



Elucidating nosocomial SARS-Co

5.1.2e

12-11-2020



Nosocomial transmission

- **WHO definition**

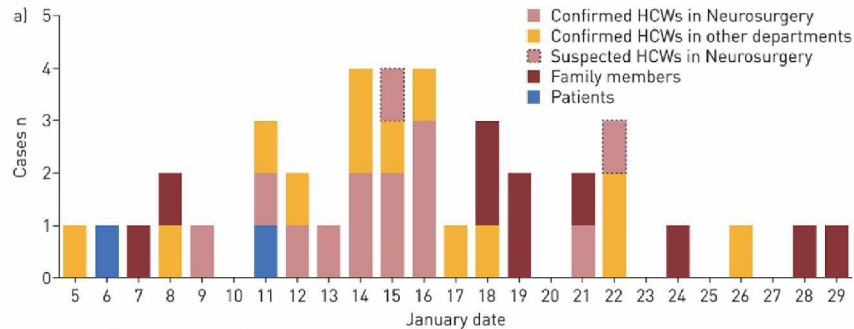
"Nosocomial infections, also called "hospital-acquired infections", are infections acquired during hospital care which are not present or incubating at admission. Infections occurring more than 48 hours after admission are usually considered nosocomial."

<https://www.who.int/csr/resources/publications/drugresist/en/whocdscsreph200212.pdf>



Nosocomial infections are common for other coronaviruses

- In MERS-CoV nearly 50% of new cases was due to nosocomial spread.
- Also described in January 2020 in Wuhan, China for SARS-CoV-2 including spread to family members

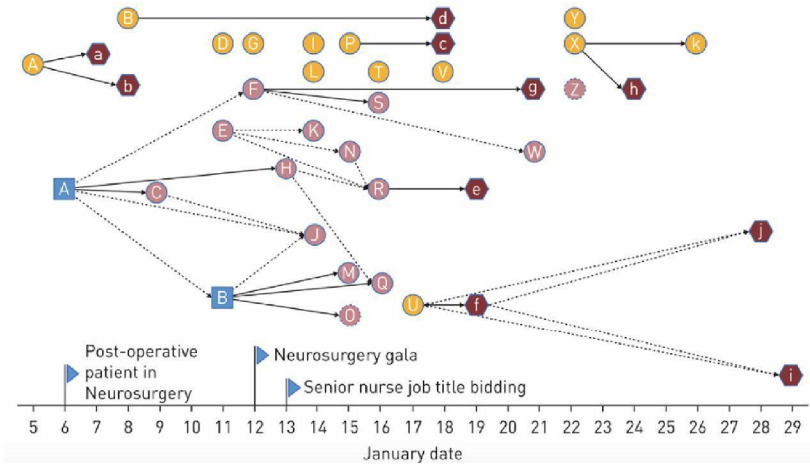


Wang et al. Nosocomial outbreak of COVID-19 pneumonia in Wuhan, China Eur Respir J 2020; 55: 2000544



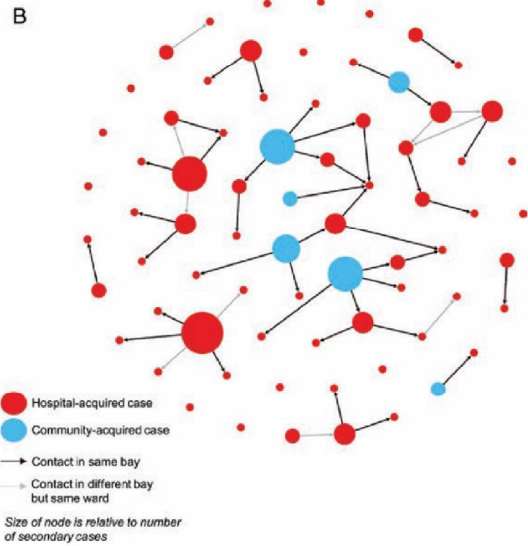
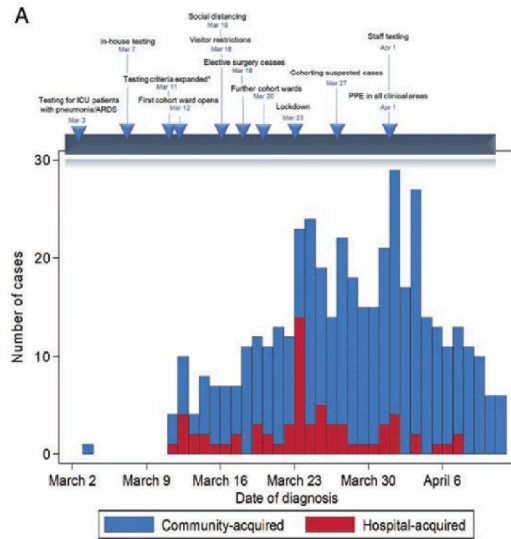
Also infection of family members

- Infected patients
- Confirmed HCWs in Neurosurgery
- Confirmed HCWs in other units
- Confirmed family members
- Probable transmission
- ⋯→ Suspected transmission
- Suspected HCWs in Neurosurgery





Nosocomial transmission in teaching hospital in England



Nearly 15% of cases were due to nosocomial transmission

Rickman et al. Nosocomial Transmission of Coronavirus Disease 2019: A Retrospective Study of 66 Hospital-acquired Cases in a London Teaching Hospital CID 2020;XX(X):1-4



Nosocomial transmission in The Netherlands

Sikkema et al. COVID-19 in health-care workers in three hospitals in the south of the Netherlands: a cross-sectional study. *Lancet Infect Dis* 2020; 20: 1273–80

"We did a cross-sectional study at two teaching hospitals (Amphia Hospital, Breda, Netherlands [700 beds], and Elisabeth-TweeSteden Hospital, Tilburg, Netherlands [800 beds]) and one regional hospital (Bravis Hospital, Roosendaal and Bergen op Zoom, Netherlands [600 beds]), at which 12 022 health-care workers in total were employed."

All health-care workers at these three hospitals who had fever or mild respiratory symptoms in the 10 days before screening for SARS-CoV-2 infection were eligible for testing, which was voluntary. All patients testing positive for SARS-CoV-2 and who had been admitted 2 days or more before the last date of onset of symptoms of healthcare workers per hospital were included.



Results

At Amphia Hospital, 42 (**5%**) of 783 health-care workers tested positive for SARS-CoV-2 RNA;

at Bravis Hospital, 10 (**2%**) of 443 health-care workers tested positive;

and at Elisabeth-TweeSteden Hospital, 44 (**8%**) of 570 health-care workers tested positive.

These percentages are likely an underestimation as asymptomatic patients were not screened.



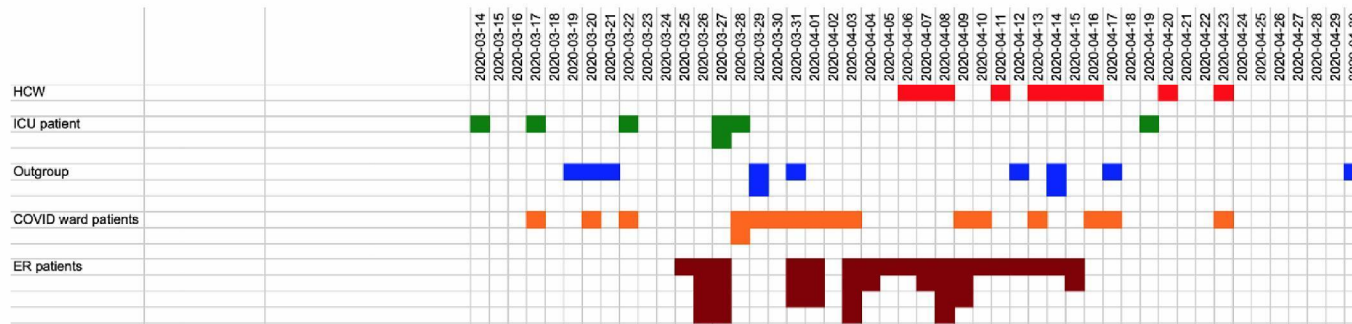
OLVG

- During the first pandemic wave OLVG was the regional SARS-CoV-2 treatment center.
- At the peak of the first wave: 5 COVID wards and 3 ICU units.
- During April 2020 several internal medicine residents and medical specialists fell ill. All had worked on ER/COVID wards. Testing showed: SARS-CoV-2 positive.
- In total 10 residents/doctors sick.



Timeline and sample selection

- In total:
 - 10 internal medicine residents/doctors
 - 78 local comparators:
 - 39 ER patient samples
 - 17 COVID ward patient samples
 - 11 outgroup samples from other hospital
 - 7 ICU patient samples





Analysis

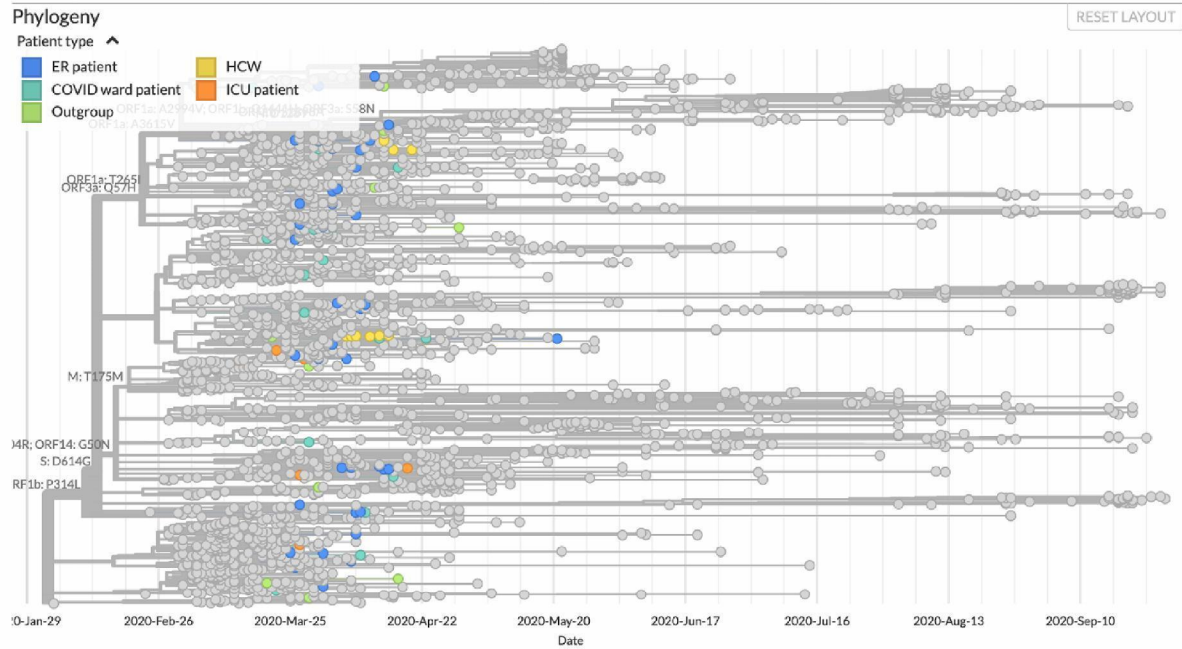
Generated 3 datasets:

All OLVG outbreak sequences +

- 1) All Dutch GISAID sequences
+ top 10 GISAID local blast per sequence
- 2) European reference set: per month / per country max 3 sequences
+ top 10 GISAID local blast per sequence
- 3) Global reference set: per month / per country max 3 sequences
+ top 10 GISAID local blast per sequence

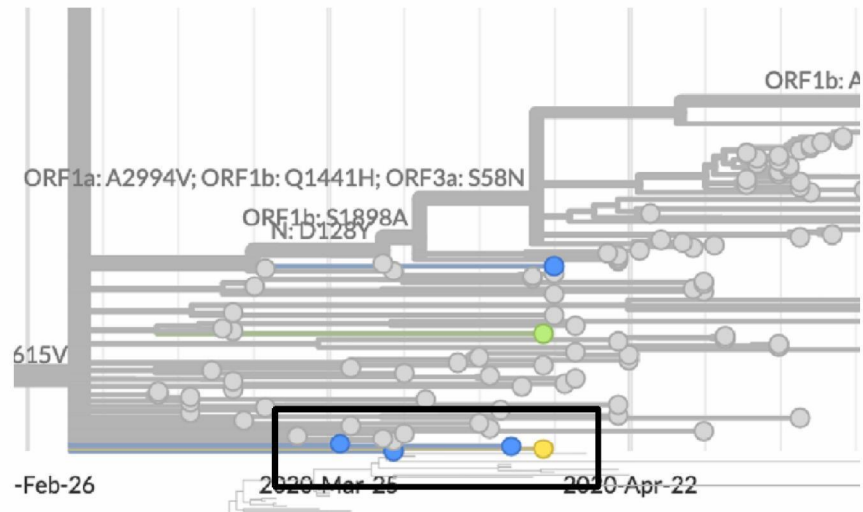


Results with Dutch sequences





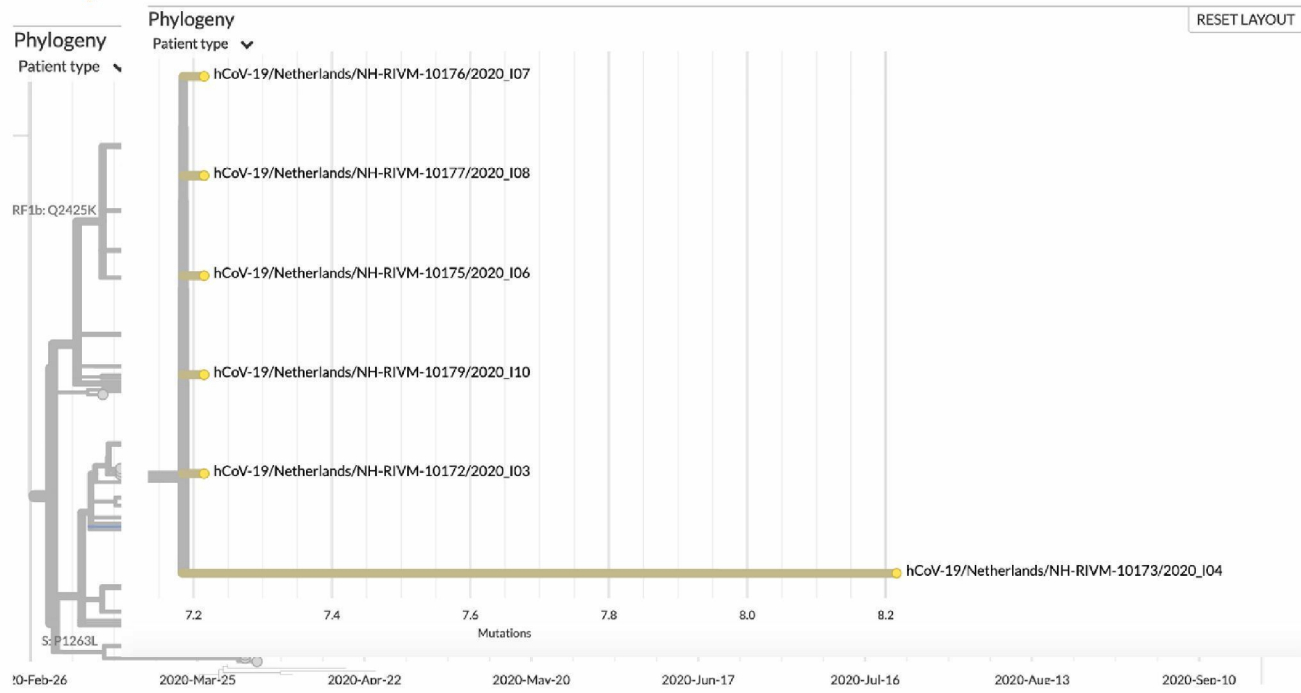
I02



Clustering I02 with three ER patient samples: however all three different nucleotide mutations. Probably/possibly not related.

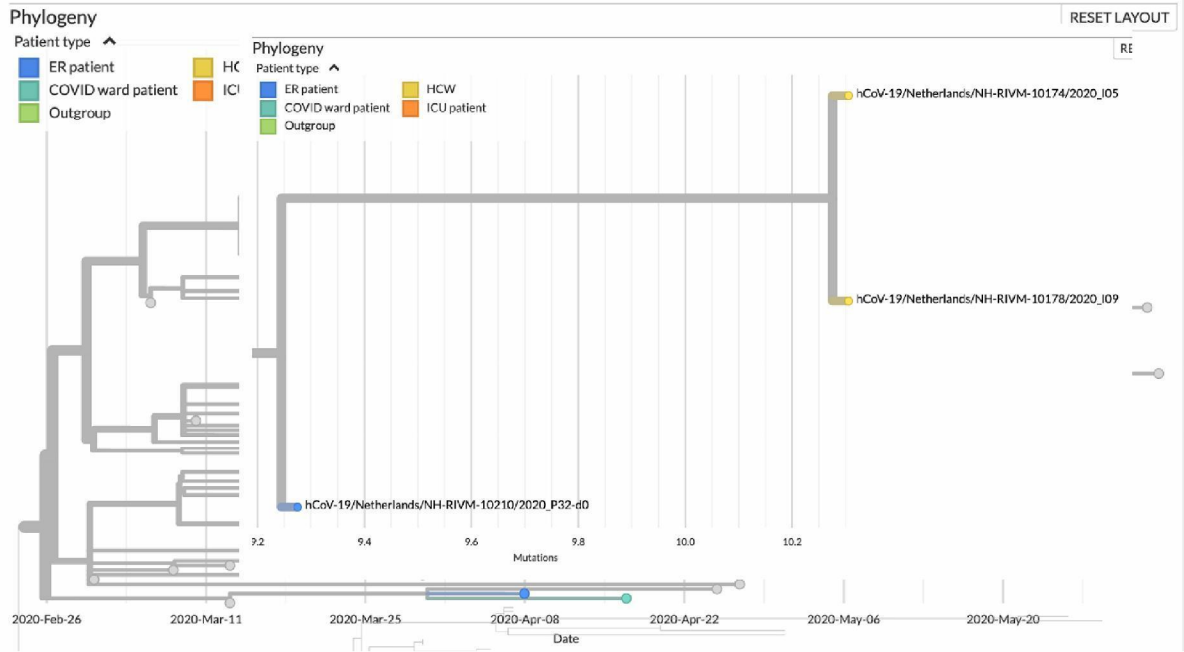


I03/I04/I06/I07/I08/I10: 1 cluster



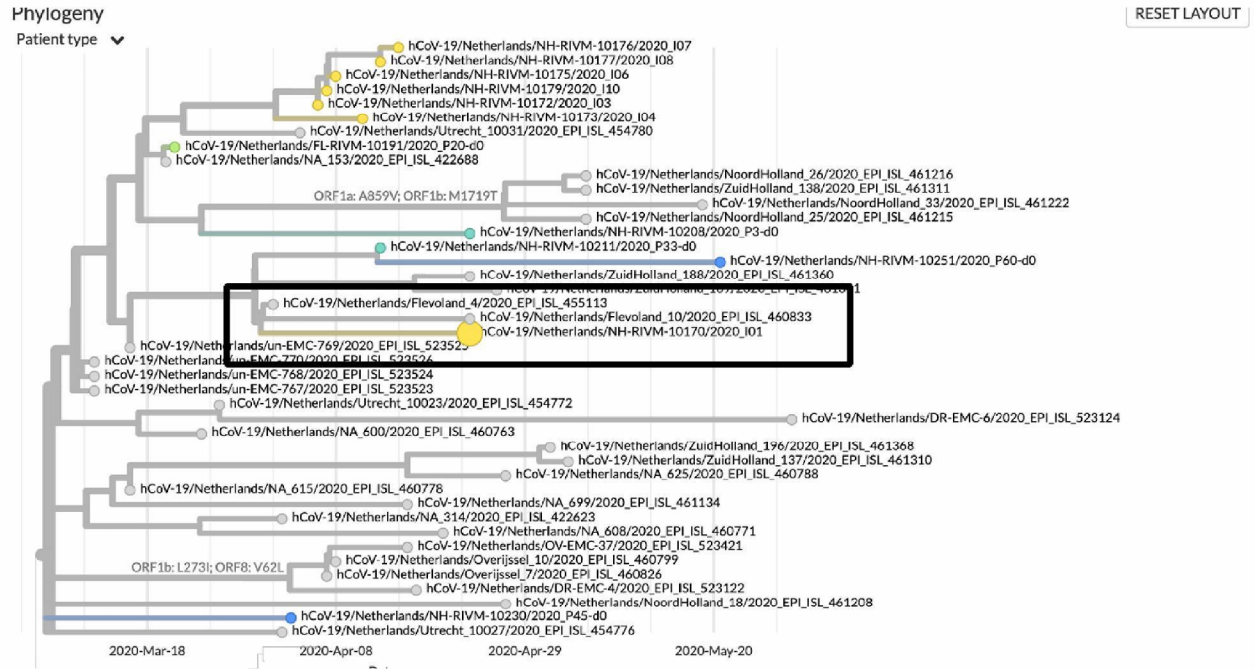


Cluster I05/I09



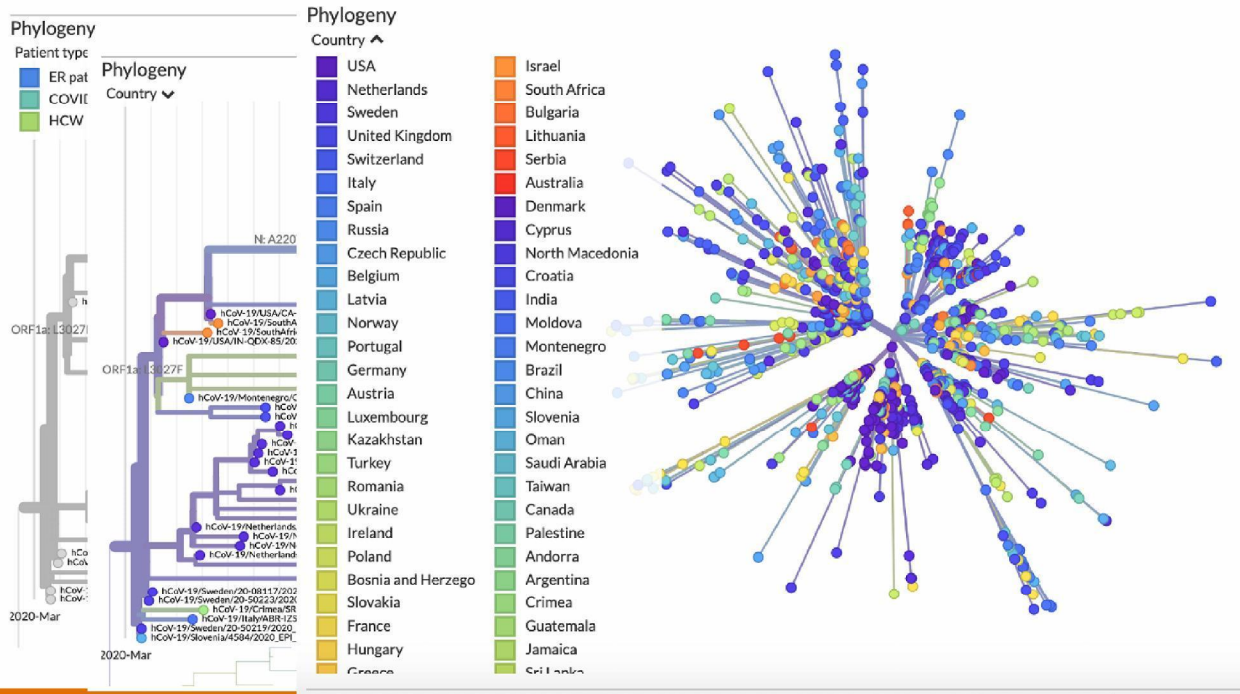


I01: separate introduction



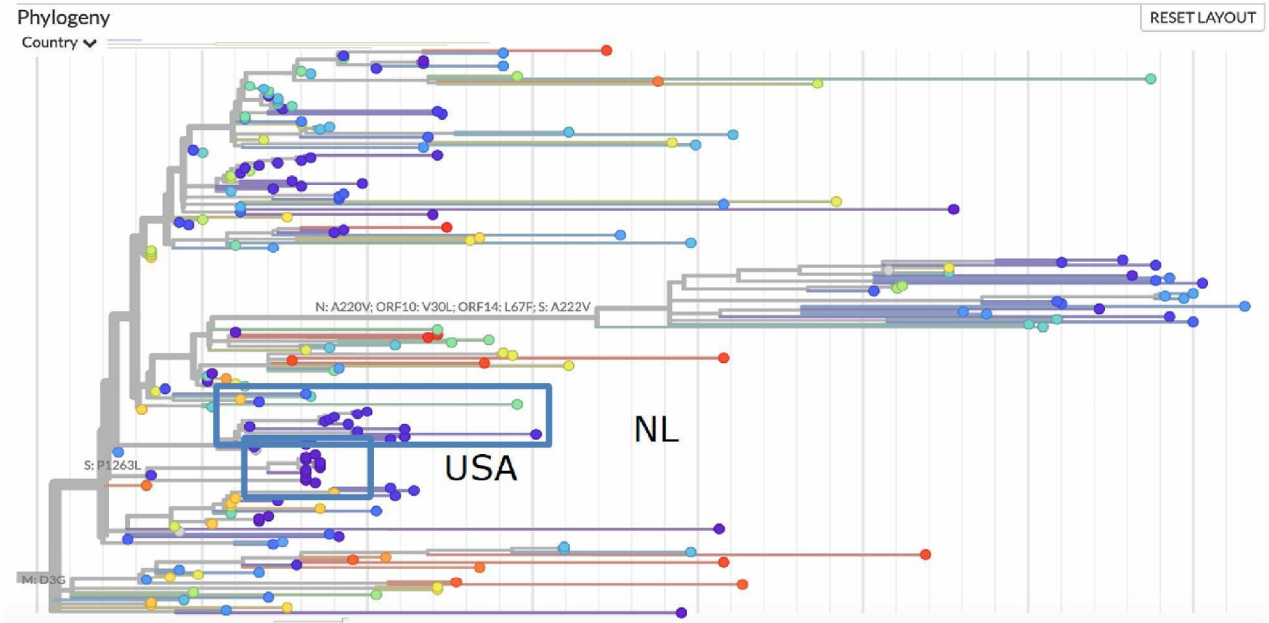


Europese set: waar kwamen OLVG virussen vandaan?



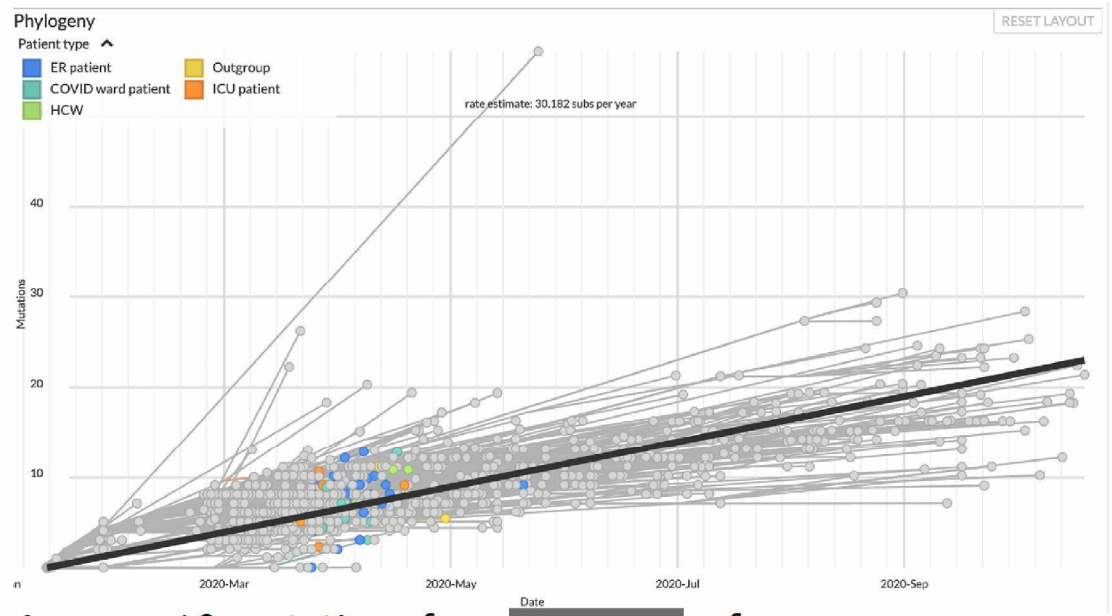


Global set





Moleculaire klok



Average 10 mutations from **5.1.2a** reference.
Matches early in the pandemic.



Acknowledgements

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