commitments.

My contributions were most needed when a new variant had been identified that was of concern, normally by an early indication of local dominance over other variants in global circulation.

c. Your role in providing research, information and advice.

I have continued to provide findings of research, information and advice on the transmission and immune escape capabilities of emerging COVID-19 variants.

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

Reports prepared solely by me for TAG, VT-TAG and / or VTG:

22/04/2021	Molecular Modelling of B.1.617
30/04/2021	Presentation for Variant Technical Group
13/05/2021	Molecular Modelling of Key Variants
15/05/2021	B-1-617-2 Summary
19/05/2021	VT-TAG Report
25/05/2021	Variants of Interest
04/06/2021	Breakthrough Infection
11/06/2021	Validation Document
16/06/2021	Delta + G142D and Delta + K417N
03/12/2021	Molecular Modelling of the Omicron Variant
14/12/2021	Protein Biology Notes on the Omicron Variant TAG
17/02/2022	Structural Biology Analysis of Omicron subvariants BA.1, BA.2 and BA.3

None of these documents are publicly available and have been shared only with TAG, VT-TAG and the UK VTG.

5. 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 Welsh Government's response to the Covid-19 pandemic. Please include links to those documents where publicly available.

No interviews given. No evidence given prior to this inquiry.

6. Your views as to whether the work of the above-mentioned groups in responding to the Covid-19 pandemic (or Wales's response more generally) succeeded in its aims. This may include, but is not limited to, your views on:

a. The composition of the groups and/or their diversity of expertise;

TAG was a highly diverse group of people with a wide range of expertise. Individuals with key roles in public health, the health service and government were complemented by university academics with expertise in the relevant fields. There was a very good balance across the areas of interest. This diverse group worked with great cohesion.

b. The way in which the groups were commissioned to work on the relevant issues;

The linkage between TAG and the VT-TAG subgroup worked well, with excellent communication both ways. For my own inputs, typically involving analysis of emerging viral variants, the reception of the contributions was seamless. TAG would on occasion provide a steer for VT-TAG in terms of matters to be discussed. Conversely, the chair of VT-TAG would often report at TAG meetings on the discussions that had been initiated at the subgroup. As a member of TAG and the subgroup, my contributions were often sought at the meetings of both groups.

c. The resources and support that were available;

For the science work itself, nothing, which was as expected for the niche work that we do. However, there was rich discussion of our findings and frequent support from the members of TAG and the wider network in application and integration of the findings, and identifying questions for further investigation.

d. The advice given and/or recommendations that were made;
e. The extent to which the groups worked effectively together;

TAG and VT-TAG meetings were conducted in a convivial and constructive atmosphere. I think that everyone felt that they could contribute at any time. The chairing was consistent and amenable, and the decision making about advice that was to be given was methodical and collective. A great rapport developed in the groups, between the chairs and the members of the group, and often between the members themselves.

In terms of the quality of the advice and recommendations given, my recollection would be that the best advice was consistently given in light of the evidence that was available at the time.

TAG was a very useful umbrella forum for learning about the considerations of all the subgroups. The knitting of the subgroup threads happened there. The communication between individual members of the different subgroups at the TAG meetings was strong and productive.

f. The extent to which applicable structures and policies were utilised and/or complied with and their effectiveness.

The policy outcomes, in the form of public health advice, were in keeping with the deliberations and decisions of TAG. Others are much better placed to comment on compliance, though this was discussed at every meeting, particularly during the period of restrictions. The overarching aim of the group was to help the Welsh Government to as much as possible limit the harms of the Covid-19 pandemic to the people of Wales.

The statistical analysis of the real effectiveness of Government interventions will go on for many years to come. It's my view that the deliberations of TAG and the Welsh Government decisions that they informed saved many lives and averted much morbidity.

7. Your views as to any lessons that can be learned from the Welsh Government'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.

The epidemiological and population-based modelling has evidently proved to be generally robust and has been extensively utilised. There is, however, plenty of scope for better integration of the molecular modelling predictors into the body of evidence used to respond to current and emerging infectious diseases and CBRN threats. There is a tremendous volume of molecular knowledge, cheaply or freely available, that could be used to help maximise response capabilities, and to maximise the effectiveness and efficiency of health protection resources and strengthen preparedness.

The application and further development of our modelling systems has become increasingly focused on emerging SARS-CoV-2 variants and developing robust approaches that can be generically applied to other pathogens / variants in the future. This work is ongoing.

Modelling the molecular pathology of disease, viral disease in particular, is a great scientific challenge due to its inherent complexity. However, there is broad consensus that the field can make an enormous contribution to national preparedness and informing public health decisions at critical times. We are still struggling to identify the appropriate vehicle to make this happen in a systematic and resilient way.

We need to target the development and maintenance of technologies to contribute to surveillance, monitoring and risk assessment of emerging viral threats, particularly for assessment of the transmission and immune escape capabilities of emerging COVID-19 variants and other viral pathogens.

The flow of information from the relevant UK bodies to Wales needs to be improved. For my work, real-time computable access to sequencing data would be of great benefit.

In Wales, we need to continue to organise ourselves in our inimitably compact way to be able to fruitfully exploit the scientific talent that we have to inform the Wales-specific response. It needs an initiative targeting technical preparedness and integrating molecular pathology with the population-based modelling. These shouldn't cost too much at all to establish, but these systems are needed. The other option of not having robust and resilient monitoring systems in place for the inevitable eventuality of the next pandemic threat could prove to be very expensive indeed, both in terms of the public health and longer-term economic impacts.

8. A brief description of documentation relating to these matters that you hold (including soft copy material held electronically). Please retain all such material. I am not asking for you to provide us with this material at this stage, but I may request that you do so in due course.

All documentation circulated by email to all the members of TAG since March, 2021, including meeting agendas, notes, minutes and presented papers, drafts and final reports. Files relating to my own work, prepared for TAG, VT-TAG and VTG, including primary data, analyses, presentations and reports.