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## Monkeypox draft genome

3 messages

Thu, May 26, 2022 at 14:55

To: guillaume.croville@envt.fr

Dear Guillaume,

My name is [REDACTED] I am a molecular biologist from Norway.

I have read your study:

"First French draft genome sequence of Monkeypox virus, may 2022"

I have some questions:

1. Did you or your colleagues try to use healthy controls (healthy persons) for NGS? (extraction of DNA from a sample, library preparation, sequencing and assembly of monkeypox genome)
2. Did you try to use a sample from other disease or other skin condition ( example: friction blister) as a control for NGS? (extraction of DNA from a sample, library preparation, sequencing and assembly of monkeypox genome)

Thank you for your answer and explanation.

Best regards,

[REDACTED]

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Guillaume Croville <guillaume.croville@envt.fr>

Fri, May 27, 2022 at 21:17

To: [REDACTED]

Dear [REDACTED]

Thank you for your email and your relevant questions.

Unfortunately, we did not carry out controls, for several reasons:

- 1- My colleagues at the hospital did not provide me with any other sample than the DNA of the sick patient;

2- The clinical and epidemiological conditions were favorable with a case of MPXV

3- A real-time PCR was first performed by the hospital to confirm the presence of poxvirus.

I totally accept that all these reasons are not good reasons but I did it with the biological material that was provided to me.

You're absolutely right about the controls we need to do for sequencing but also for the bioinformatics process and that's something I'm thinking about in order to do robust analyzes in the near future.

What limitations do you think my results have?

Best regards

**Guillaume CROVILLE**

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**De:** [REDACTED]

**À:** "Guillaume Croville" <[guillaume.croville@envt.fr](mailto:guillaume.croville@envt.fr)>

**Envoyé:** Jeudi 26 Mai 2022 14:55:06

**Objet:** Monkeypox draft genome

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[REDACTED]  
To: Guillaume Croville <[guillaume.croville@envt.fr](mailto:guillaume.croville@envt.fr)>

Sun, May 29, 2022 at 13:37

Hello Guillaume,

Almost no one carries out the necessary controls. That really shocked me. (There is about 250000 sars-cov-2 publications...for example)

There are very few examples of implemented necessary controls, however, the results are frightening.


Scientists from Switzerland have extracted RNA from uninfected supernatant / cells (cell cultures) treated the same way as infected cells / supernatant but virus-free and applied "de novo" approach. The result is whole-genome sars-cov-2.

Scientists from China get a lot of sars-cov-2 sequences, without the presence of any virus, from cell cultures.

I have documentation, but I do not share it at the moment. If you are interested I could ask to share with you.

Also, with raw reads used to assemble sars-cov-2 genome it is possible to assemble other viruses (it is control experiment in the field of bioinformatics)

Best regards,

  
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