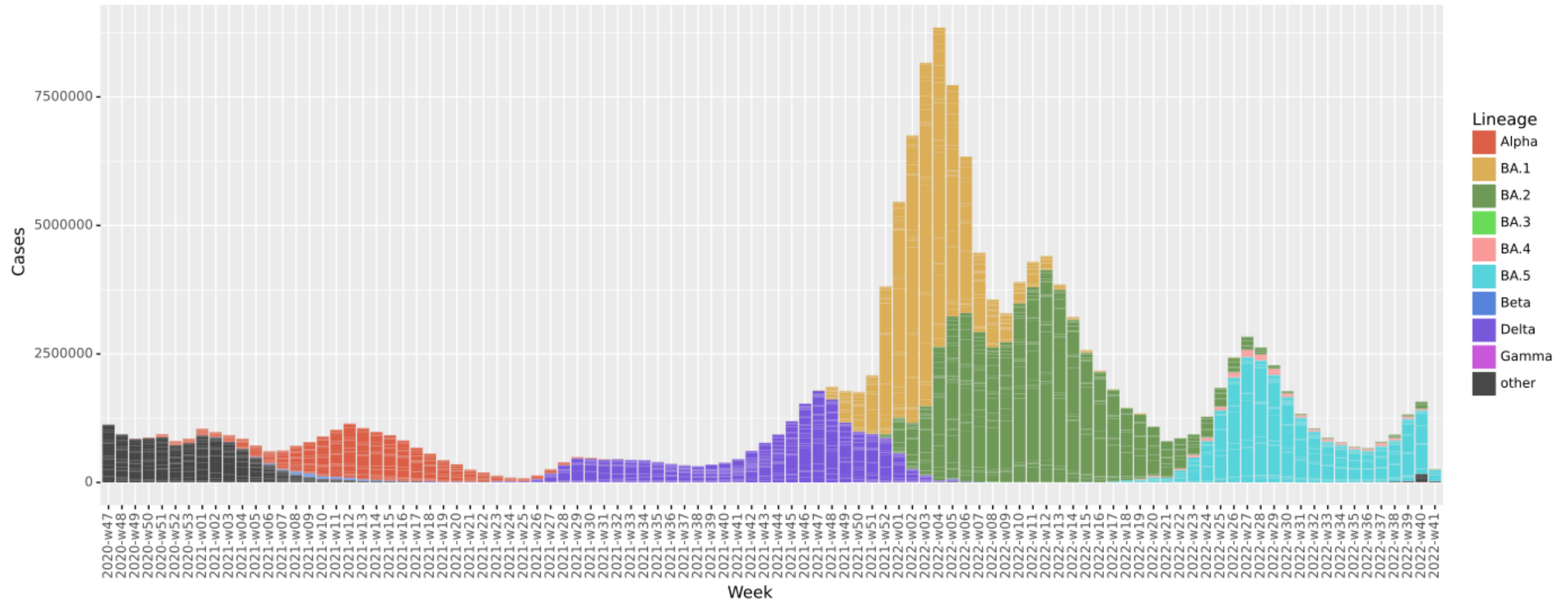


# SARS-CoV-2 variants: current situation and future scenarios

Luca Freschi, ECDC  
20 October 2022

# Current situation

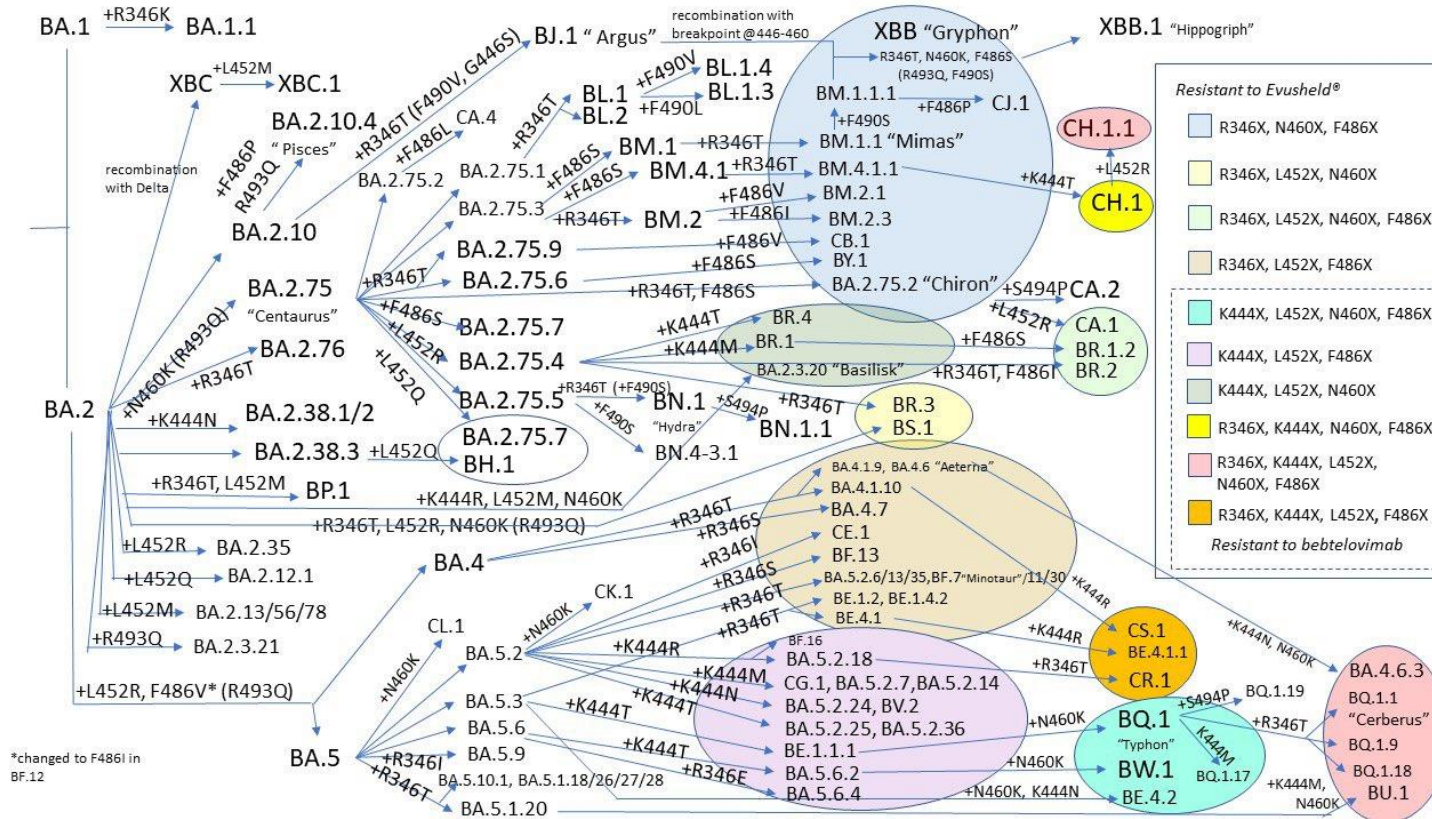
EU/EEA



Breakdown of SARS-CoV-2 cases by variant in the EU/EEA

# Current situation: characteristics

**1. Diversification** – a lot of new Omicron-derived lineages are emerging (parental lineages are mostly BA.2, BA.4 and BA.5).



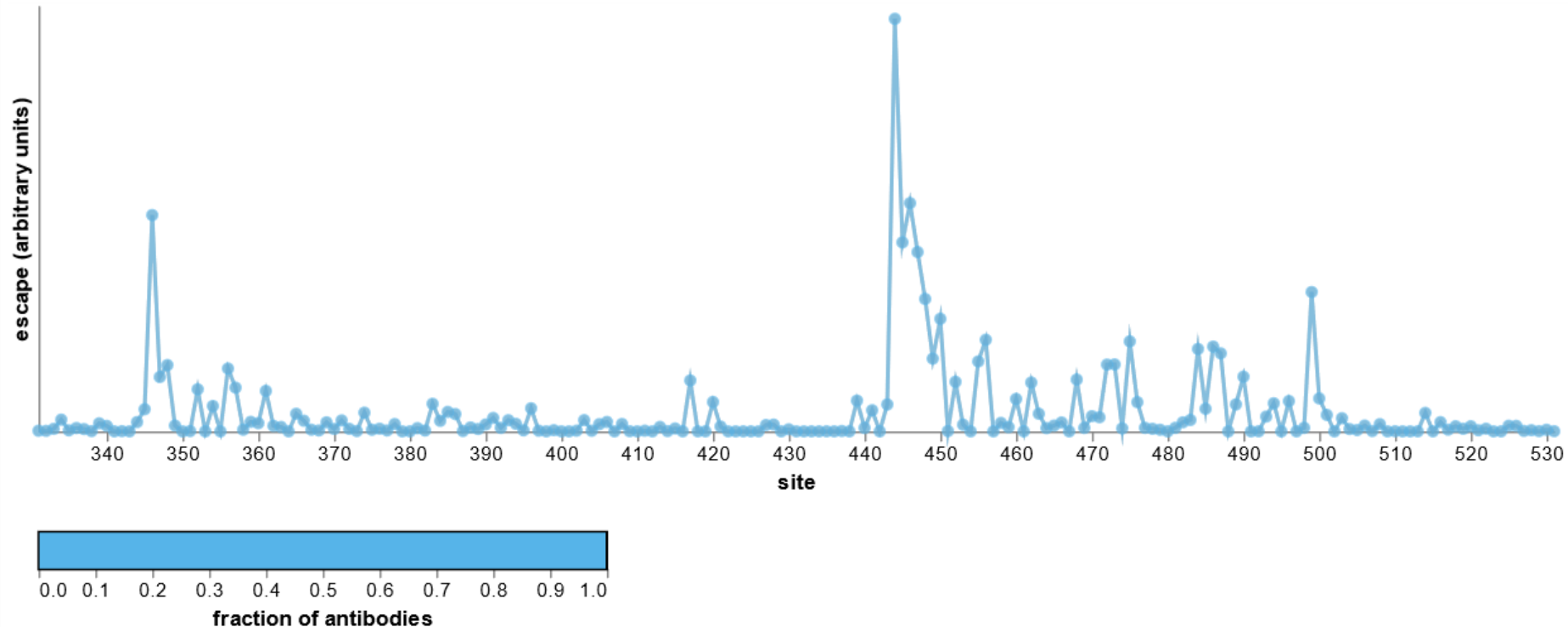
\*changed to F486I in BF.12





# Current situation: characteristics

- Such mutations have been shown to contribute to confer immune evasion properties.



# Current situation: emerging lineages

pango_lineage	description	major_omicron_ancestor	346	356	444	452	460	486	490
BN.1	BA.2.75 sub-lineage	BA.2	●	●			●		●
BN.2	BA.2.75 sub-lineage	BA.2		●			●		●
● XBB	BA.2.10.1.1 x BA.2.75.3.1.1.1	BA.2	●				●	●	●
● XBB.1	XBB sub-lineage	BA.2	●				●	●	●
CA.1	BA.2.75.2 sub-lineage	BA.2	●			●	●	●	
BR.2	BA.2.75.4 sub-lineage	BA.2	●			●	●	●	
BA.2.3.20	BA.2 sub-lineage	BA.2			●	●	●		
● BQ.1	BA.5.3 sub-lineage	BA.5			●	●	●	●	
● BQ.1.1	BA.5.3 sub-lineage	BA.5	●		●	●	●	●	
BU.1	BA.5.2 sub-lineage	BA.5			●	●	●	●	
BW.1	BA.5.6 sub-lineage	BA.5			●	●	●	●	

# BQ.1.1 and XBB

## BQ.1.1 (BA.5 subvariant)

- Substitutions on top of BA.5 within the Spike: **R346T, K444T, N460K**
- 747 sequences from 29 countries
- No severe disease reported so far

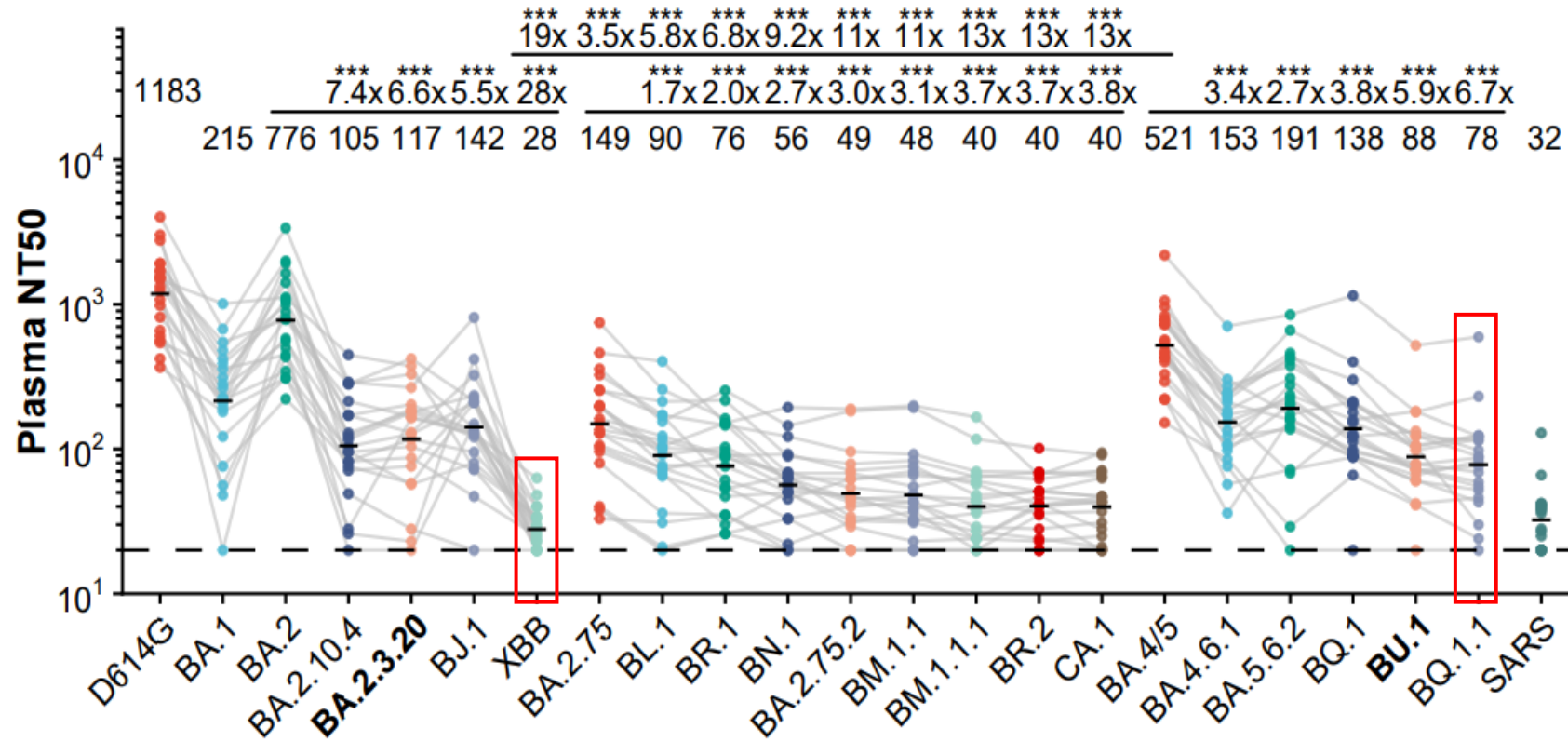
## XBB (BA.2.10.1 and BA.2.75 recombinant)

- Substitutions on top of BA.2 within the Spike: **V83A, Y144-, H146Q, Q183E, V213E, G252V, G339H, R346T, L368I, V445P, G446S, N460K, F486S, F490S**
- 827 sequences from 26 countries (as of 17 Oct 22)
- No severe disease reported so far

Likely responsible for the recent increase in cases observed in Singapore.

# Emerging lineages: neutralization data

**f CoronaVac × 3 → BA.5 infection**





# Emerging lineages: Ab

COV2-2196+COV2-2130 (Evusheld - tixagevimab and cilgavimab)

LY-CoV1404 (bebtelovimab)

SA55+SA58 is a pair of broad NABs isolated from vaccinated SARS convalescents

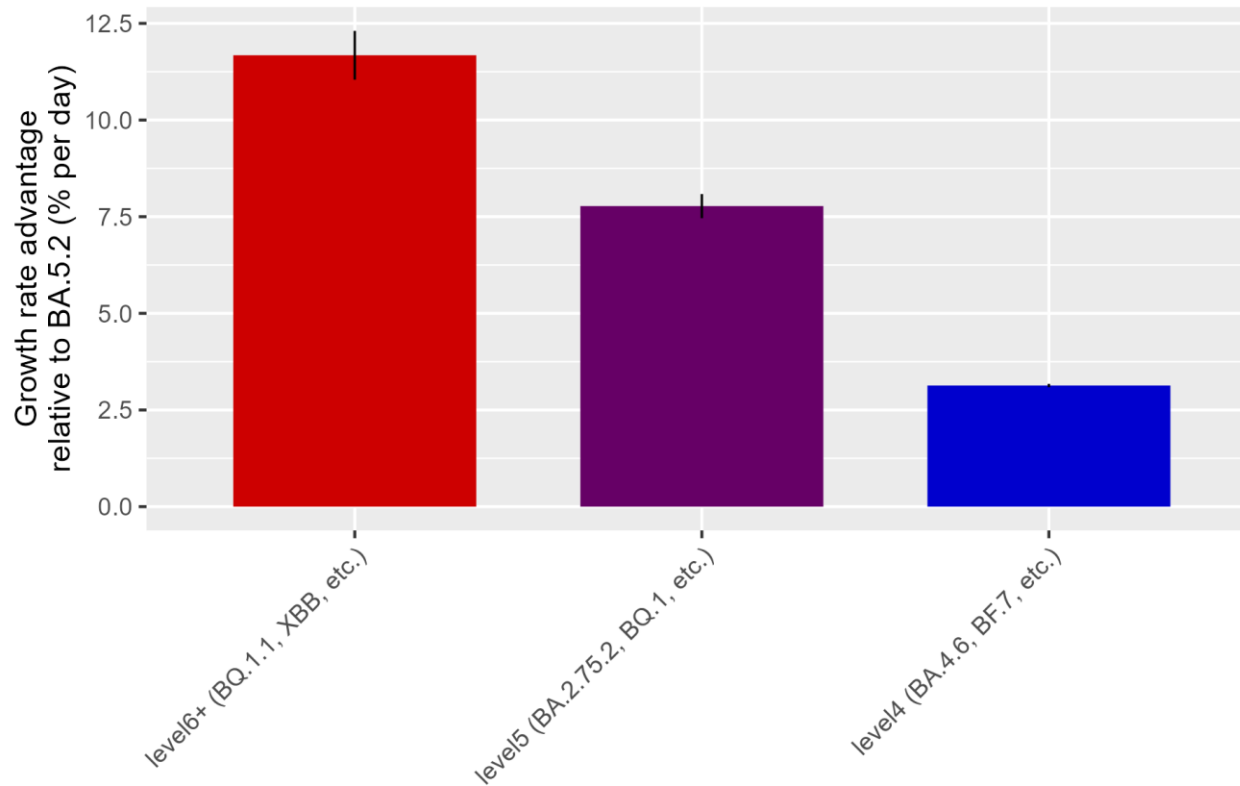
Pango lineages	REGN 10933	REGN 10987	REGN10933 +10987	COV2-2196	COV2-2130	COV2-2196+2130	BRII-196	BRII-198	BRII-196+198	S309	DXP-604	LY-CoV 1404	SA58	SA55	SA55+SA58	Additional RBD mutations
BA.2	*	590	821	4312	6.3	8.2	8530	8990	8610	852	219	0.9	5.1	7.2	7.8	
BA.2.3.20	121	*	199	15	*	26	14	*	24	897	181	9.7	20	4.6	7.8	K444R+N450D+L452M+N460K+R493Q
BA.2.10.4	*	*	*	*	289	501	2109	7990	3984	706	6348	1.3	4.3	4.9	5.0	G446S+F486P+R493Q+S494P
BJ.1	*	*	*	3076	*	5985	7609	*	*	709	166	*	8163	3.7	8.6	D339H+R346T+L368I+V445P+G446S+V483A+F490V
XBB	*	*	*	*	*	*	*	*	*	963	*	*	8805	5.3	9.8	D339H+R346T+L368I+V445P+G446S+N460K+F486S+F490S+R493Q
BA.2.75	278	*	410	119	352	121	1730	6622	3861	672	5920	2.2	246	4.3	9.6	
BL.1	260	*	511	93	*	174	1251	*	3075	508	7193	2.8	7975	6.3	10	R346T
BR.1	319	*	679	117	*	170	1992	*	3160	564	6689	*	1616	5.9	9.7	L452R+K444M
BN.2.1	390	*	701	59	303	109	4101	*	8444	6979	8901	1.7	4960	5.7	9.4	K356T+F490S
BN.1	344	*	599	70	*	166	3683	*	7791	*	6012	3.3	8295	4.9	9.0	R346T+K356T+F490S
BA.2.75.2	*	*	*	*	*	*	*	*	*	852	*	3.0	6922	5.9	9.7	R346T+F486S
BM.1.1	*	*	*	*	*	*	*	*	*	879	*	2.3	8823	5.2	8.9	R346T+F486S
BM.1.1.1	*	*	*	*	*	*	*	*	*	956	*	1.9	8082	4.8	10.5	R346T+F486S+F490S
BR.2	*	*	*	*	*	*	*	*	*	921	*	2.6	7263	4.7	10.5	R346T+L452R+F486I
CA.1	*	*	*	*	*	*	*	*	*	897	*	3.2	6927	6.0	11.5	R346T+L452R+F486S
BA.4/5	*	520	709	*	23	40	7124	*	*	1055	6264	0.8	3.9	5.0	4.5	
BA.4.6.1	*	2338	5402	*	*	*	4763	*	7809	4456	4634	1.2	50	4.8	9.9	R346T
BA.5.6.2	*	*	*	*	*	*	4636	*	7883	1408	5892	1662	58	5.1	8.9	K444T
BQ.1	*	*	*	*	*	*	*	*	*	1709	*	1905	44	6.6	9.2	K444T+N460K
BU.1	*	*	*	*	*	*	*	*	*	1082	*	26	56	5.3	10.5	K444M+N460K
BQ.1.1	*	*	*	*	*	*	*	*	*	5581	*	*	900	5.9	10.3	R346T+K444T+N460K

Pseudovirus IC50 (ng/mL) <100 100~1,000 >1,000

# Emerging lineages: growth advantages

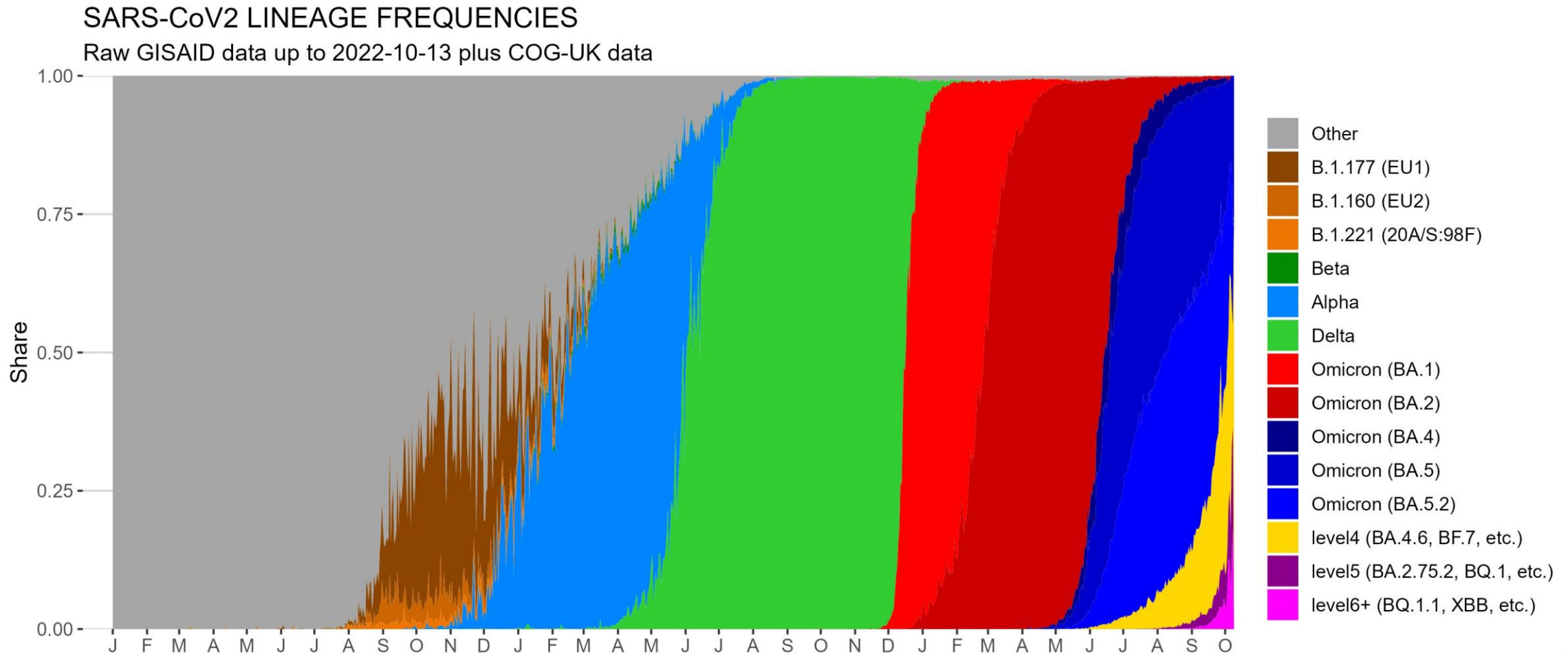
## GROWTH RATE ADVANTAGE OF SARS-CoV2 VARIANTS

based on multinomial fit variant  $\sim ns(\text{date}, df=2) + ns(\text{date}, df=2):continent + country$   
GISAID & COG-UK data, using data from countries with  $\geq 50$  level5 or level6+ variants



@TWenseleers  
2022-10-13

# Lineage proportions in the EU/EEA

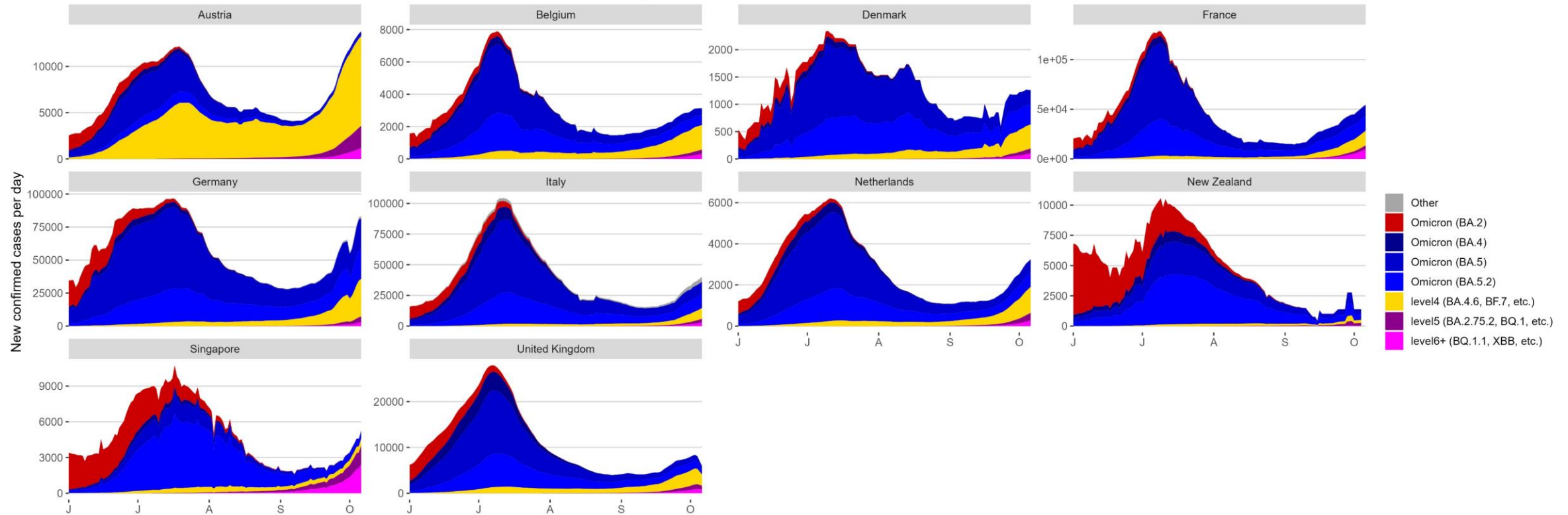


@TWenseleers  
 2022-10-13

# Current situation: characteristics

## NEW CONFIRMED SARS-CoV2 CASES BY VARIANT

case data accessed via the covidregionaldata package  
 lineage frequencies based on GISAID data up to 2022-10-13 plus COG-UK data  
 and multinomial fit variant  $\sim ns(\text{date}, df=2) + ns(\text{date}, df=2): \text{continent} + \text{country}$ ,  
 selected countries with  $\geq 50$  level5 or level6+ variant sequences shown

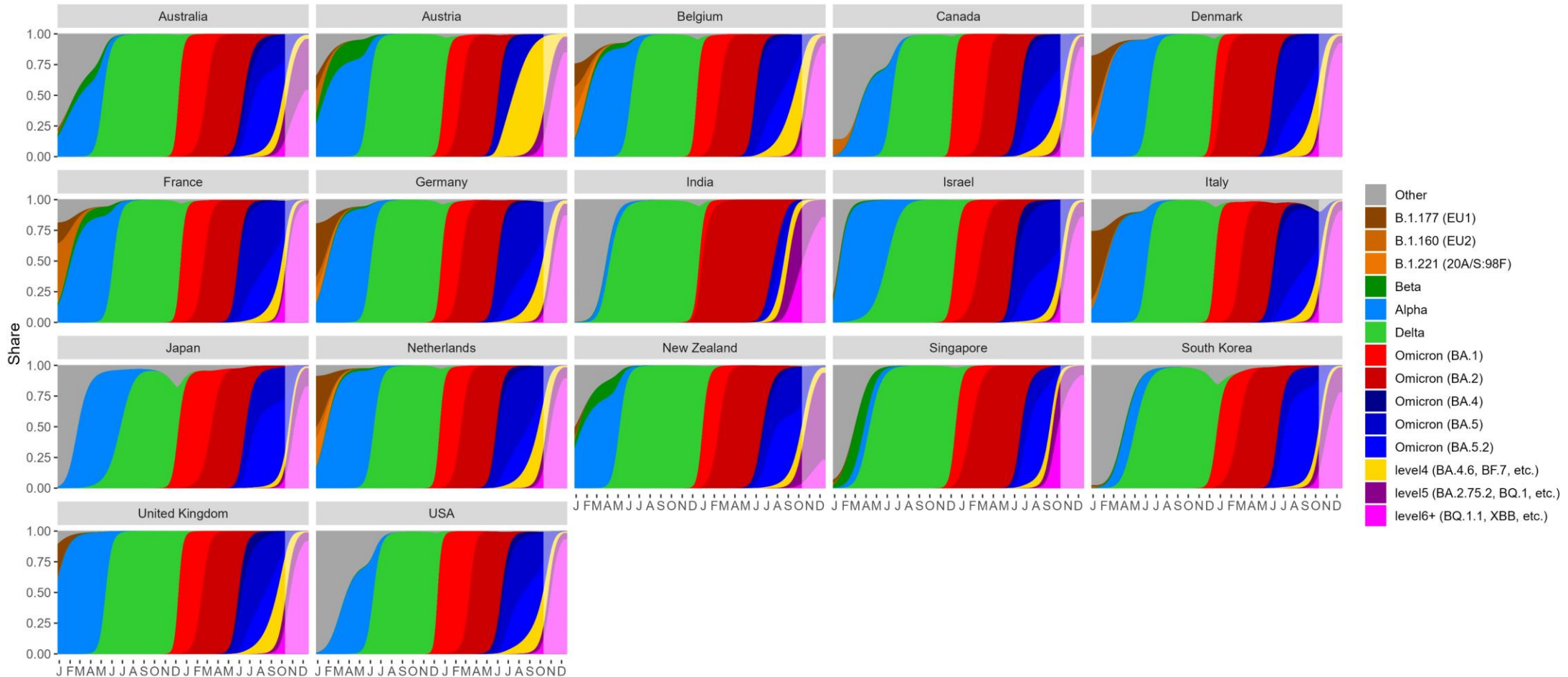




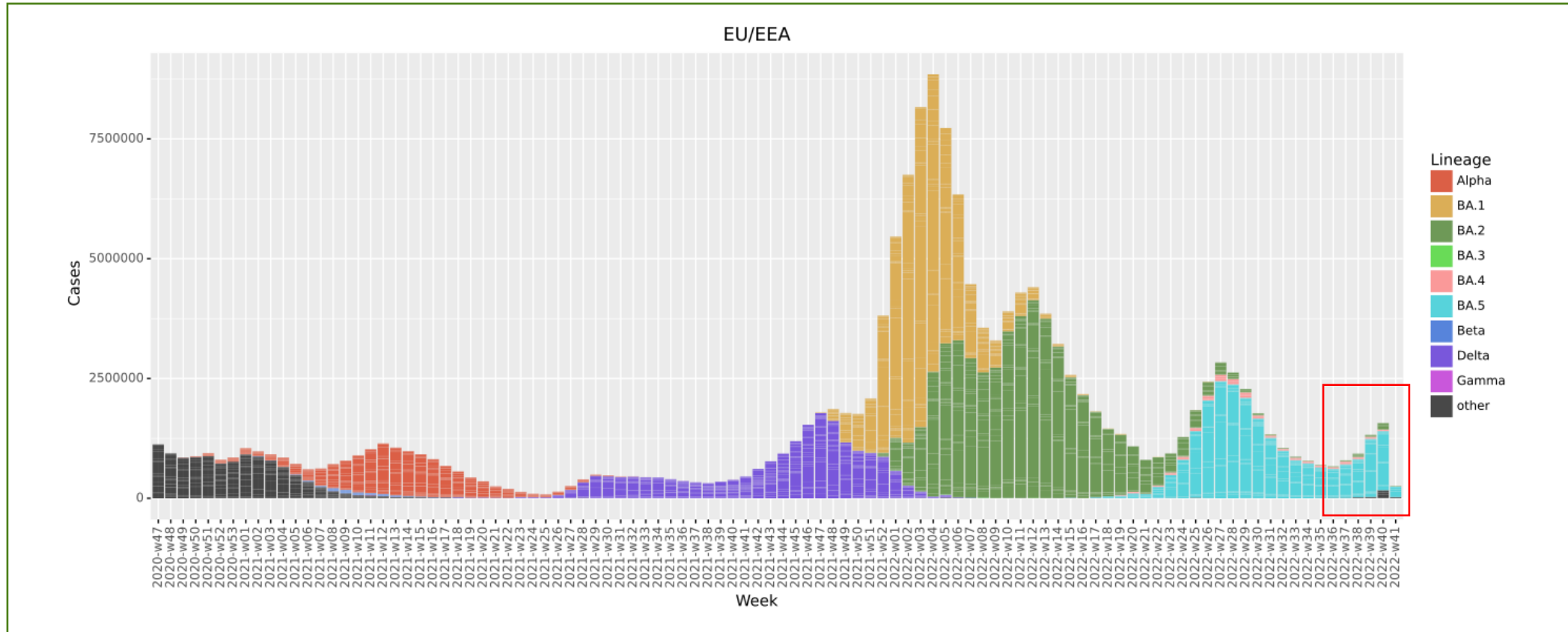
# Current situation: characteristics

## SARS-CoV2 LINEAGE FREQUENCIES

GISAID data up to 2022-10-13 plus COG-UK data, multinomial fit variant  $\sim ns(\text{date}, df=2) + ns(\text{date}, df=2): \text{continent} + \text{country}$ , all countries with  $\geq 50$  level5 or level6+ variant sequences shown

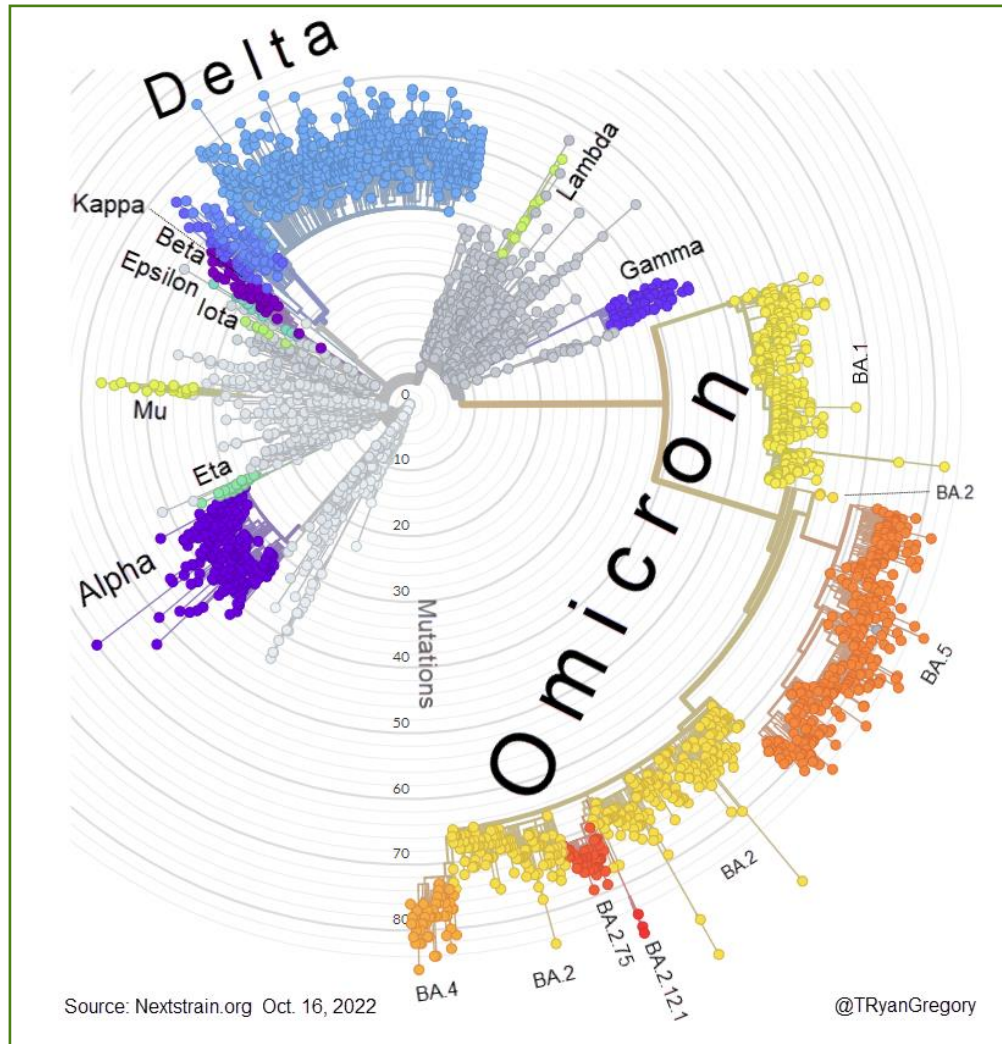


# Future scenarios



So far we have always observed a pattern where a new variant sweeps through every few months. Whether that variant will rise to the level of a variant of concern remains an open question.

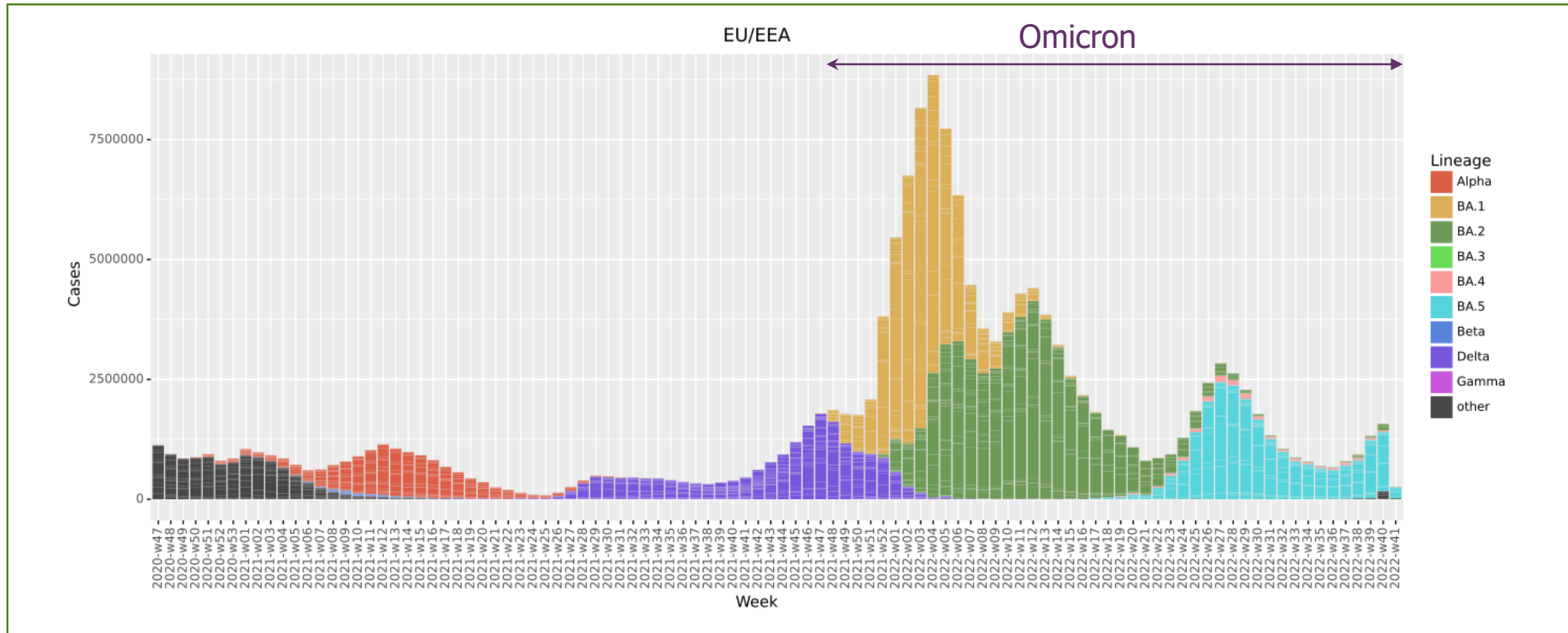
# Future scenarios



SARS-CoV-2 evolutionary path remains unclear.

So far new VOCs have not evolved from the dominant preceding ones, but rather they have emerged from separate lineages.

# Future scenarios

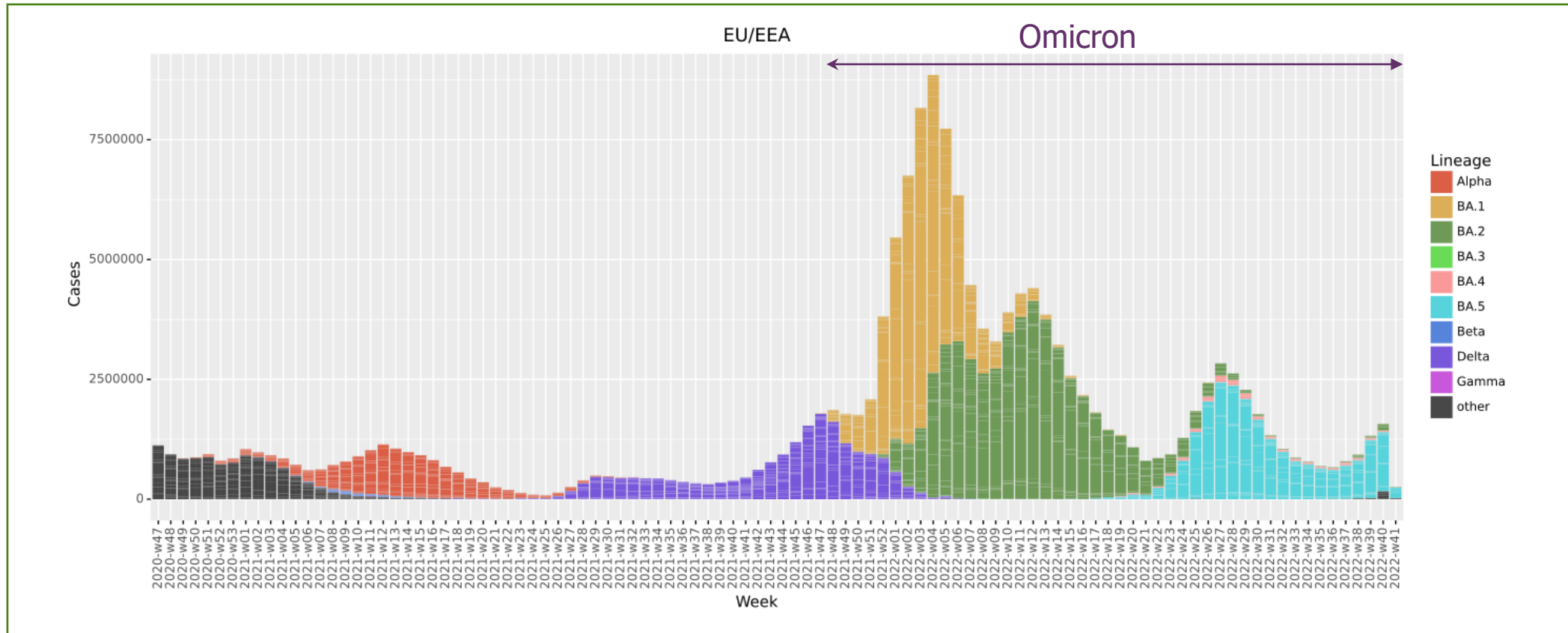


Omicron has dominated the variant landscape for longer time than any other previous SARS-CoV-2 variant.

What is a VOC right now? A SARS-CoV-2 variant capable to produce a new wave, or should we should only look at changes in severity?



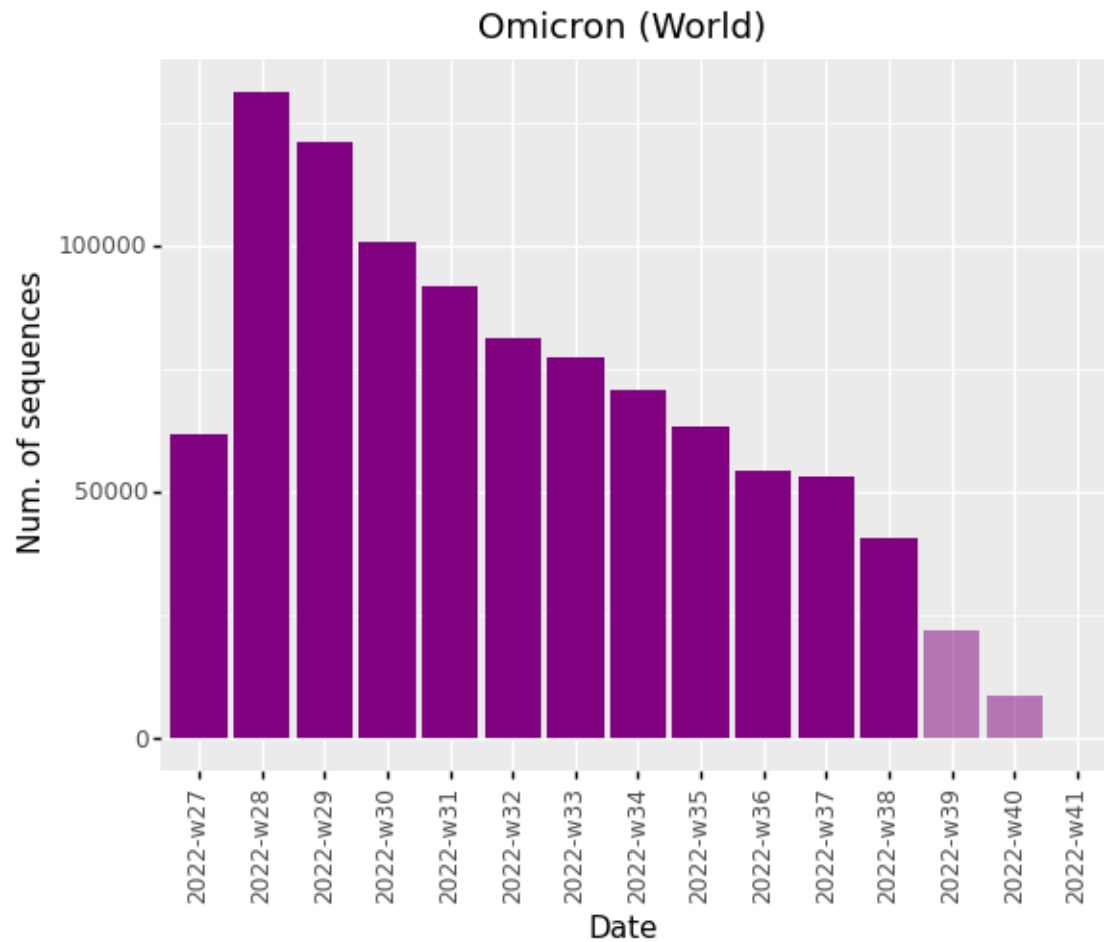
# Future scenarios



Omicron has dominated the variant landscape for longer time than any other previous SARS-CoV-2 variant.

Does this mean that the virus cannot make huge evolutionary jumps anymore? Probably not or at least it is too early to assume that!

# Future scenarios



In the near future, the testing policies will change.

It could take weeks longer to realize a new variant of concern is afoot due to the changes in surveillance strategies, with limited availability for testing and sequencing.

**Thank you!**