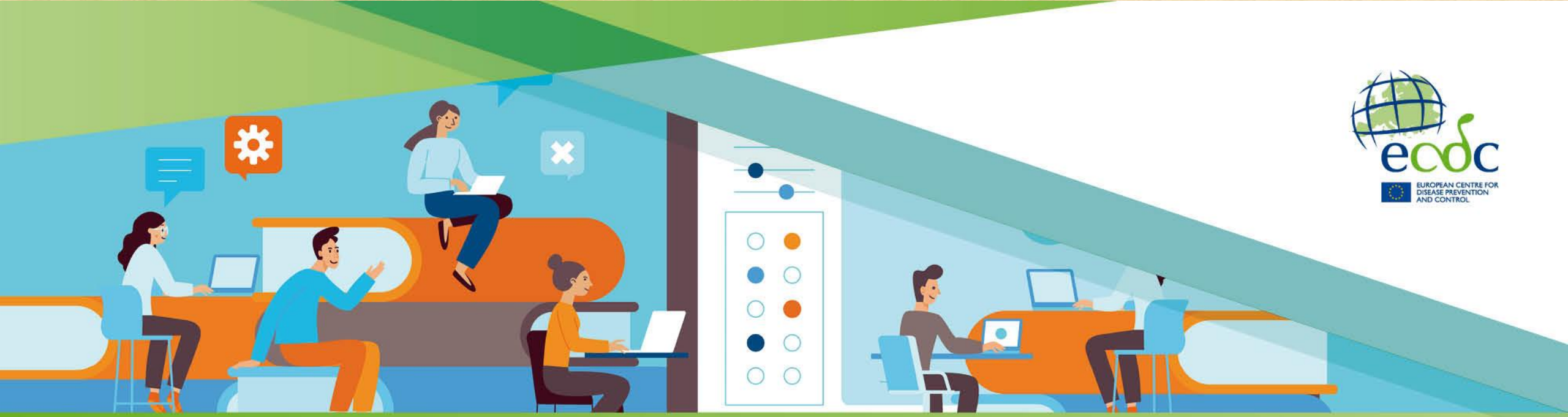


GenEpi-BioTrain Virtual Training 29 - Genomic epidemiology of mpox

Comparative Analysis and Troubleshooting

12-10-2026

David Nieuwenhuijse and Bas Oude Munnink

Aim and learning objectives

Aim

Live discussion on the advantages and limitations of NGS for outbreak investigations

Discuss the difficulties in doing this in LMIC settings (presentation by Hayley)

Troubleshooting: Which challenges were encountered

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Can you think of any advantage of NGS for outbreak investigations?

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Advantages of NGS for outbreak investigations
Rabies virus example

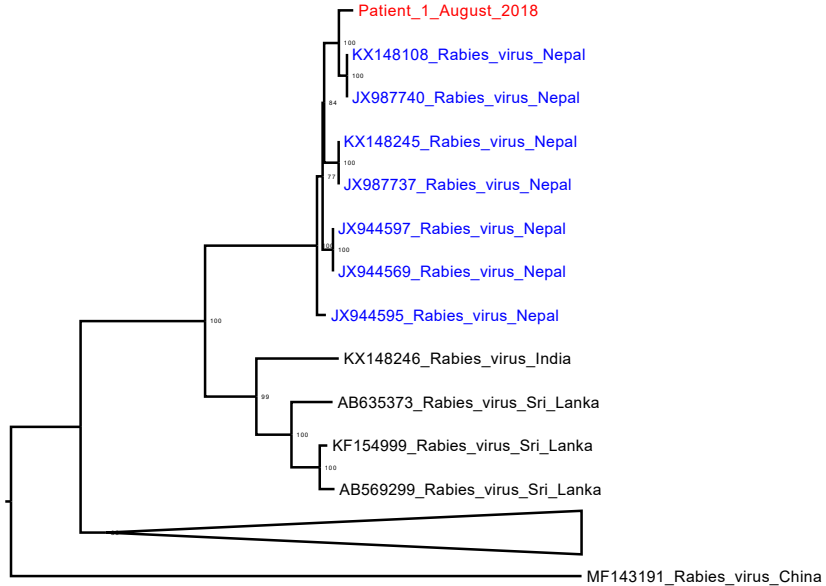
- On July 18th 2018, a 33 year old Nepali, was admitted at the Emergency Department in the Hamad General Hospital. The patient had arrived in Qatar one month before, and reported an animal bite by an unknown animal 3 months ago in Nepal.

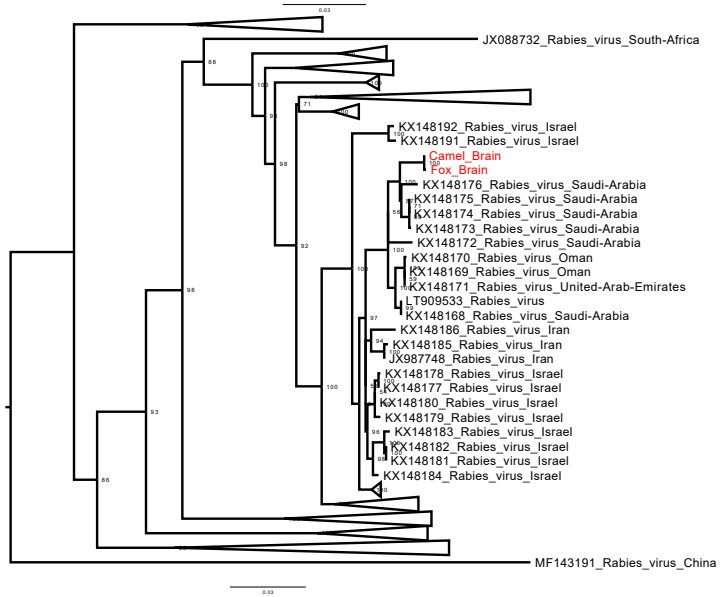
- On February 24th 2019, a second patient, a 25 year old Nepali, was transferred to the Emergency Department at the Hamad General Hospital. According to relatives reports, he had been bitten by a raccoon around early October 2018 in Nepal.

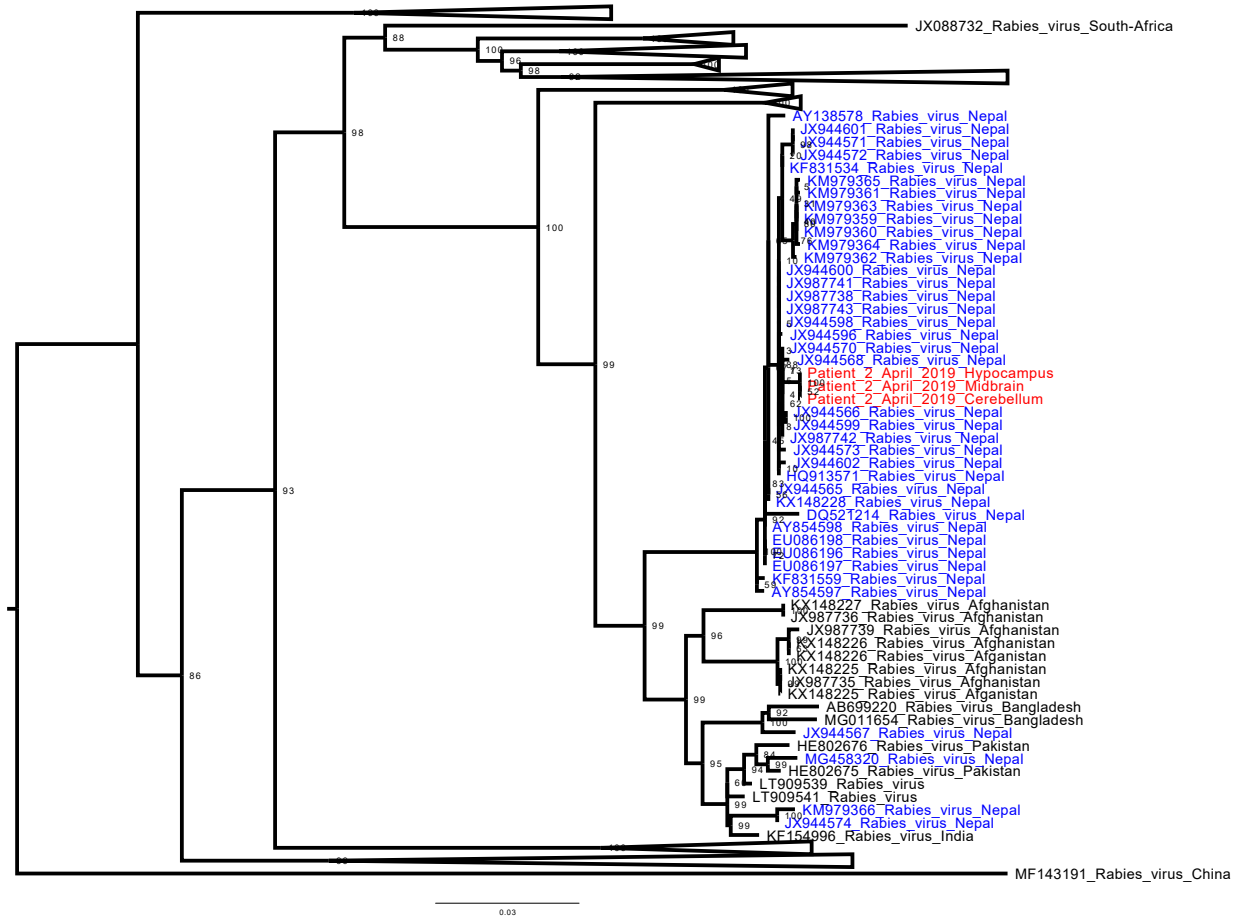
- In the same period, there was a fox attack at a camel farm in the Alkharsah area in September 2018 (Qatar). Approximately two weeks after the fox bite, a camel started to develop neurological symptoms, and died later on. The fox and the camel both tested positive for RABLV by RT-PCR

- **Did the patient acquire the infection in Qatar or in Sudan?**

Whole genome sequencing



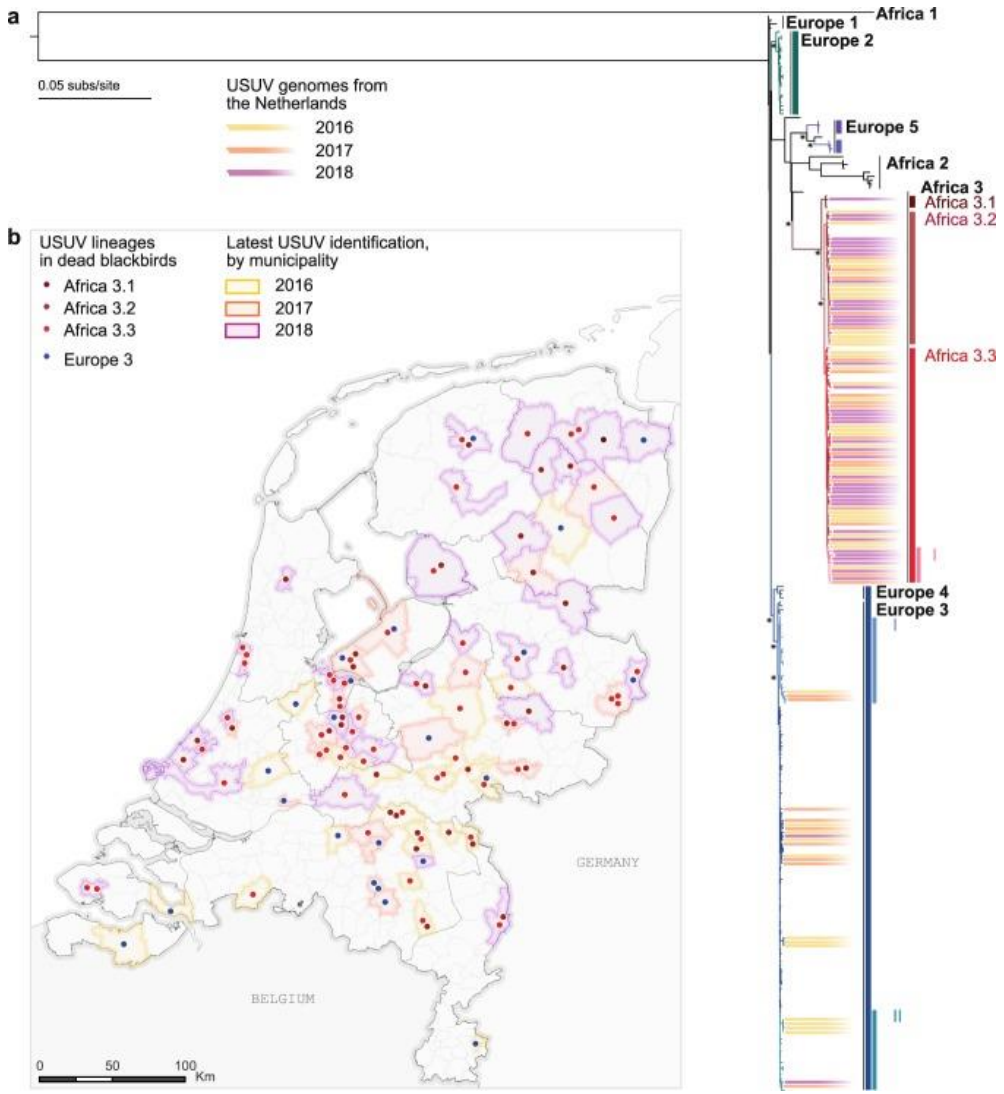




Oude Munnink et al, IJID, 2020

Usutu virus

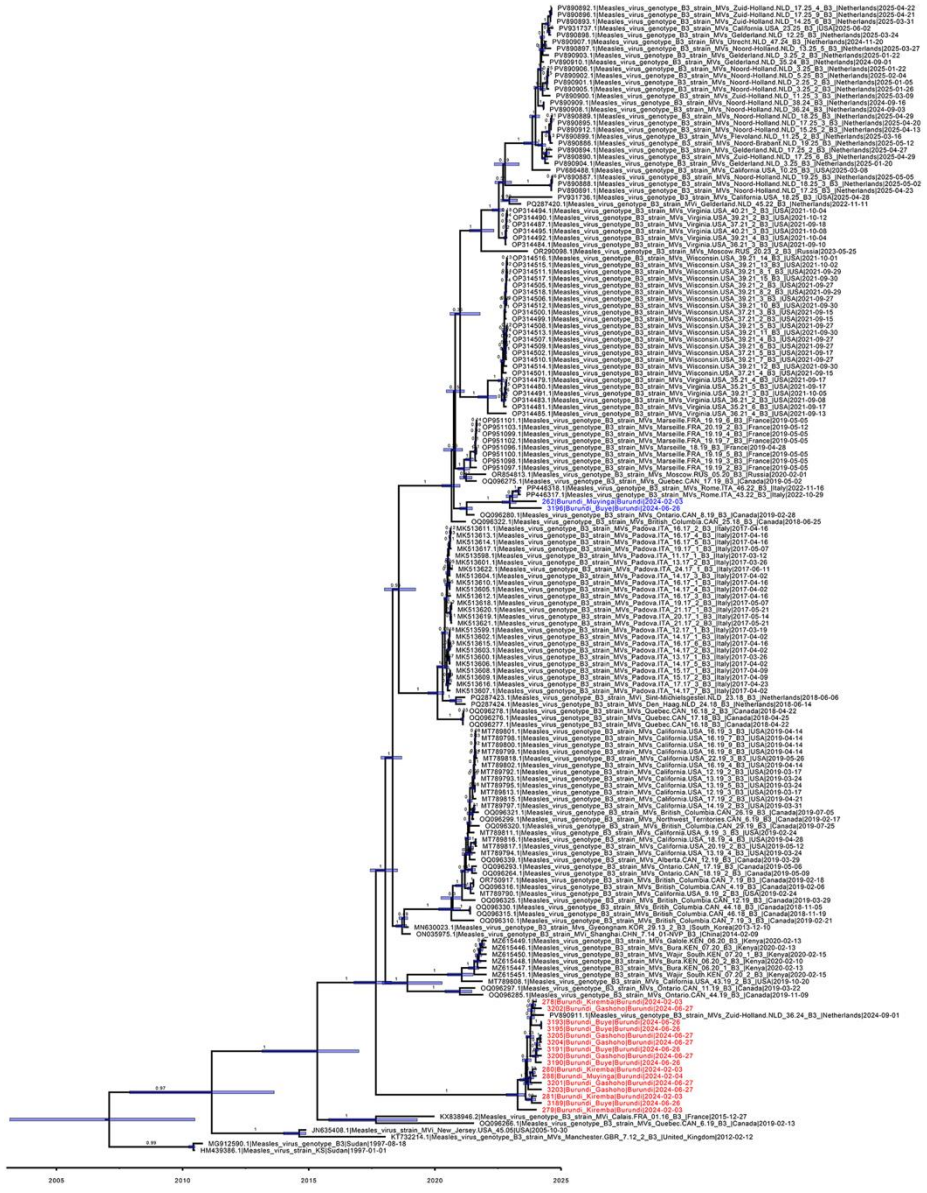
- In the Netherlands, USUV was first detected in 2016, when it was identified as the likely cause of an outbreak in birds.
- Here we showed that several lineages of USUV are already co-circulating
- Molecular clock analysis evaluated their most recent common ancestor to 10 to 4 years before first detection of USUV in the Netherlands



Oude Munnink et al, Scientific Reports, 2020

Measles virus

- Despite progress towards measles elimination in Burundi, the country has seen a resurge in cases since 2019.
- Unclear if all measles cases involved in recent outbreaks were linked or caused by multiple independent events including introductions from other countries.
- Using WGS we demonstrated that measles viruses genotype B3 were already circulating in Burundi since the beginning of 2023 well before the outbreak in 2024 was noted.
- There are recurrent measles outbreaks in Burundi ignited from different sources, showing that measles in Burundi is sustained by multiple introductions and emphasizing the importance of ongoing molecular surveillance for elimination efforts.



Nzoyikorera et al, Plos One, 2026

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Can you think of any limitations in the use of NGS for outbreak investigations?

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Limitations of NGS for outbreak investigations

- Costs
- Turnaround time
- Dependence on sample quality
- Bioinformatic challenges

More generalising this leads to:

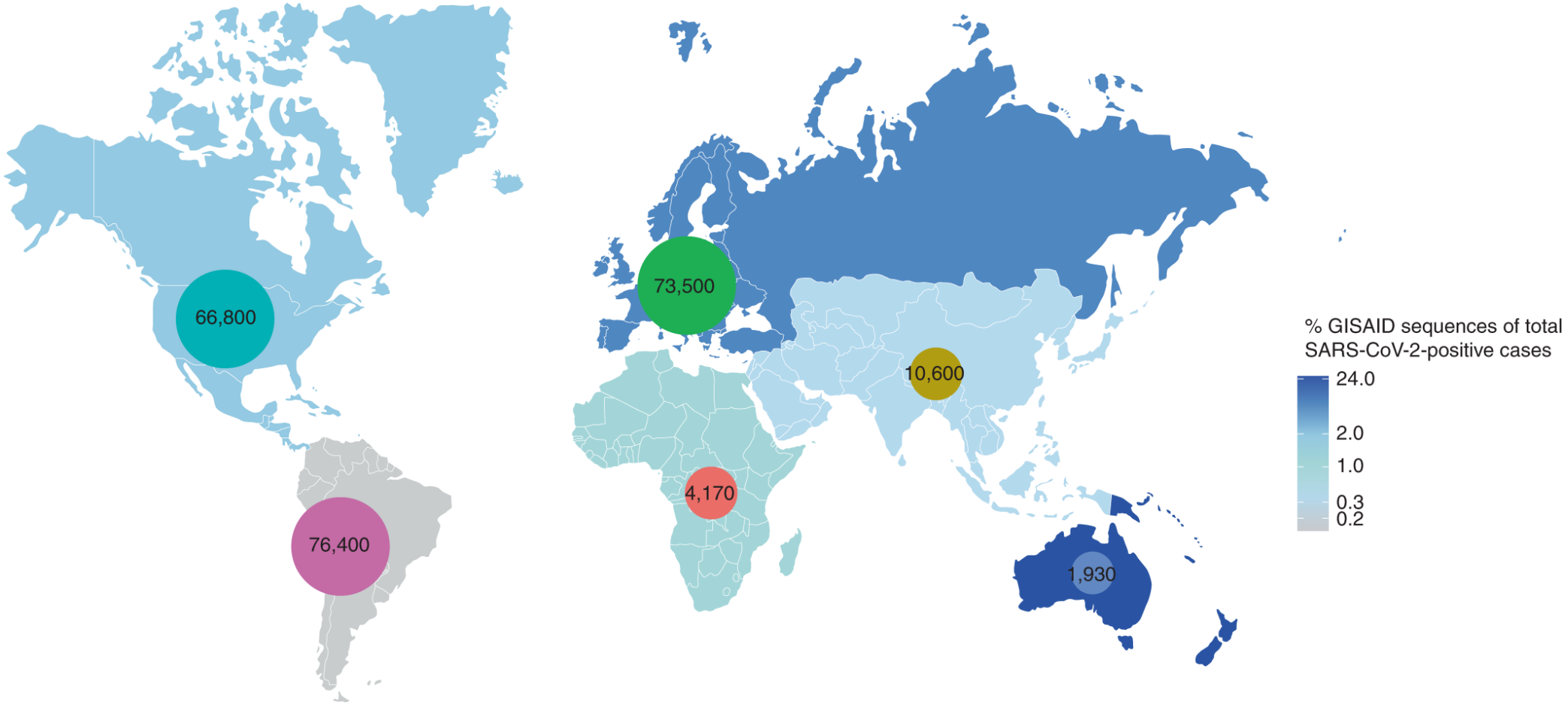
- Inequal access to pathogen genomics
- Data sharing disparities
- Surveillance bias

Results of these limitations in surveillance bias

- Phylogenetic analyses may incorrectly suggest that a pathogen variant originated in a particular country simply because that location has more extensive genomic surveillance, rather than because it was the true source of emergence.

- Areas with limited sequencing capacity may be underrepresented, obscuring transmission pathways and delaying detection of novel variants.

Percentage of WGS generated and shared on GISAID compared to the total number of COVID-19 cases per continent as of 5 July 2021.



Oude Munnink et al, Nature Medicine, 2021

SARS-CoV-2

01/04/2020 3,169 sequences on GISAID

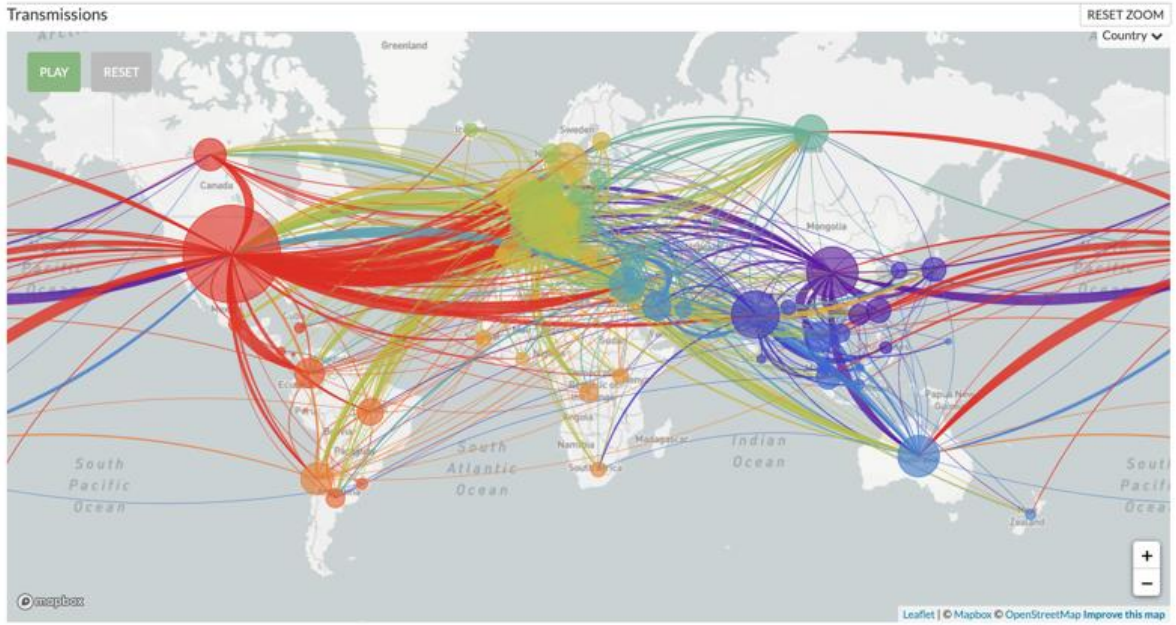
- 425 UK sequences
- 190 Dutch sequences

01/05/2020 15,959 sequences on GISAID

- 5,686 UK sequences
- 586 Dutch sequences

01/07/2020 57,965 sequences on GISAID

- 27,558 UK sequences
- 1,603 Dutch sequences



Nextstrain visualisation

SARS-CoV-2

- "UK" variant
- "South Africa" variant

- Travel bans/restrictions

- These countries perform the most dense sequencing in their continent



There are already huge lorry queues to enter Dover port in Kent because of Christmas stockpiling and Brexit concerns

France suspended all travel links, including freight lorries, with the UK for 48 hours from midnight on Sunday (23:00 GMT).

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Ideas

SOUTHERN AFRICA: LAST IN LINE FOR VACCINES, FIRST IN LINE FOR TRAVEL BANS

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Is a travel ban the right thing to do?

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Modelling study shows a delay

- "Compared to no travel ban a 14-day delay in reaching 10,000 Omicron cases was achieved"

- "However, given that the importation of Omicron pre-dated the initiation of travel restrictions, we found that measures to reduce the R_e of the virus played a more important role in influencing its initial spread."

BMJ Open. 2025 May 21;15(5):e089610. doi: 10.1136/bmjopen-2024-089610

Estimating the effect of South Africa travel restrictions in November 2021 on the SARS-CoV-2 Omicron outbreak in the Netherlands: a descriptive analysis and modelling study

Elke Wynberg [1,2,✉,0,1], Sherman Lee [1,3,0,1], Roisin Bavalia [1], Valerie Eijrond [1], Luc E Coffeng [4], Anne de Vries [5], Saskia van Egmond [5], Lobke Brals [5], Noud A J Schel [6], Lotte Harbers [7], Bas Kolen [8,9], Sake De Vlas [4], Anja Schreijer [1]

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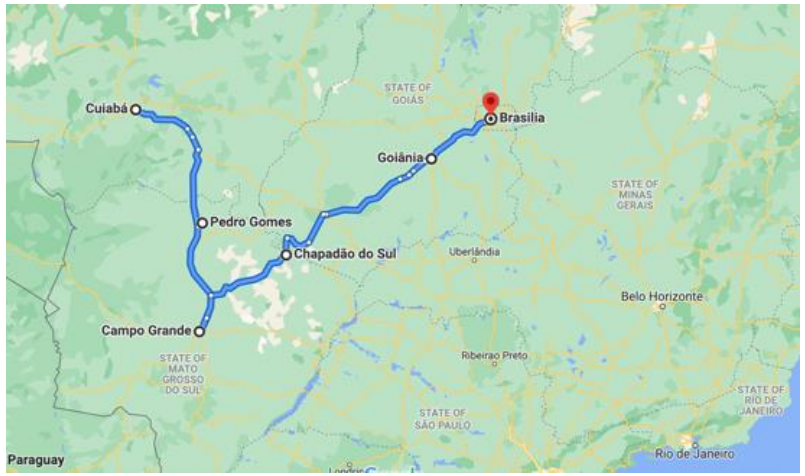
PMCID: PMC12097087 PMID: 40398937

Mpox

- Data generation and sharing is improving

Country	Cases since 2025	Sequences on GISAID
DRC	25.825	2.800
Uganda	7.160	655
Sierra Leone	5.442	356
Madagascar	3.436	11
Guinea	2.310	18
Burundi	1.797	111
Liberia	1.618	8
Kenya	1.229	2
Ghana	1.000	55

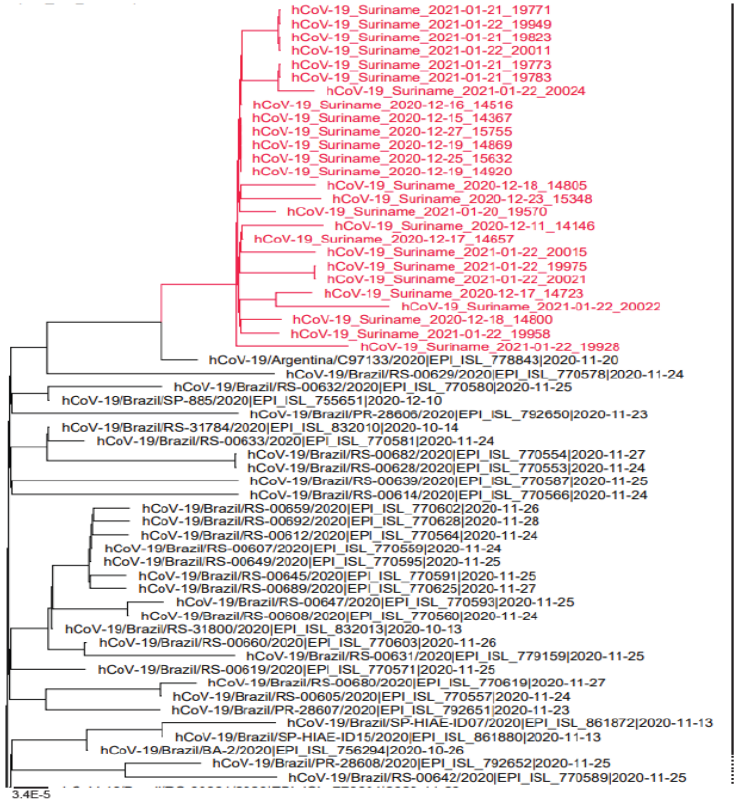
How to solve these inequaties?

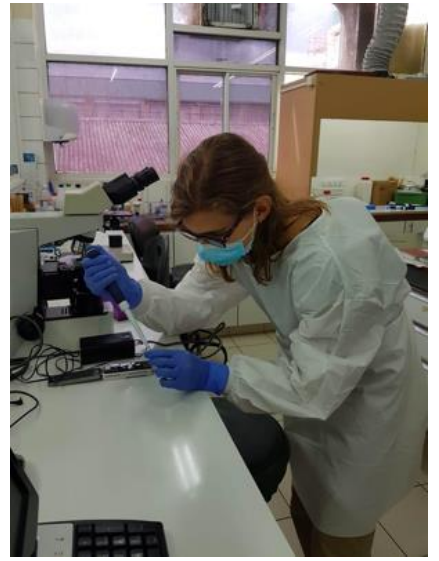














Presentation by dr. Hayley Cassidy

Challenges encountered in your situation

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What challenges do you encounter in setting up WGS?

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Interactive discussion on TEAMS

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