

To: [REDACTED] [REDACTED]@rivm.nl
From: [REDACTED]
Sent: Mon 11/16/2020 7:43:12 PM
Subject: Fw: Breach of Terms of Use
Received: Mon 11/16/2020 7:43:24 PM
[GISAID letter to OUP re Welkers et al.pdf](#)
[GISAID letter to Welkers et al.pdf](#)
[GISAID_DAA.pdf](#)

[REDACTED]

[REDACTED]



P.O. box 2040, 3000 CA Rotterdam, The Netherlands

Office address: [REDACTED] Dr. Molewaterplein 40, 3015 GD Rotterdam, The Netherlands

E-mail: [REDACTED]@erasmusmc.nl | Phone [REDACTED]

From: [REDACTED] <[REDACTED]@gisaid.org>
Sent: 16 November 2020 03:06
To: [REDACTED] <[REDACTED]@erasmusmc.nl>; [REDACTED] <[REDACTED]@erasmusmc.nl>; [REDACTED] <[REDACTED]@erasmusmc.nl>
 <[REDACTED]@erasmusmc.nl>
Cc: [REDACTED] <[REDACTED]@gisaid.org>; [REDACTED] <[REDACTED]@gisaid.org>
Subject: Re: Breach of Terms of Use

Dear [REDACTED] and colleagues,

Please find attached our letters from the GISAID Secretariat to the authors and the publisher. We ask that you keep these confidential.

Sincerely,

[REDACTED]

From: [REDACTED] <[REDACTED]@gisaid.org>
Date: Friday, November 13, 2020 at 13:58
To: "[REDACTED]" <[REDACTED]@erasmusmc.nl>; "[REDACTED]" <[REDACTED]@erasmusmc.nl>; [REDACTED] <[REDACTED]@erasmusmc.nl>
 <[REDACTED]@erasmusmc.nl>
Cc: GISAID Secretariat <[REDACTED]@gisaid.org>; [REDACTED] <[REDACTED]@gisaid.org>
Subject: Re: Breach of Terms of Use

Dear [REDACTED] and colleagues,

We have received the manuscript and reiterate that we will keep it confidential. We are working on this internally and intend to communicate with the publisher. In the meantime, feel free to contact us with any additional information or questions.

Sincerely,

5.1.2e

From: "5.1.2e" <5.1.2e@erasmusmc.nl>

Date: Friday, November 13, 2020 at 3:01 AM

To: 5.1.2e <5.1.2e@gisaid.org>, "5.1.2e" <5.1.2e@erasmusmc.nl>, "5.1.2e" <5.1.2e@erasmusmc.nl>

Cc: 5.1.2e <5.1.2e@gisaid.org>, "5.1.2e@gisaid.org" <5.1.2e@gisaid.org>

Subject: Re: Breach of Terms of Use

Dear colleagues,

Please find attached the manuscript (still confidential). We have also contacted the head of the RIVM, who is responsible for this research group. This email was partially in Dutch but we also included an English version for our international partners which is pasted below.

We will also contact the corresponding author directly with a similar email.

Dear 5.1.2e 5.1.2e

Through this message we want to inform you formally of our disappointment about the recent presentation of work done by researchers from RIVM on data shared by us through the global database GISAID. This is data that has been generated through a research consortium working on the mink SARS COV 2 outbreak, which is ongoing and has been presented in periodic updates to RIVM with mention of ongoing deeper analysis, in the presence of the scientist involved. None of the members of the consortium has been approached about the plans for additional analysis by the RIVM, nor has any of the intermediate results been shared in relevant meetings in which members of the core mink research team were present. We are presently analysing the data on virus evolution with an international partner.

The sharing of data through GISAID is encouraged to allow public health action while respecting ownership rights of primary data generators. It is a clear agreement that data can be used to support one's own novel data and analyses, but that producers need to be contacted in case of analysis for which a full set of primary data is re-used, to discuss rules of engagement. It is exactly this type of (mis)use of data that creates barriers to the data sharing for public health.

We note that RIVM – as public health institute- has set a poor example with this paper. We will inform GISAID as well as the editor of the journal as soon as we have access to the paper. For the remainder of the studies, we will contact you to make more formal arrangements for the sharing of updates from the consortium. For now, we propose to postpone release of the publication until we have been able to finish our primary analyses. This is a solution that has been proposed in similar situations by GISAID and the journal involved.

On behalf of the consortium,

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Best regards,

5.1.2e

Van: 5.1.2e <5.1.2e@gisaid.org>

Datum: donderdag 12 november 2020 om 23:11

Aan: "5.1.2e" <5.1.2e@erasmusmc.nl>, "5.1.2e" <5.1.2e@erasmusmc.nl>, "5.1.2e" <5.1.2e@erasmusmc.nl>

CC: GISAI Secretariat <5.1.2e@gisaid.org>, "5.1.2e@gisaid.org" <5.1.2e@gisaid.org>

Onderwerp: Re: Breach of Terms of Use

Dear Colleagues,

Thank you for bringing this to our attention. We share your concerns regarding complying with the code of conduct and use of data obtained from GISAI, and we appreciate the steps you have taken.

Can you please provide us with the attachment of the paper, so that we may understand how they are using data? This will greatly help our assessment of this situation. Again, we reiterate that we will keep it in the utmost confidence. Also, have you sent any communications to the author or the journal yet? If you have, please send those to us as well.

Once we receive more information, we will then get back to you as soon as possible regarding our opinion and next steps.

Thank you,

5.1.2e

From: "5.1.2e" <5.1.2e@erasmusmc.nl>

Date: Thursday, November 12, 2020 at 01:15

To: 5.1.2e <5.1.2e@gisaid.org>

Cc: "5.1.2e" <5.1.2e@erasmusmc.nl>, 5.1.2e <5.1.2e@erasmusmc.nl>, "5.1.2e" <5.1.2e@erasmusmc.nl>

Subject: Breach of Terms of Use

Dear GISAI team,

Recently, we were informed of a study describing the mutations observed in Dutch and Danish mink sequencing which is accepted for publication in Virus Evolution. This study is solely based on the sequence data we have submitted to GISAI. This data has been generated by a research consortium working on the mink SARS-CoV-2 outbreak, which is ongoing at the moment, but we found it important to share the sequence information in (near to) real-time while we are still working on analysis and a manuscript describing this data. In addition, we have shared our findings at regular intervals with the national institute of public health as part of the national response effort. This included mention of the planned and ongoing analytical work.

This data of course became of special interest after hearing about the SARS-CoV-2 outbreak in mink in Denmark and several authorities urged the Danish researchers to put their data online to enable international experts to form their own opinion about the risk assessments in their countries, in Europe and globally. We also are working on additional farm and human sequence data that will be shared, but in the meantime have been asked to present our data to the national authorities, ECDC, WHO and others.

In one of these meetings, we learned of the above mentioned analysis, and were informed of a paper in press. It

was shared with us but since this has not been shared through a preprint service, we have not attached it but can do so if needed in confidential communication. It is a manuscript by Welkers et al, accepted for publication in virus evolution. In conflict with GISAID regulations, none of the members of the consortium has been approached about the plans for this analysis, nor has any of the intermediate results been shared in relevant meetings in which members of the core mink research team were present. This is especially problematic since one of the authors has been present at all meetings at the national response team in which we have shared our findings. We also noted that the publication has some misleading conclusions, since the authors don't have a complete overview of the data generated and relevant metadata and did not reach out to discuss that. They also did not share the analysis in a preprint, as has been customary for all SARS COV 2 related work, and as we have done consistently. We have been working on an in-depth analysis on the data on virus evolution in mink and mink farm employees with an international partner.

We think that this constitutes a breach of the code of conduct when accessing GISAID shared data. The sharing of data through GISAID is encouraged to allow public health action while respecting ownership rights of primary data generators. It is a clear agreement that data can be used to support one's own novel data and analyses, but that producers need to be contacted in case of analysis for which a full set of primary data is re-used, to discuss rules of engagement. This is now the third time where we feel the full set of data that we have generated has been used on ways that raise questions, and decided to not let this one pass. Therefore, we have sent a formal complaint to the national institute and bring this matter to your attention. We propose to at least withhold the publication until we have finalized our primary analysis. We will also send this to the journal where the manuscript is published and ask them to withdraw the manuscript.

We would like to ask GISAID their opinion with regards of to this use of the data and advice on what steps we can take to make our objections against this manuscript visible.

Best regards,

The Dutch mink SARS-CoV-2 research consortium

5.1.2e