



# **Molecular surveillance of pandemic SARS-CoV-2 in Germany: Sampling approach and specimen logistical issues (affecting downstream virus characterization)**

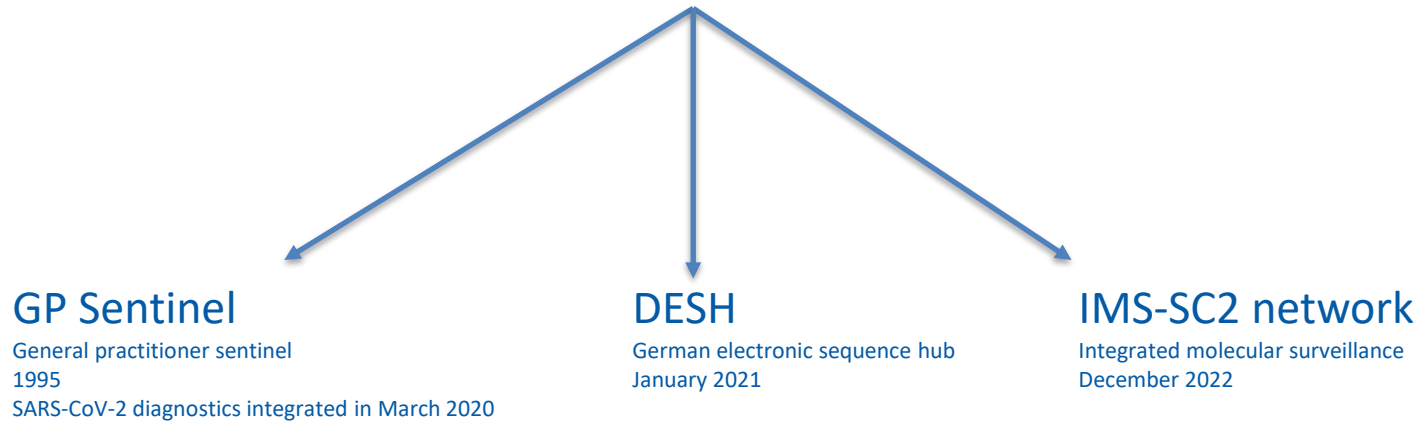
07.10. 2022

WHO/ECDC - Annual European Influenza and COVID-19 Surveillance Meeting 2022

Ralf Dürrwald, Unit 17 „Influenza and other Respiratory Viruses,  
National Influenza Centre, Robert Koch-Institut, Berlin



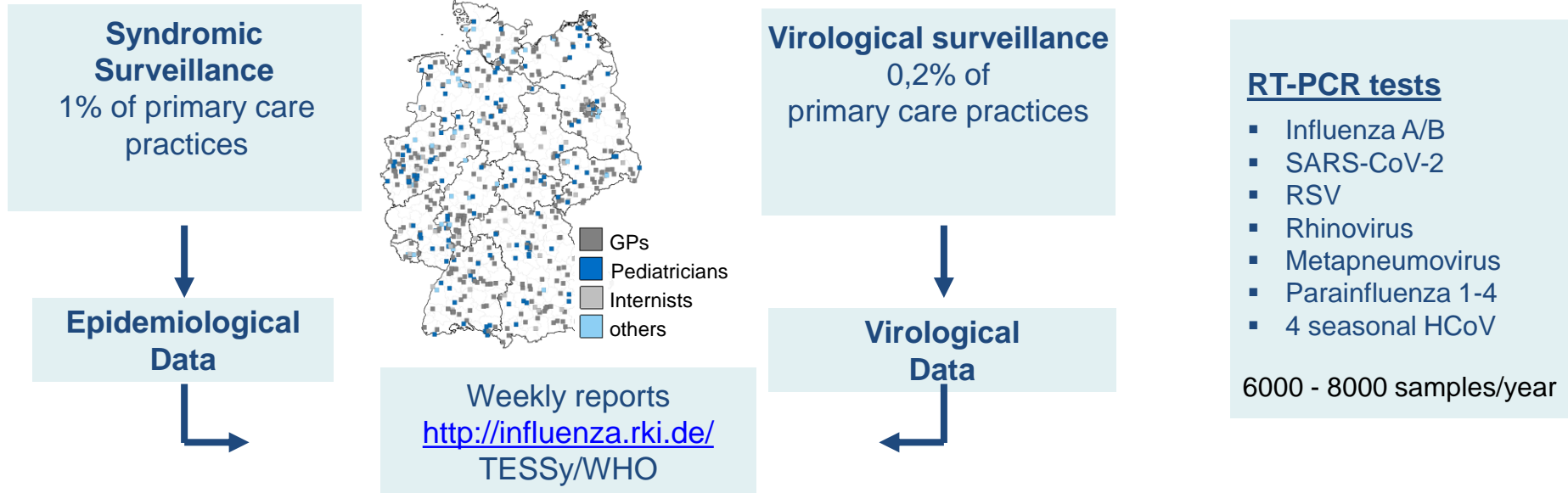
# Molecular surveillance of SARS-CoV-2 in Germany



# Sentinel surveillance of acute respiratory infections in Germany

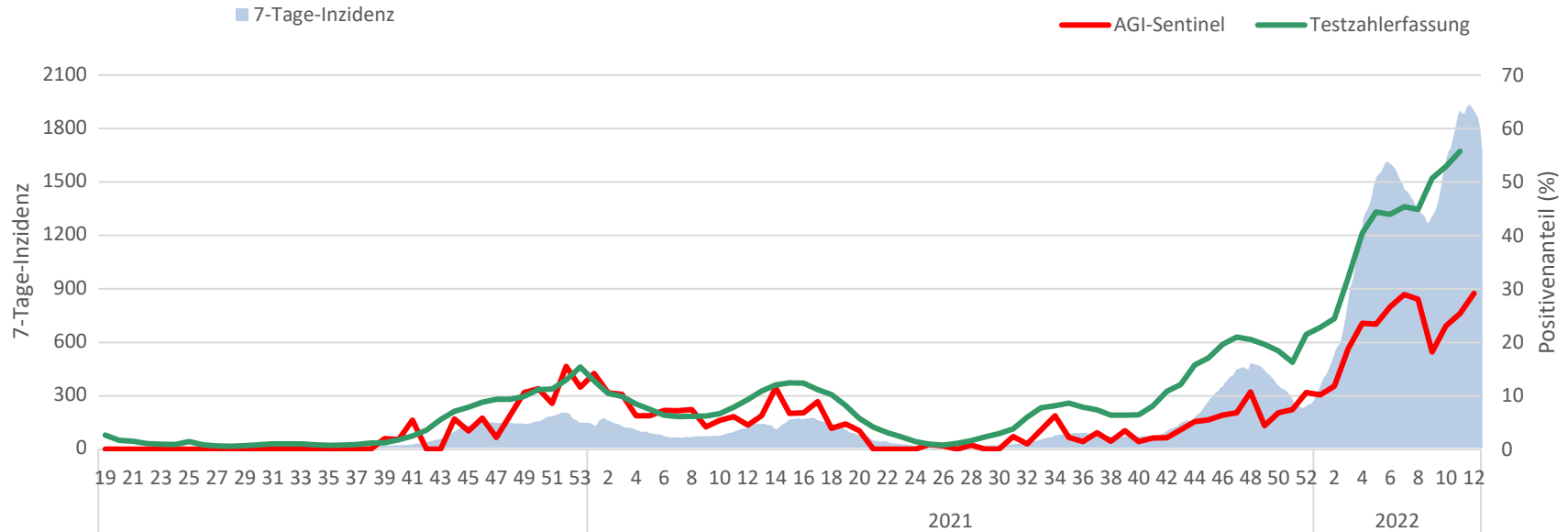


Patients with acute respiratory symptoms



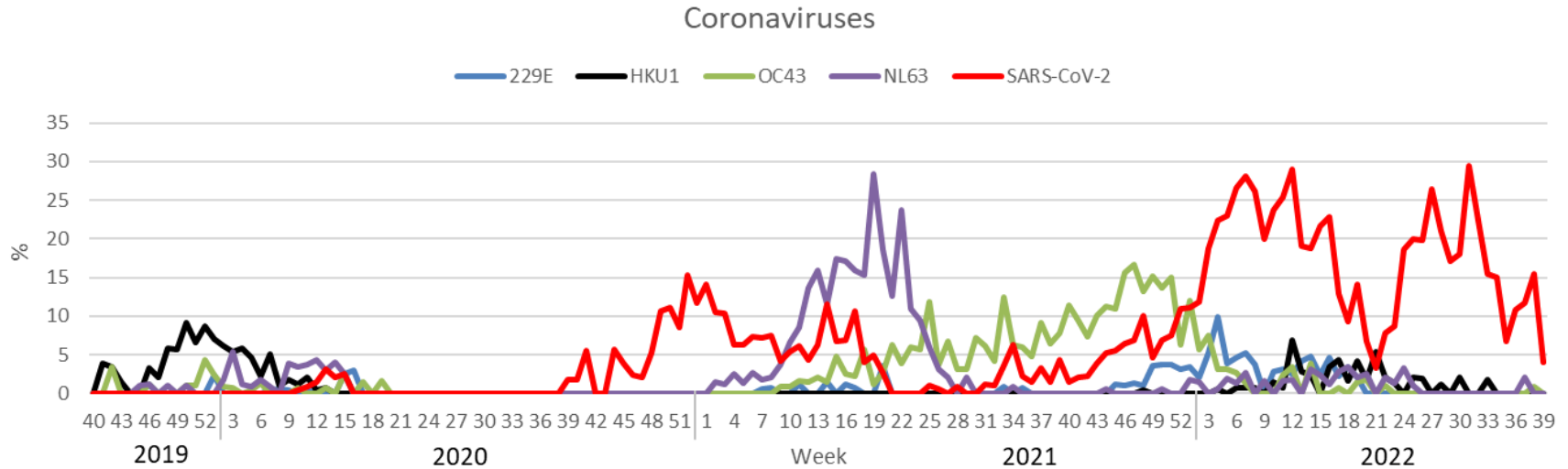


# Comparing SARS-CoV-2 detection by sentinel surveillance and national mandatory reporting



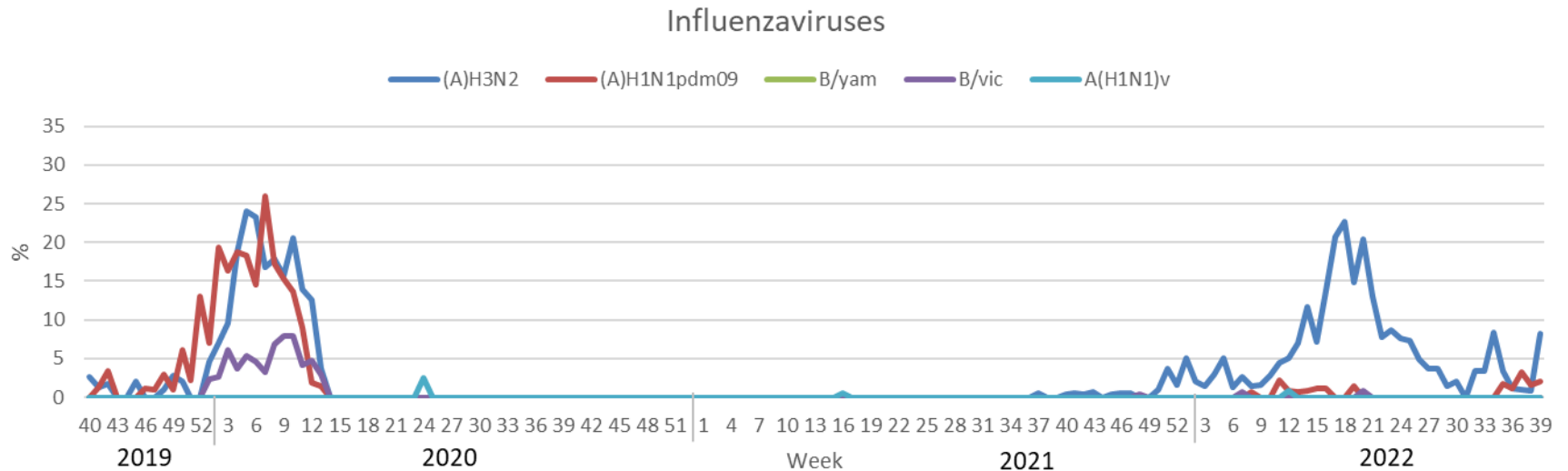


# Coronaviruses



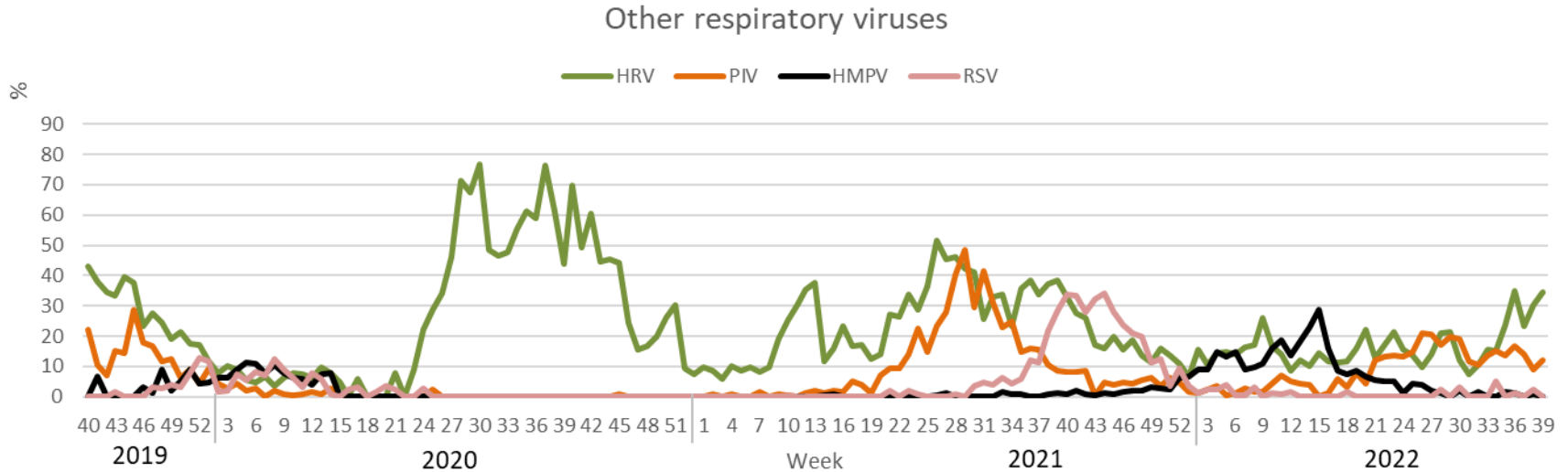


# Influenzaviruses





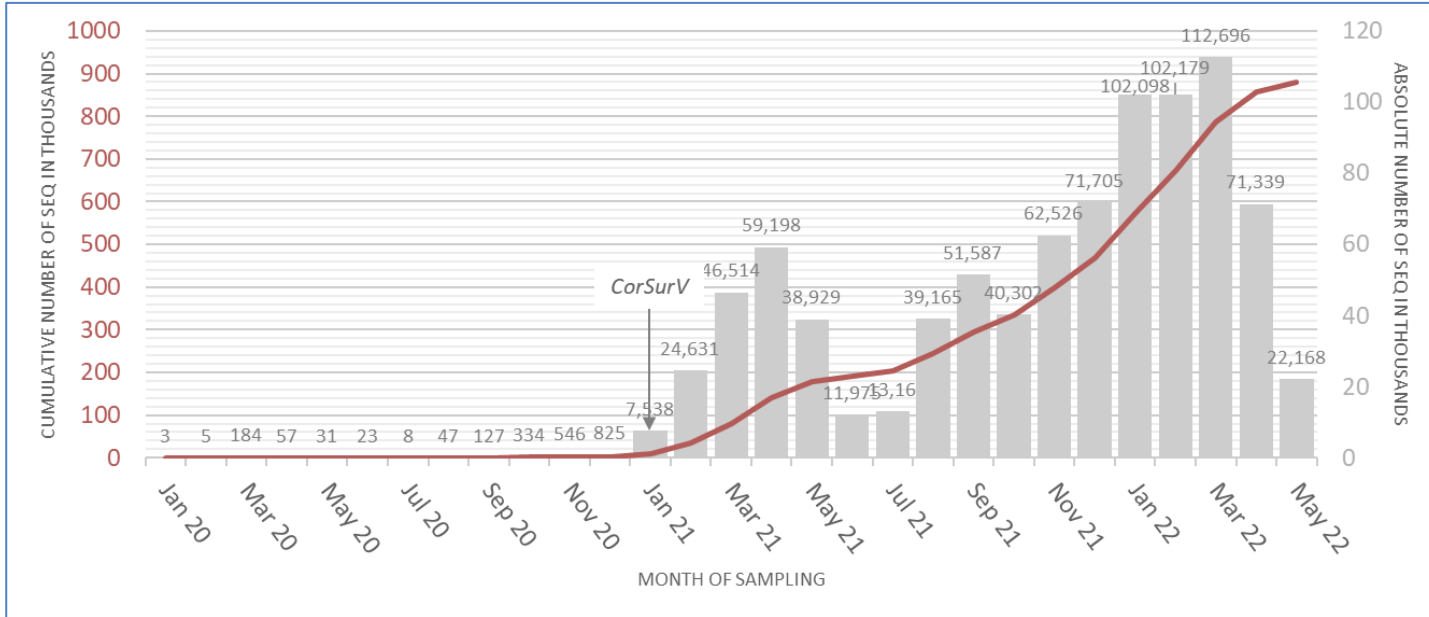
## Other respiratory viruses



# DESH: Genomic surveillance of SARS-CoV-2 in Germany



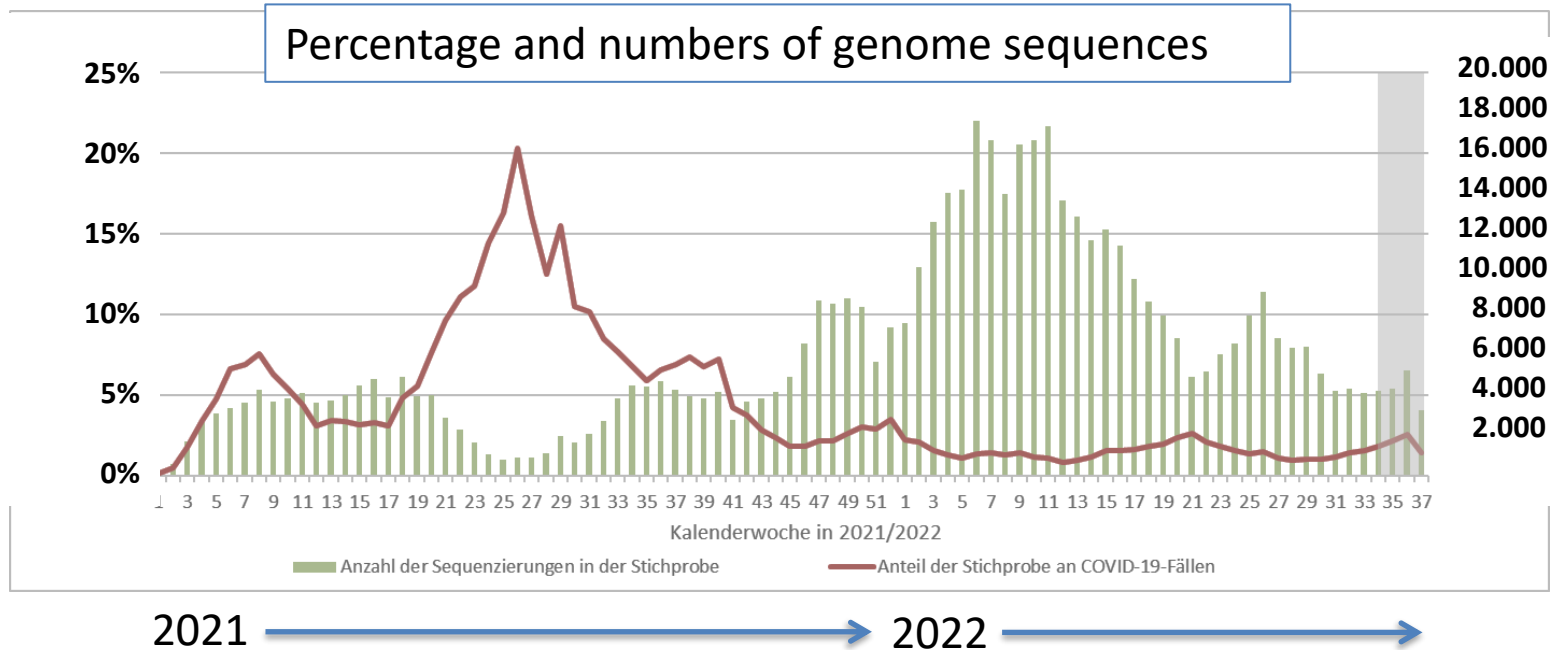
- Statutory order, January 2021 (CorSurV) → sequencing increased via DESH (“German Electronic Sequence Hub”).
- Peripheral labs report viral genome sequences to RKI



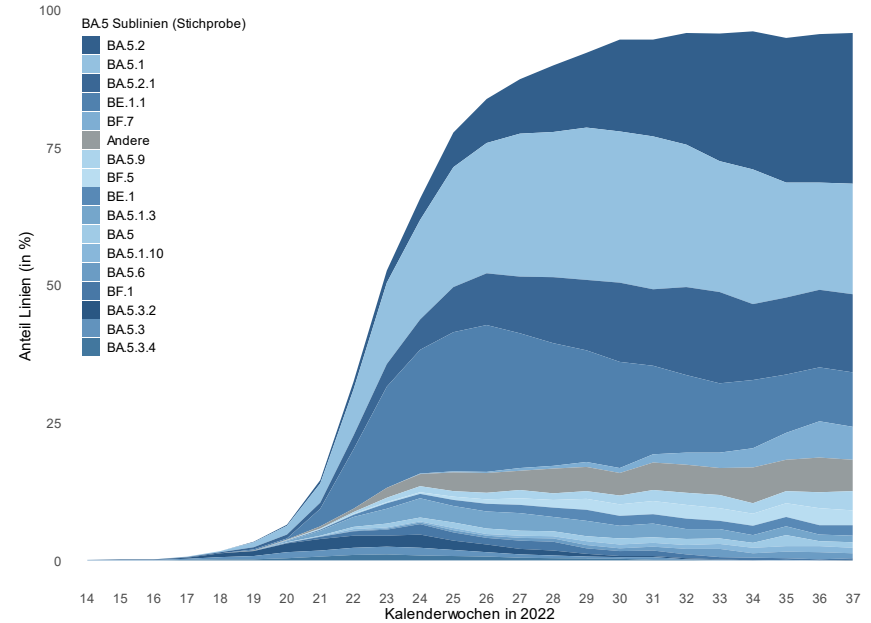
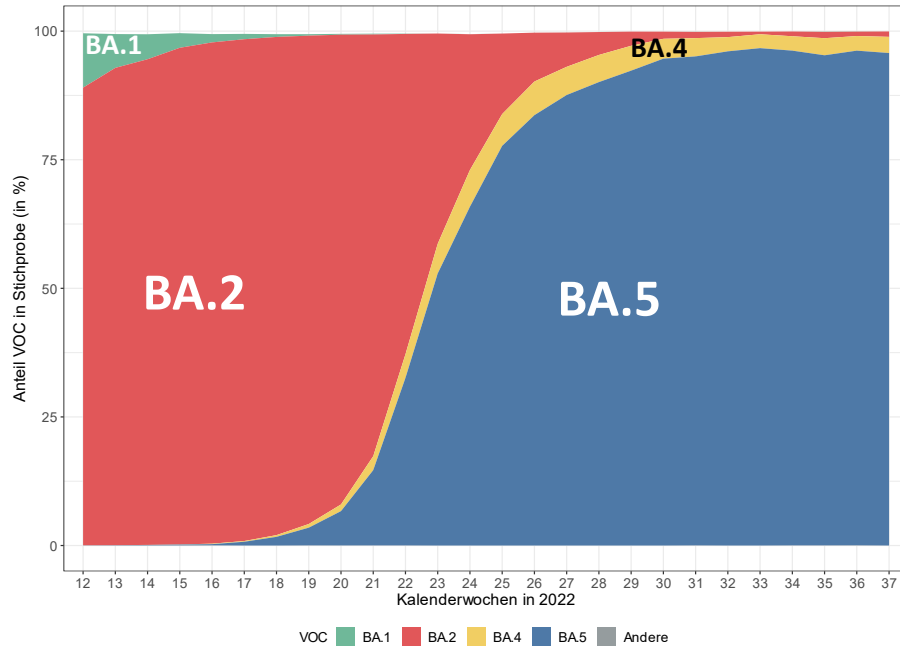
[https://www.rki.de/DE/Content/InfAZ/N/Neuartiges\\_Coronavirus/DESH/DESH.html](https://www.rki.de/DE/Content/InfAZ/N/Neuartiges_Coronavirus/DESH/DESH.html)



# Percentage of randomly sequenced genomes among SARS-CoV-2-(+ve) samples per week



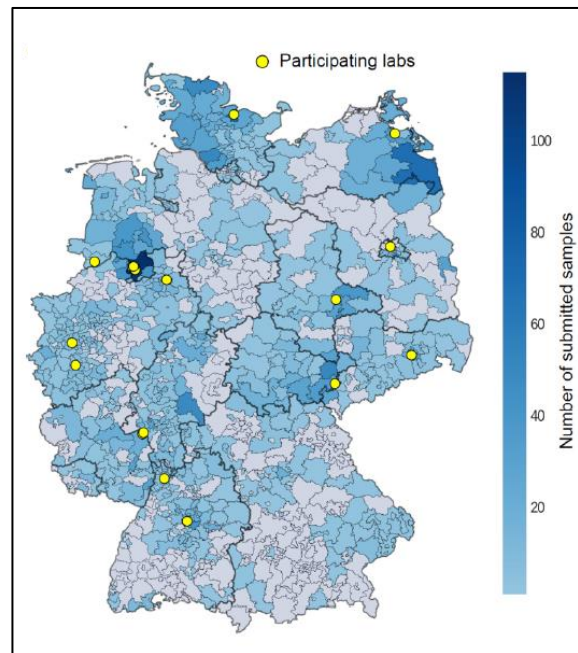
# Weekly reporting on the SARS-CoV-2 genomes via RKI website and submission to GISAID and ENA



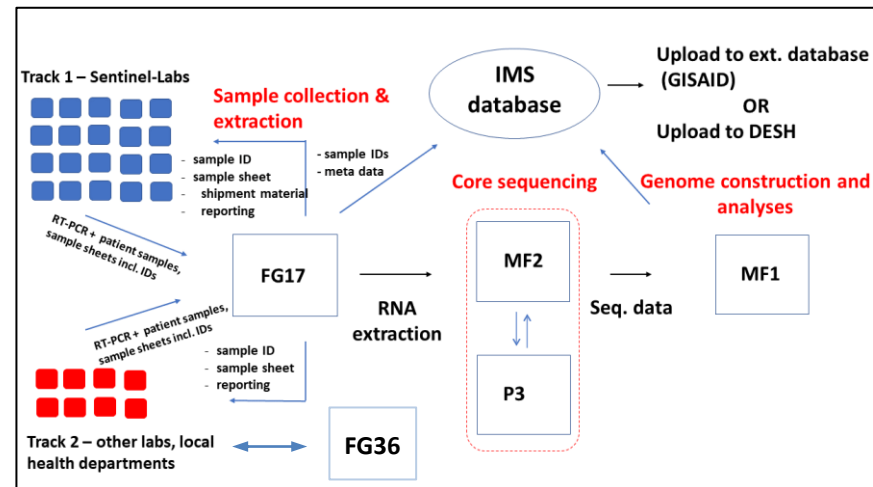
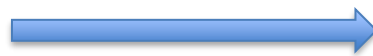
[https://www.rki.de/DE/Content/InfAZ/N/Neuartiges\\_Coronavirus/Situationsberichte/Gesamt.html?nn=2386228](https://www.rki.de/DE/Content/InfAZ/N/Neuartiges_Coronavirus/Situationsberichte/Gesamt.html?nn=2386228)



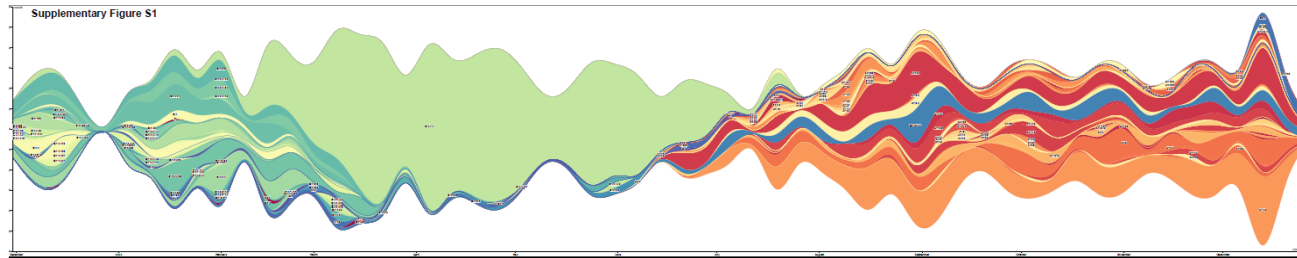
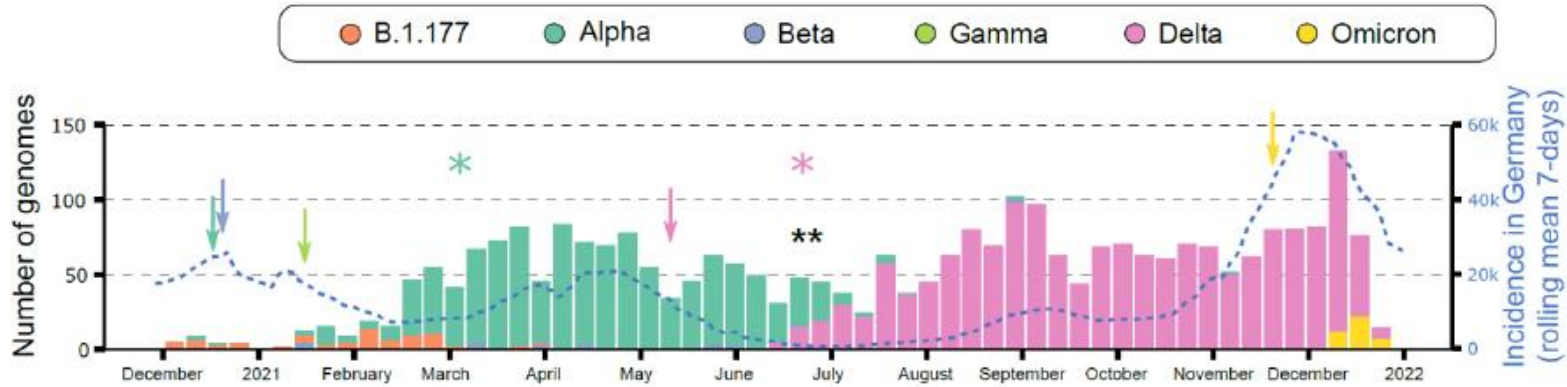
# IMS-SC2 laboratory network for surveillance of circulating SARS-CoV-2 coordinated by RKI (16 labs, 10 states)



Weekly shipment  
of RT-PCR (+)  
samples  
(native/denatured)



Oh et al., Clin Infect Dis. 2022 ,75; doi: 10.1093/cid/ciac399



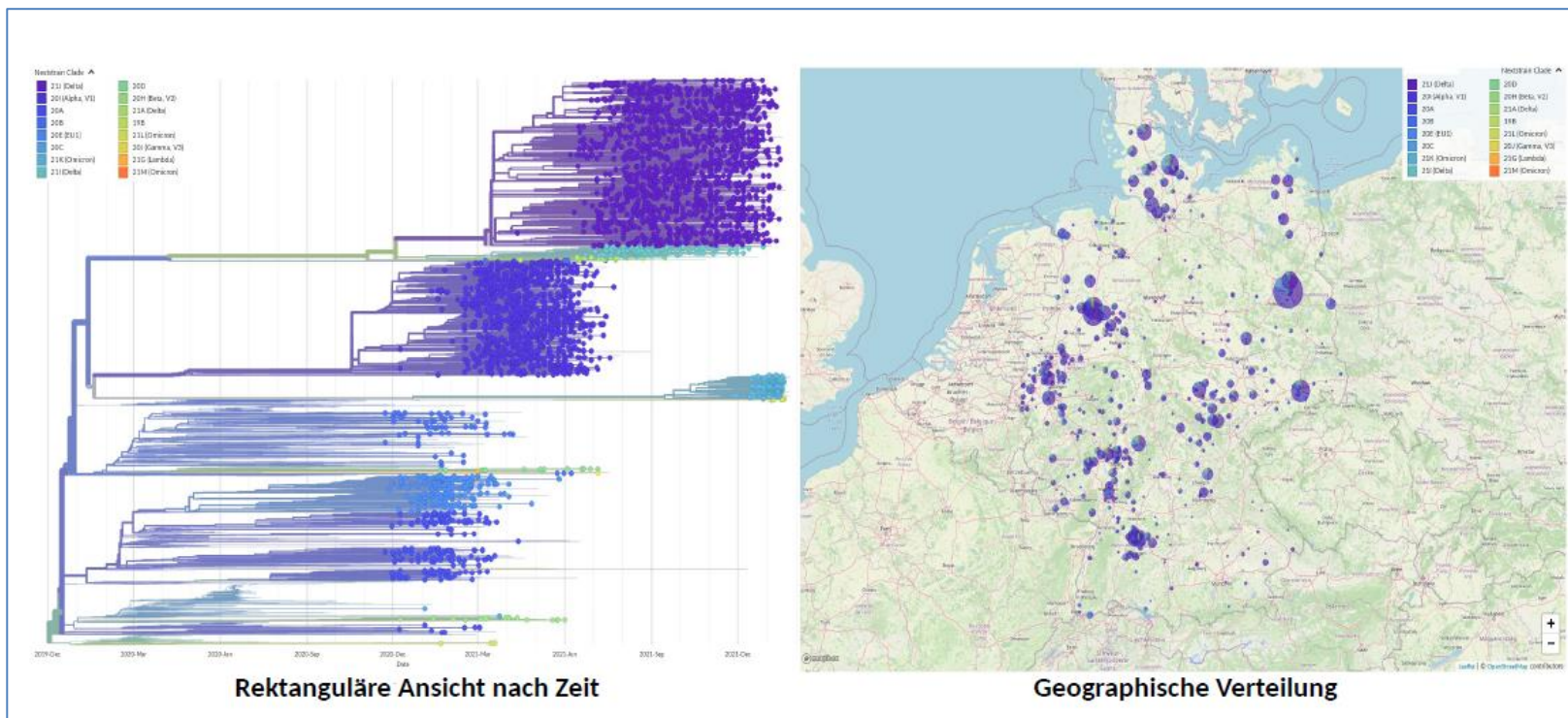
**Detection of > 90 lineages/sublineages in 2021**

01.12. 2020 – 31.12. 2021: **3282** random samples

Oh et al., Clin Infect Dis. 2022 ,75; doi: 10.1093/cid/ciac399



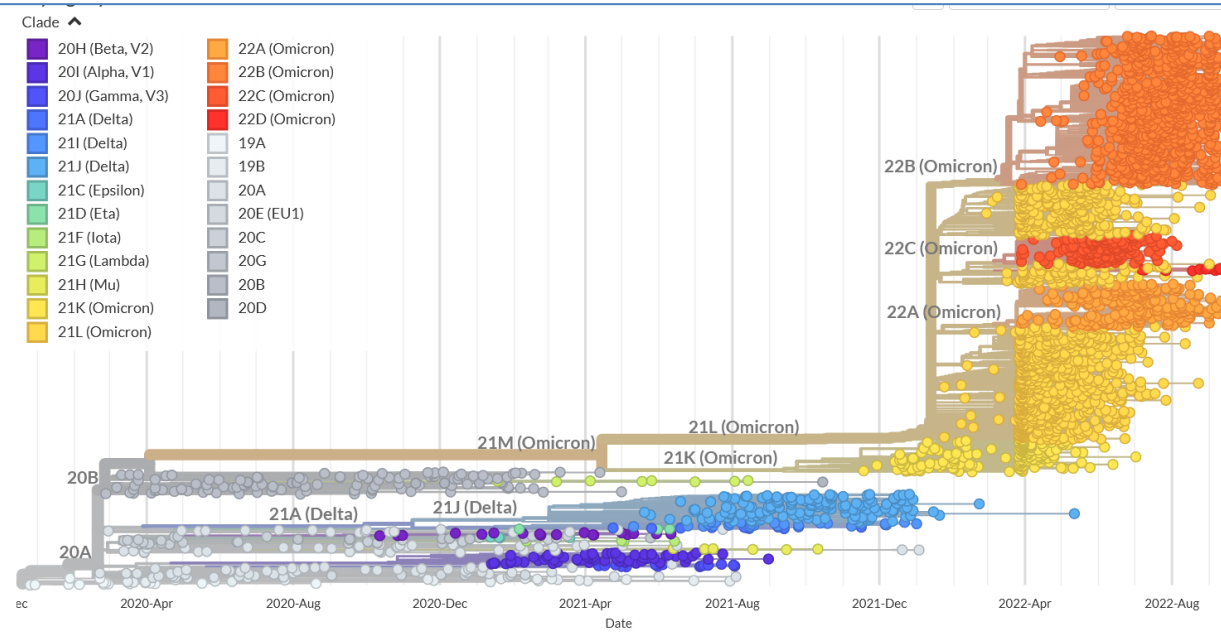
# Phylogeny and sampling sites of genomes constructed within the IMS-SC2 laboratory network (2021)



01.12. 2020 – 31.12. 2021: **3282** random samples

# SARS-CoV-2: Genetic diversity

Built with [nextstrain/ncov](#). Maintained by the [Nextstrain team](#). Enabled by data from [GISAID](#).



## SARS-CoV-2 genomes in GISAID database (20.09.2022):

- **11.945.214 (Global)**
- **765.525 (Germany)**

Alpha: 86.872

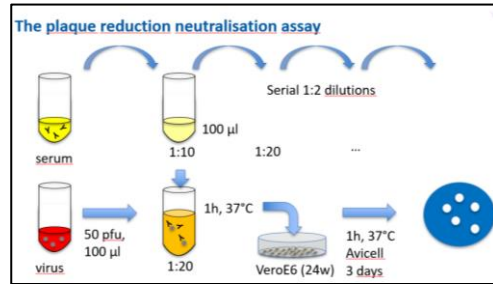
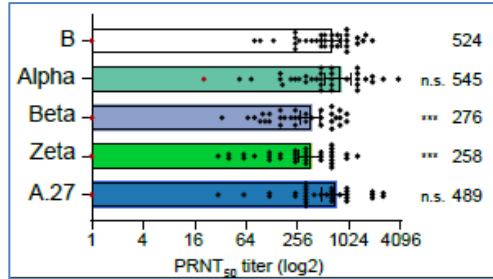
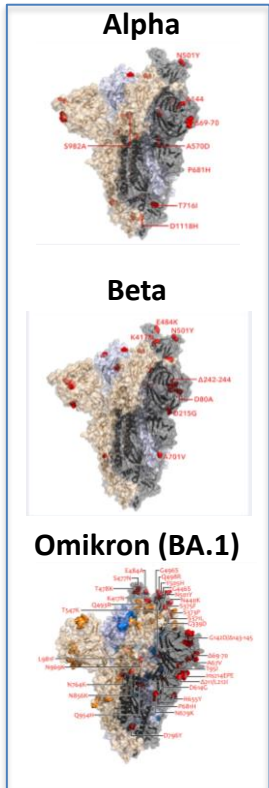
Delta: 208.105

Omicron: 437.486

## Index virus

[https://nextstrain.org/ncov/gisaid/global?c=pango\\_lineage&l=scatter&scatterY=S1\\_mutations&tl=S1\\_mutations](https://nextstrain.org/ncov/gisaid/global?c=pango_lineage&l=scatter&scatterY=S1_mutations&tl=S1_mutations)

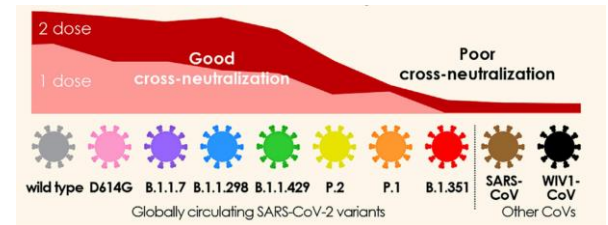
# IMS-SC2 network samples are a source for isolation of SARS-CoV-2 variants and phenotypic analysis



Hein et al., 2021; Allergy; doi: 10.1111/all.15189

## Limitations:

- Rare variants are unlikely to be sampled
- Not all diagnostic labs provide native samples suitable for virus growth
- Shortage of staff trained for BSL-3 work





## Summary and outlook

Non-sentinel laboratory networks can complement sentinel surveillance efforts for SARS-CoV-2 in a meaningful manner by:

- Increasing the number of viral genomes available for WGS and SNP PCR analysis
- Enabling NGS specialists and bioinformaticians to get hands on experiences for genome reconstruction and quality assessments (primer sets,
- Providing a source for native patient samples suitable for virus isolation and characterization





## Summary and outlook

- What are the challenges and limitations that countries are facing in terms of phenotypic analysis? E.g. when new drugs are introduced
  - lab capacity (BSL3)
  - personal resources (establishment of a NCC in preparation)
  - increase of bureaucracy during pandemic (meetings, meetings, meetings, meetings ... - also by ECDC and WHO - and no time to work)
- Linkages to genomic surveillance
  - genomic surveillance is established
  - insufficient phenotypic data (markers for resistance, virulence, escape from neutralization) to be linked with genotypic data
- Frequency, representativeness and coverage of testing for phenotypic virus characterisation
  - currently at low level; it is intended to perform it similar to influenza virus phenotypic testing in future

# Thank you !



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