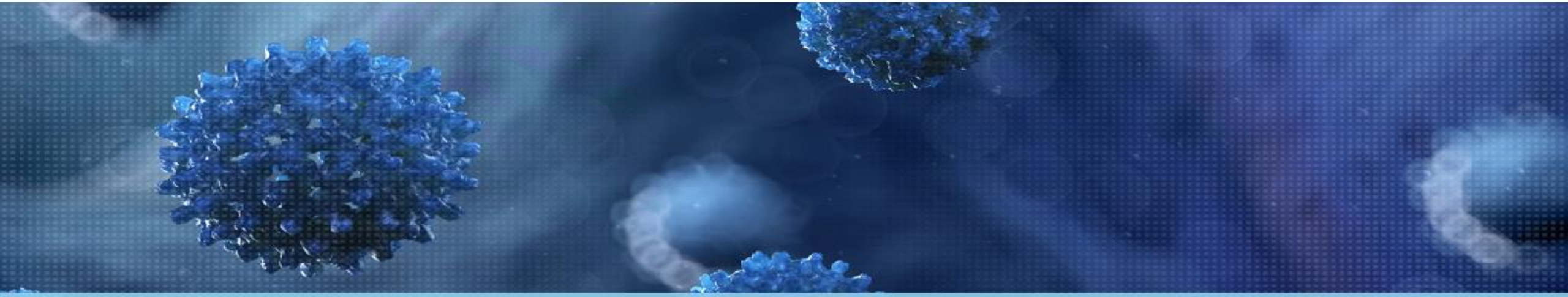
Erasmus MC

WHO collaborating centre for
Arbovirus and Hemorrhagic
Fever Reference and Research

Viroscience lab

WHERE SKILLS MEET TO STUDY & PROTECT



Considerations from viral evolution studies

Prof Dr Marion Koopmans

m.koopmans@erasmusmc.nl

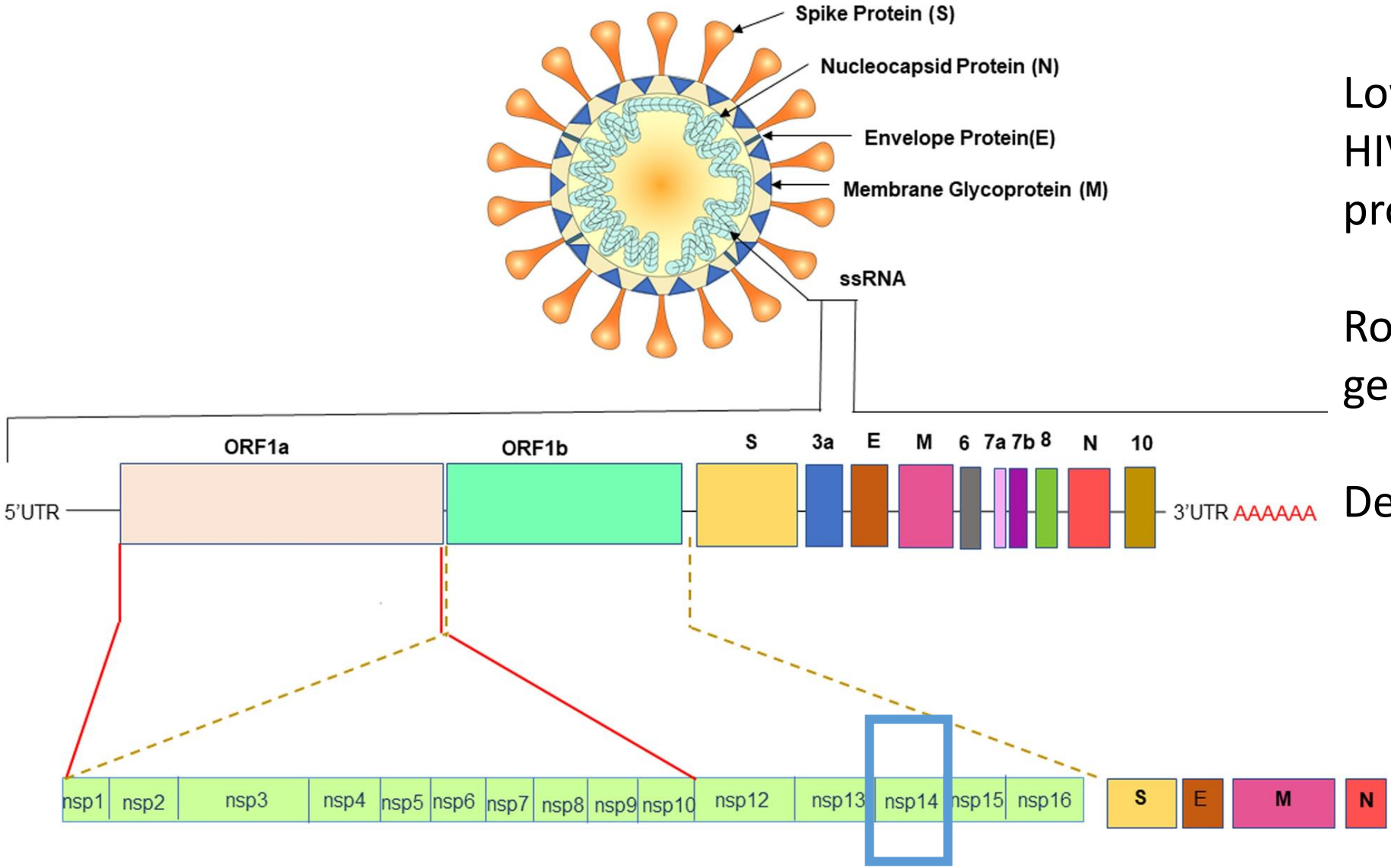
Virus genetics

- The COVID-19 pandemic is a breakthrough for the use of virus genetics
- Has generated new insights in evolution of an emerging virus
- Used for many questions:

  - How does it transmit?
  - Who infected whom?
  - Has the phenotype changed?
    - Transmissibility
    - Antigenicity
    - Virulence
    - Treatability

Variant emergence may occur without or with limited antigenic escape

Oude Munnink et al, 2021



Coronaviruses evolve

Lower frequency than for HIV, influenza due to proofreading (nsp14)

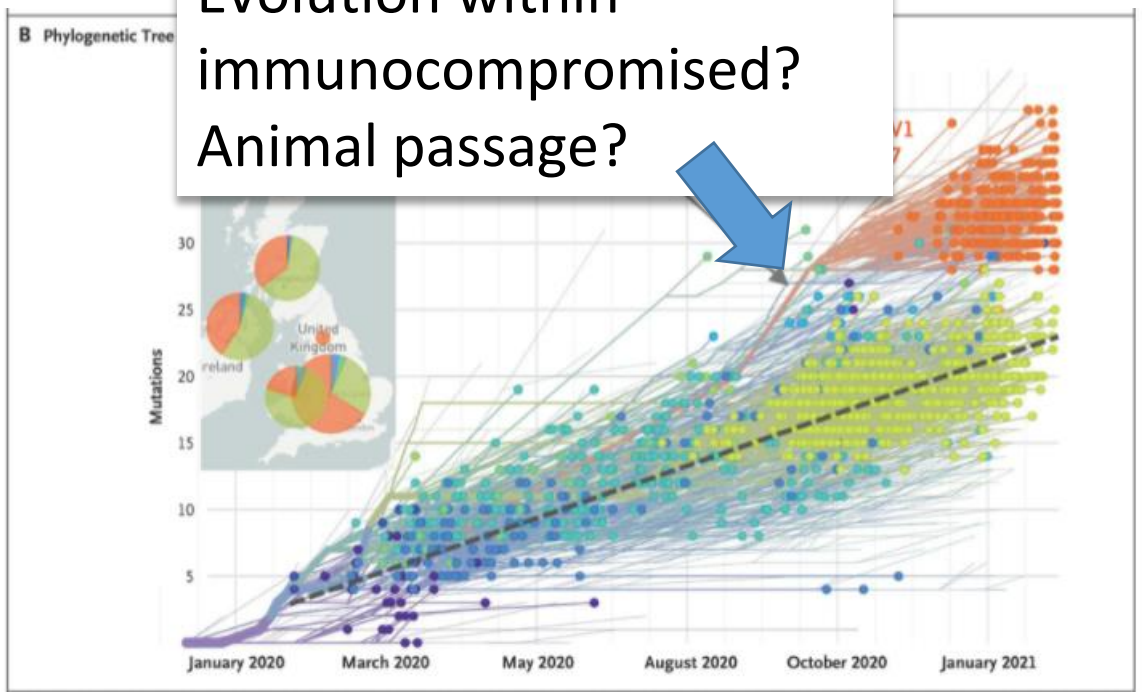
Roughly 2 mutations / genome / month

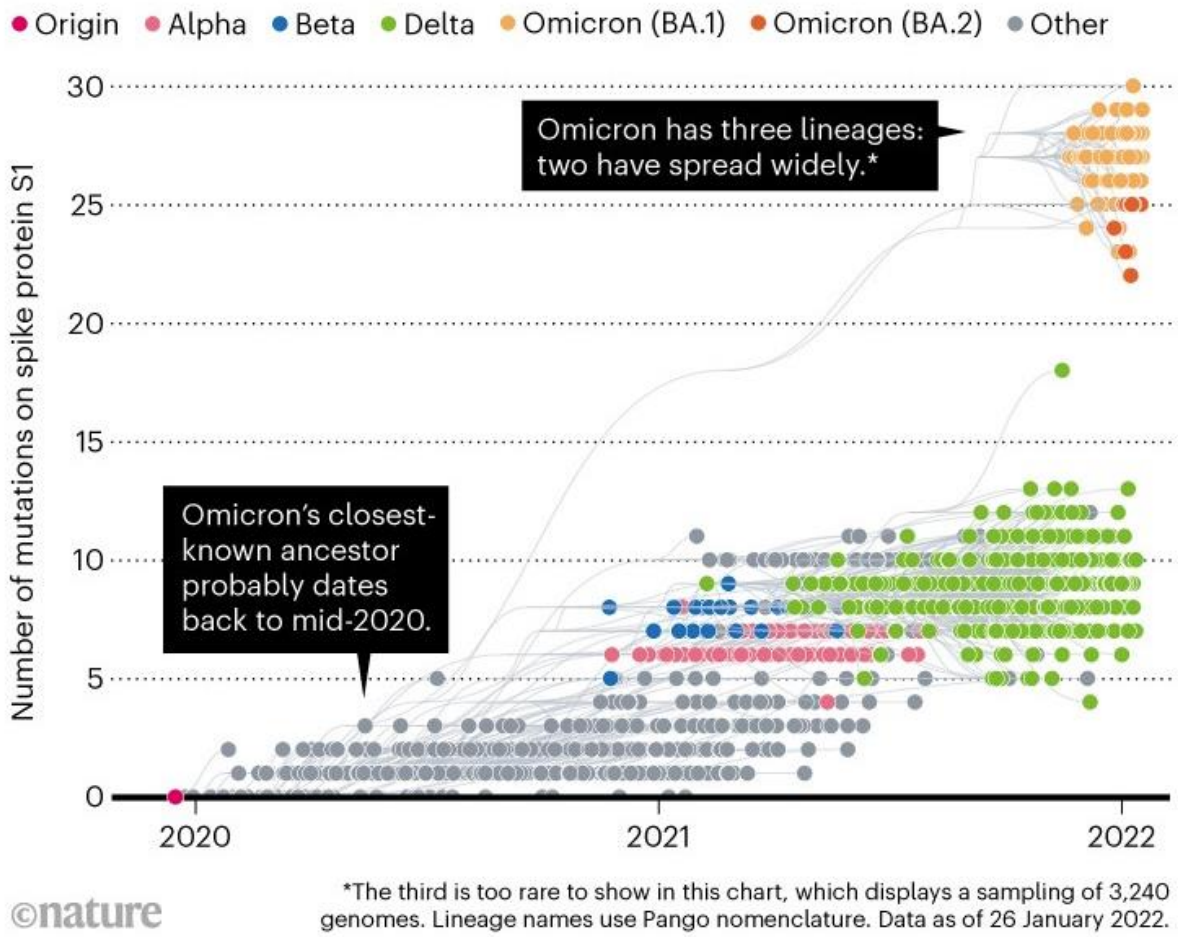
Deletions, recombination

Rastogi et al, 2020 https://respiratory-research.biomedcentral.com/articles/10.1186/s12931-020-01581-z/figures/2

Emergence of VOI/VOC

New introduction?
Evolution within immunocompromised?
Animal passage?



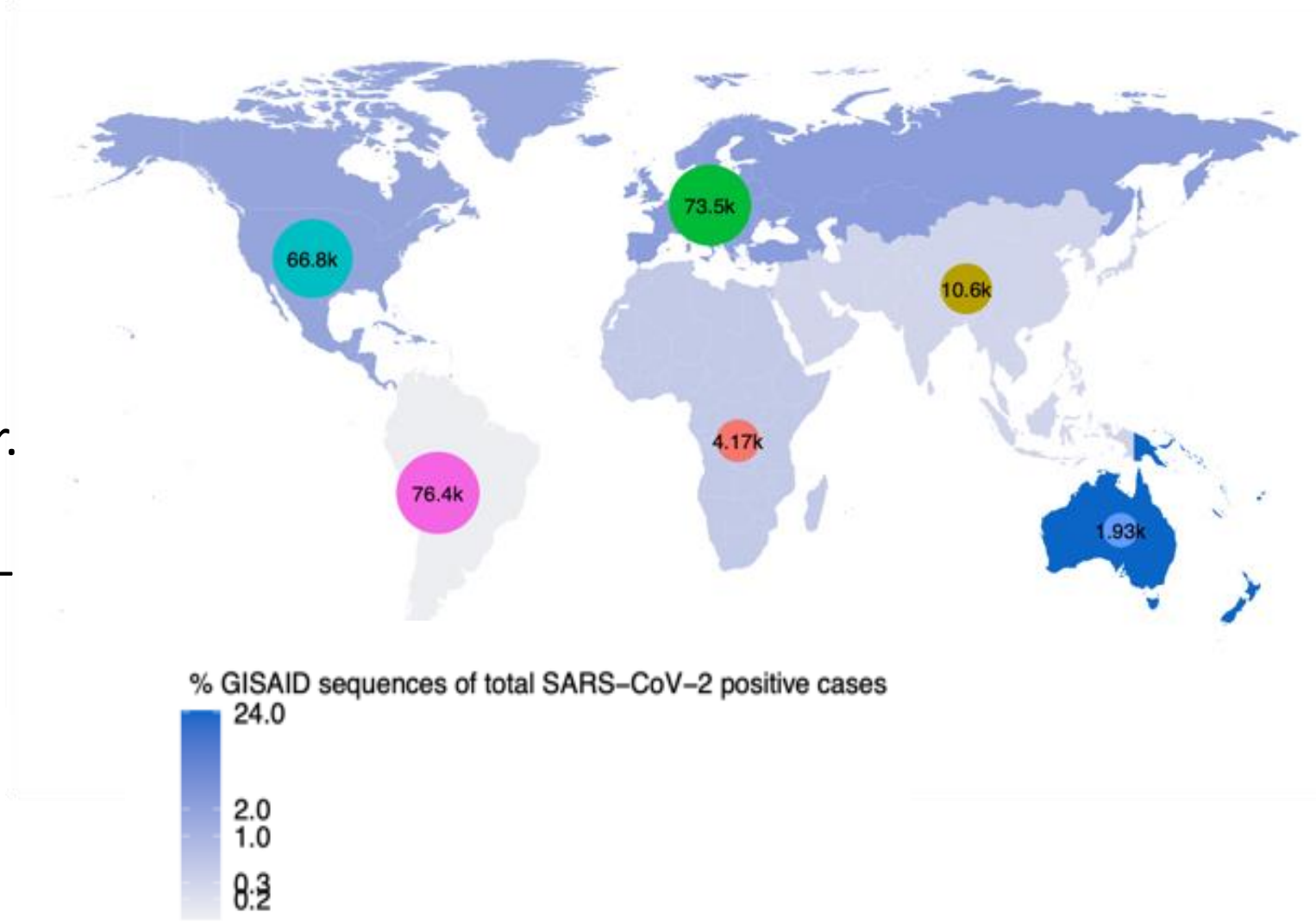


https://www.nejm.org/doi/full/10.1056/NEJMsb2104756

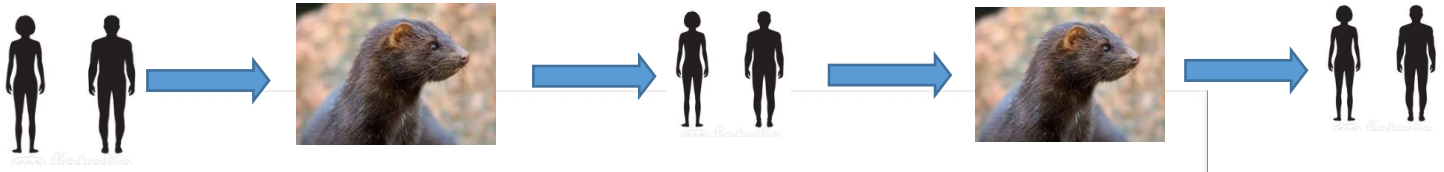
https://www.nature.com/articles/d41586-022-00215-2

Hypotheses regarding the origin of variants of concern

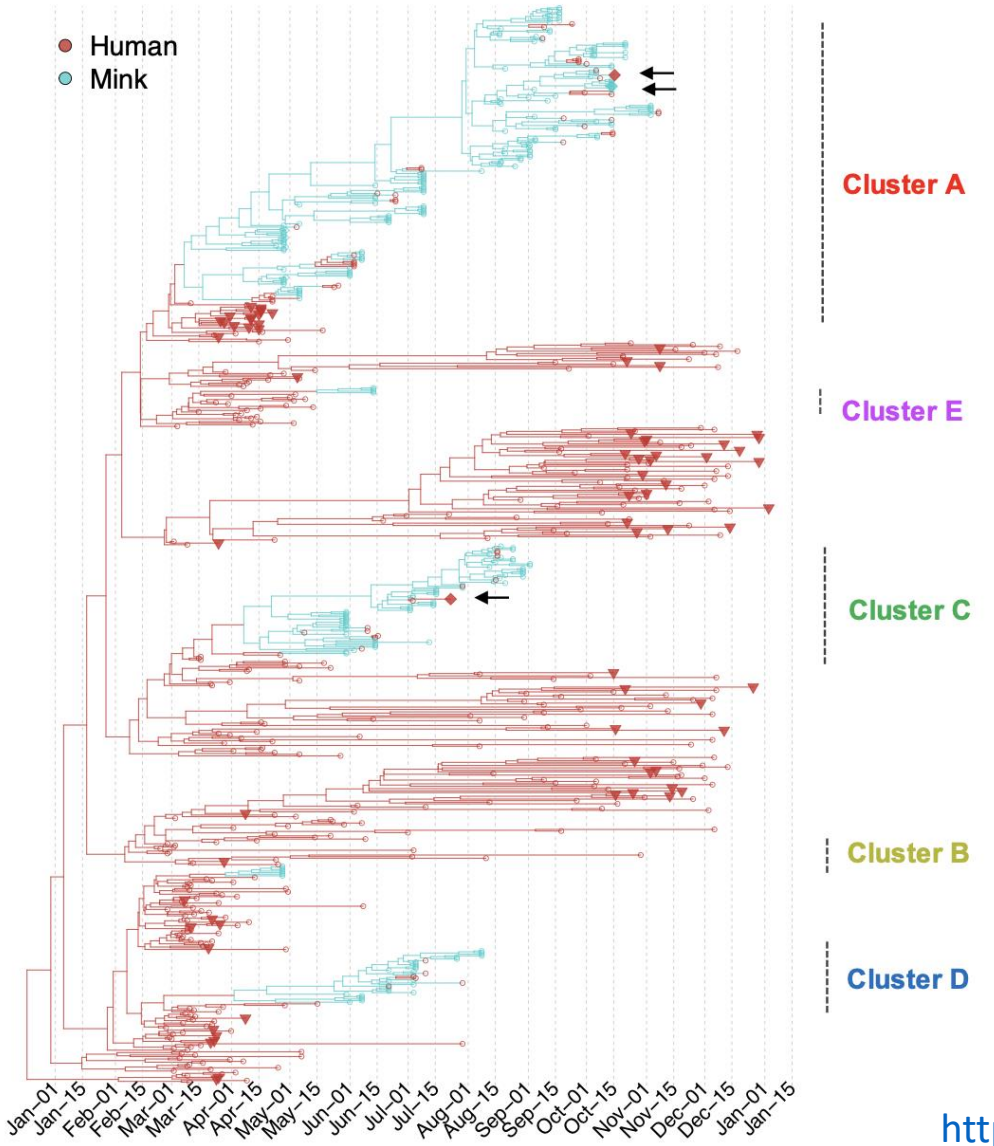
- Circulation and evolution in undersampled human populations
- (Unknown) animal reservoir.
- Persistent infection of SARS-CoV-2 in immunocompromised individuals

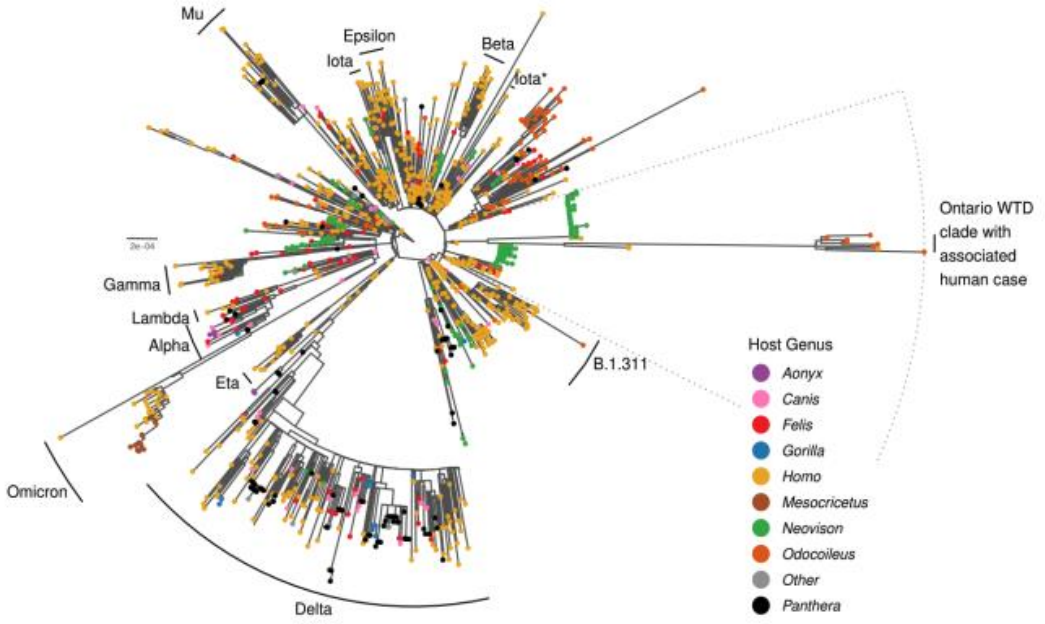


Oude Munnink et al 2021



Associated with RBD mutations

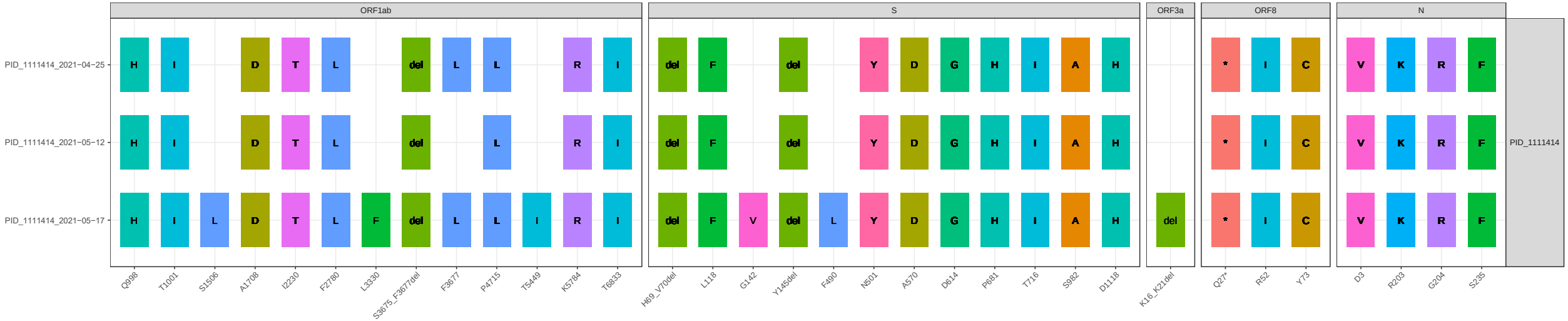




LuLu, Sikkema et al, Nature Comms, 2021

https://www.biorxiv.org/content/10.1101/2022.02.22.481551v1.full.pdf

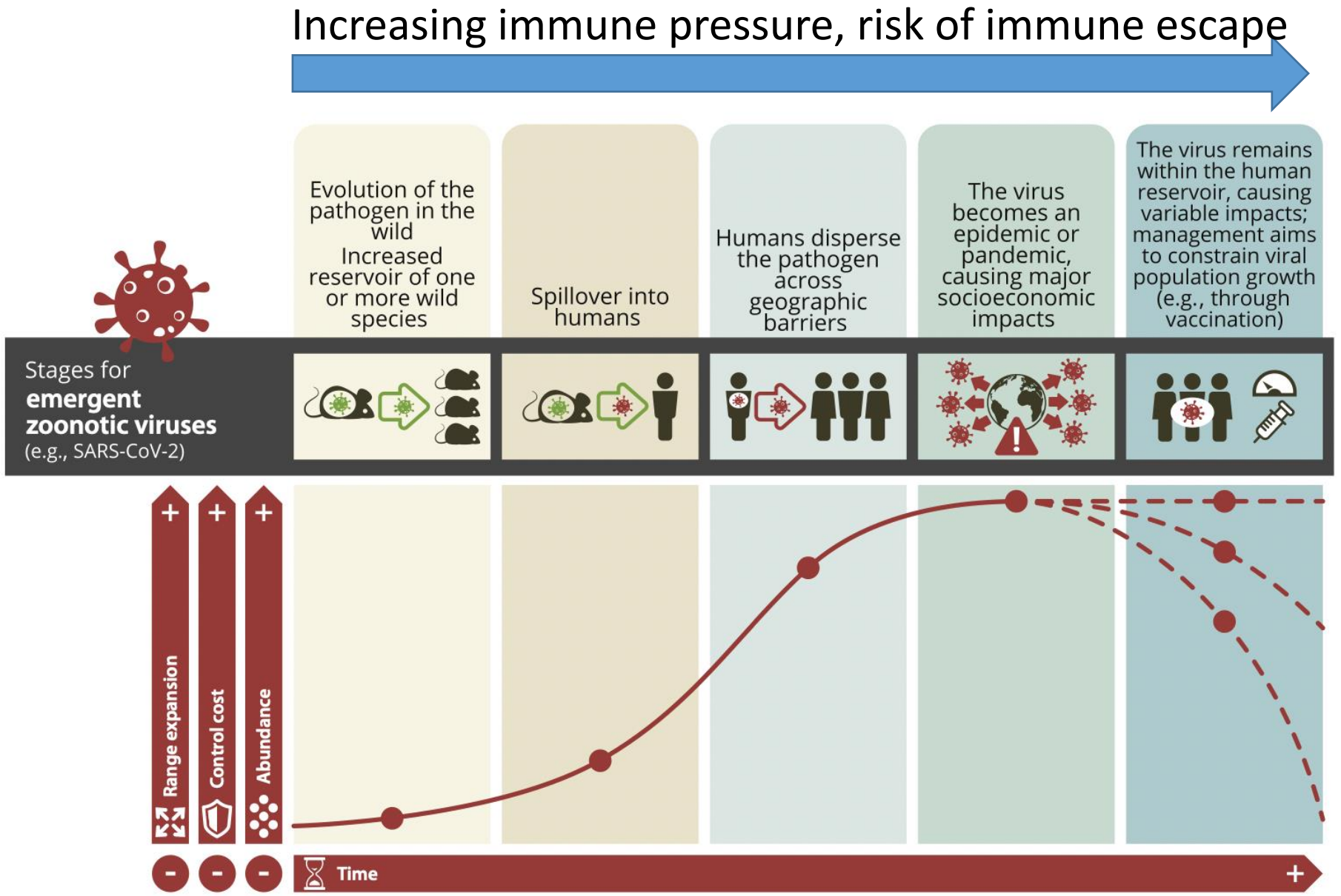
Feb 2022 Case, chronic lymphocytic leukemia (CLL) who currently is infected for 296 days with SARS-CoV-2



Alpha (B.1.1.7) variant, which has not been detected anymore in the Netherlands since the 13th of October 2021.

- G142V G142D in Delta and Omikron

Oude Munnink et al, unpublished



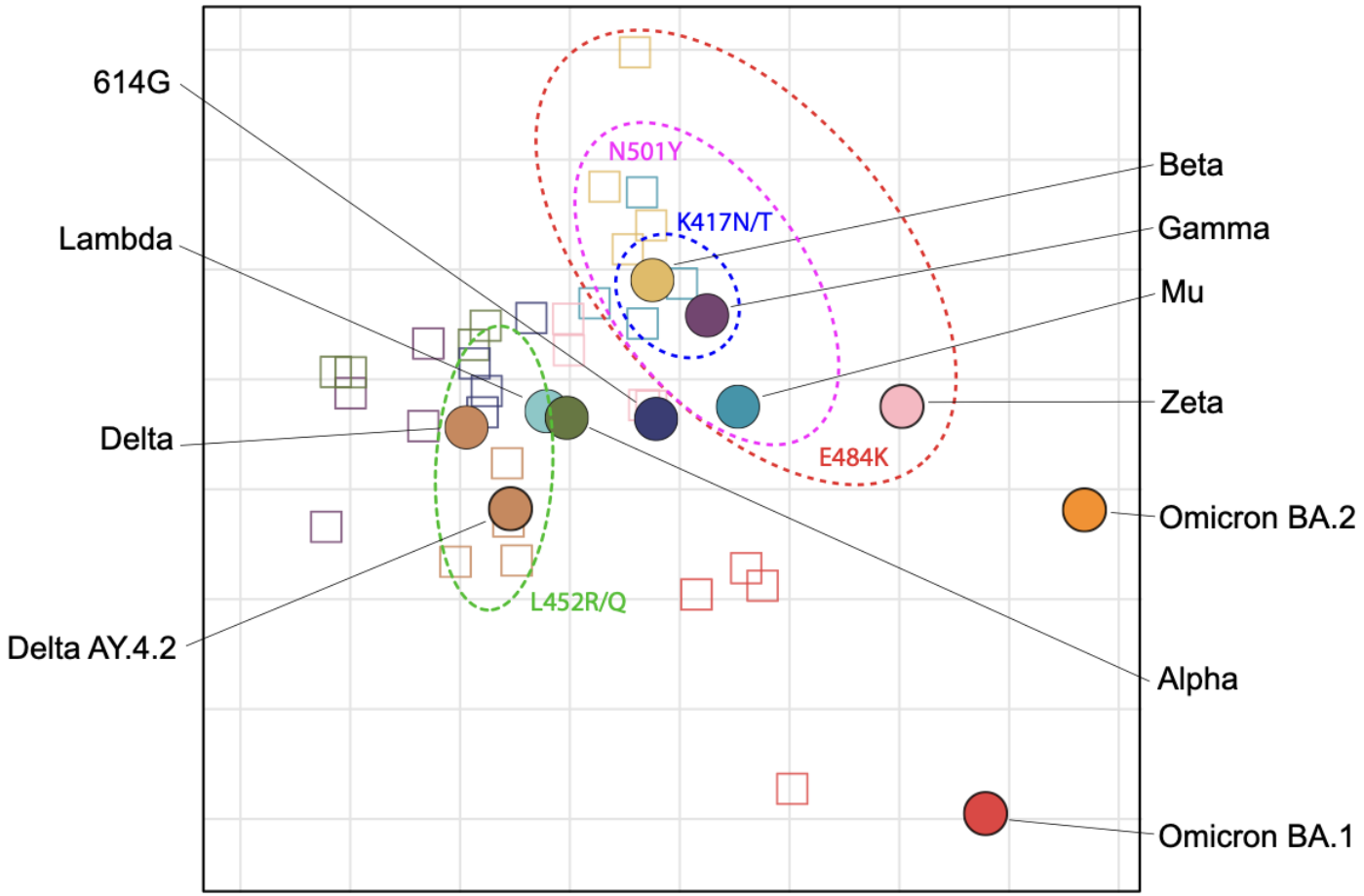
The interplay between virus and host immune selection changes over time

> Variants escape by different mechanims

Nuñez et al https://www.cell.com/action/showPdf?pii=S0169-5347%2820%2930134-8

Overview SARS-CoV-2 variants of concern

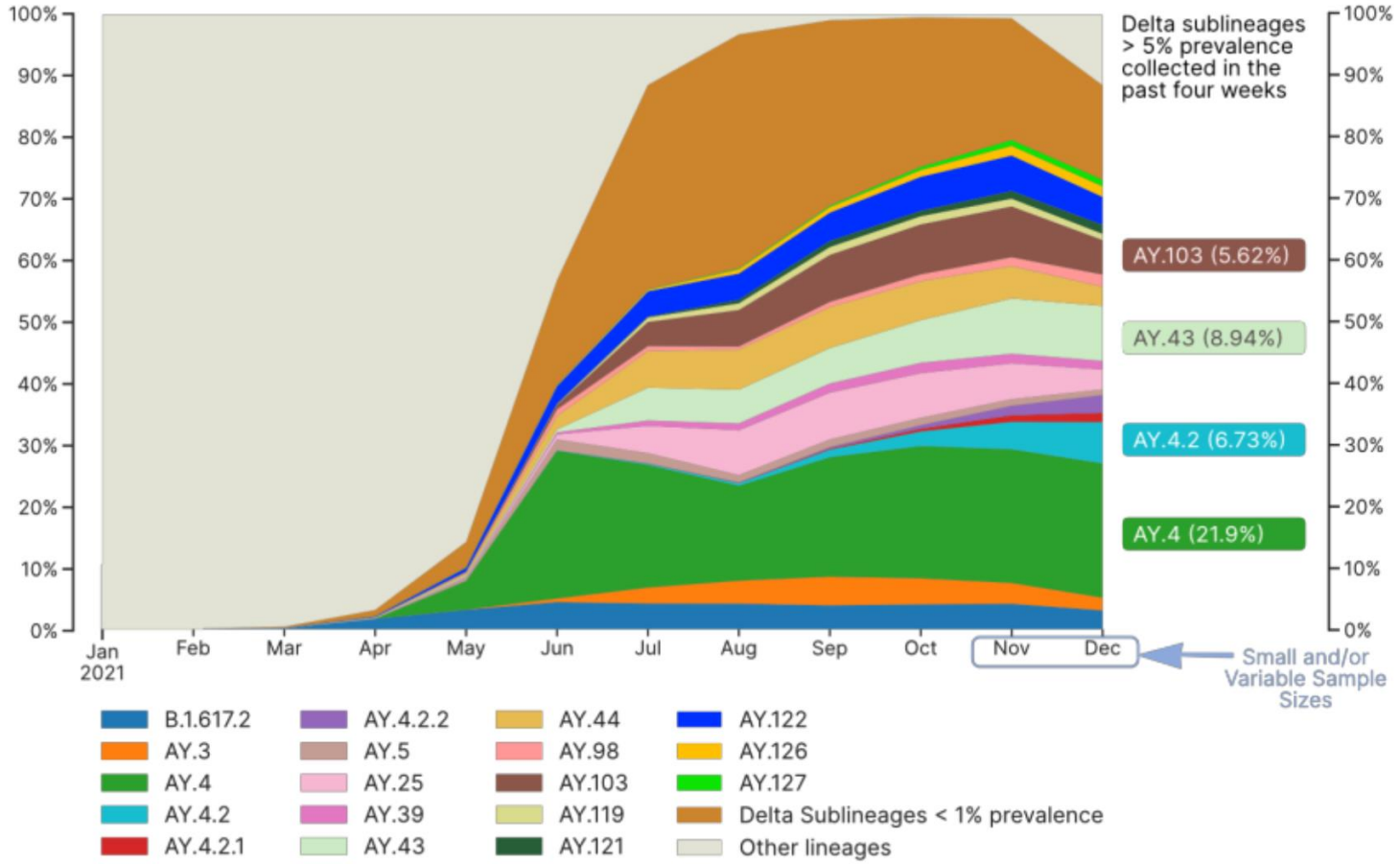
Omikron and pre-Omikron viruses may be distinct serotypes



Mykytyn et al https://www.biorxiv.org/content/10.1101/2022.02.23.481644v1.full.pdf

Note: Variants are a swarm of viruses, with multiple sublineages

Frequency of sub-lineages of Delta (GISAID)



> Deriving conclusions from experiments with specific viruses needs to be done with caution

Summary

- SARS COV 2 is evolving
- Direction of evolution is still uncertain
- Sources of emerging variants need to be resolved > enhanced surveillance
- We are at the start of discussions on vaccine updates, similar to influenza
- The thinking about broader vaccines can also benefit the current SARS COV 2 response