

3. **Email from Dr. Andrew Rambaut to Drs. Jeremy Farrar, Anthony Fauci, Patrick Vallance, Christian Drosten, Marion Koopmans, Edward Holmes, Kristian Andersen, Paul Schreier, Mike Ferguson, Francis Collins, and Josie Golding**

From: '(b) (6)'
Date: Sunday, 2 February 2020 at 09:38
To: Jeremy Farrar <(b) (6)>
Cc: (b) (6)>, "Fauci, Anthony (NIH/NIAID) [E]" (b) (6), Patrick Vallance (b) (6)>, "Drosten, Christian" (b) (6), Marion Koopmans <(b) (6)>, Edward Holmes (b) (6), "Kristian G. Andersen" (b) (6), Paul Schreier (b) (6) Michael FMedSci (b) (6)>, Francis Collins (b) (6) (b) (6) Josie Golding (b) (6)
Subject: Re: Teleconference

Dear Jeremy, Ron and all,

Thanks for inviting me on the call yesterday. (b) (5)
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Best,
Andrew

Thanks for inviting me on the call yesterday. I am also agnostic on this – I do not have any experience of laboratory virology and don't know what is likely or not in that context. From a (natural) evolutionary point of view the only thing here that strikes me as unusual is the furin cleavage site. It strongly suggests to me that we are missing something important in the origin of the virus. My inclination would be that it is a missing host species in which this feature arose because it was selected for in that host. We can see this insertion has resulted in an extremely fit virus in humans – we can also deduce that it is not optimal for transmission in bat species.

... The biggest hinderance at the moment (for this and more generally) is the lack of data and information. There have been no genome sequences from Wuhan for cases more recent than the

beginning of January and reports, but no information, about virus from non-human animals in Wuhan. If the evolutionary origins of the epidemic were to be discussed, I think the only people with sufficient information or access to samples to address it would be the teams working in Wuhan.