

Dear [REDACTED] 5.1.2e

Thank you for contacting us regarding the use of data obtained from the GISAID data sharing platform that were used in our Perspective titled "*Possible host-adaptation of SARS-CoV-2 due to improved ACE2 receptor binding in mink*".

We acknowledging the obvious importance of GISAID as an open science platform and the importance of trust and rules to keep this afloat. We would like to emphasize that the Dutch National Institute for Public Health and the Environment (RIVM) is pleased to contribute for many years to the success of GISAID, both directly by depositing human influenza and SARS-CoV-2 sequences as well as indirectly by facilitating sequence analyses by collaborating institutes through sample collections within the Dutch public health network.

First of all, we should emphasize that we have been acting in good faith, with no intended wrongdoing, in our research and the writing of our perspective. In this spirit we have openly communicated our findings in a national public health meeting attended by members of the Dutch 'mink consortium' in early October and more recently in a meeting attended by [REDACTED] 5.1.2e the latter of which seems to have ignited the current predicament.

In reply to your question about the pre-publication of our perspective on a pre-print server, we can assure you that we have tried to do so but were rejected because BioRxiv does not accept perspectives. The same goes for MedRxiv. Please find the message from Biorxiv attached.

In our manuscript, which is written as a 'Perspective', we discussed possible phenotypic changes in the SARS-CoV-2 spike protein as a result of substitutions mentioned in two peer-reviewed and published papers. To place the importance of the investigated substitutions in perspective and provide *context* about prevalence, we have analyzed available mink derived SARS-CoV-2 sequences obtained from GISAID.

Unfortunately, it became apparent that the interpretation of the DAA to this matter is ambiguous, leading to the complaints of our usage of GISAID data. It seems that the current situation is caused by ambiguous interpretation of the current GISAID terms of use of deposited sequences, whereby we assumed liberties in the spirit of open data sharing in order to advance science while others, perhaps understandably since they have contributed the sequences, may have more restrictive opinions. We would like to engage in an open discussion with GISAID to better understand what can and can't be done and help make this clearer to the scientific community.

In the mean time we feel it is important that the findings and important conclusion reported in our manuscript will be published and shared with the scientific and public health communities asap. In order to do this in the context of the current situation we propose to withdraw the sequences by [REDACTED] 5.1.2e team deposited in the public domain of GISAID from our manuscript, and base our perspective solely on observations described in published manuscripts and available sequences in Genbank (available since 12 may 2020 and as discussed by [REDACTED] 5.1.2e and colleagues in Eurosurveillance on 11 June 2020).

Awaiting your answer,

Dr. [REDACTED] 5.1.2e also on behalf of the co-authors

