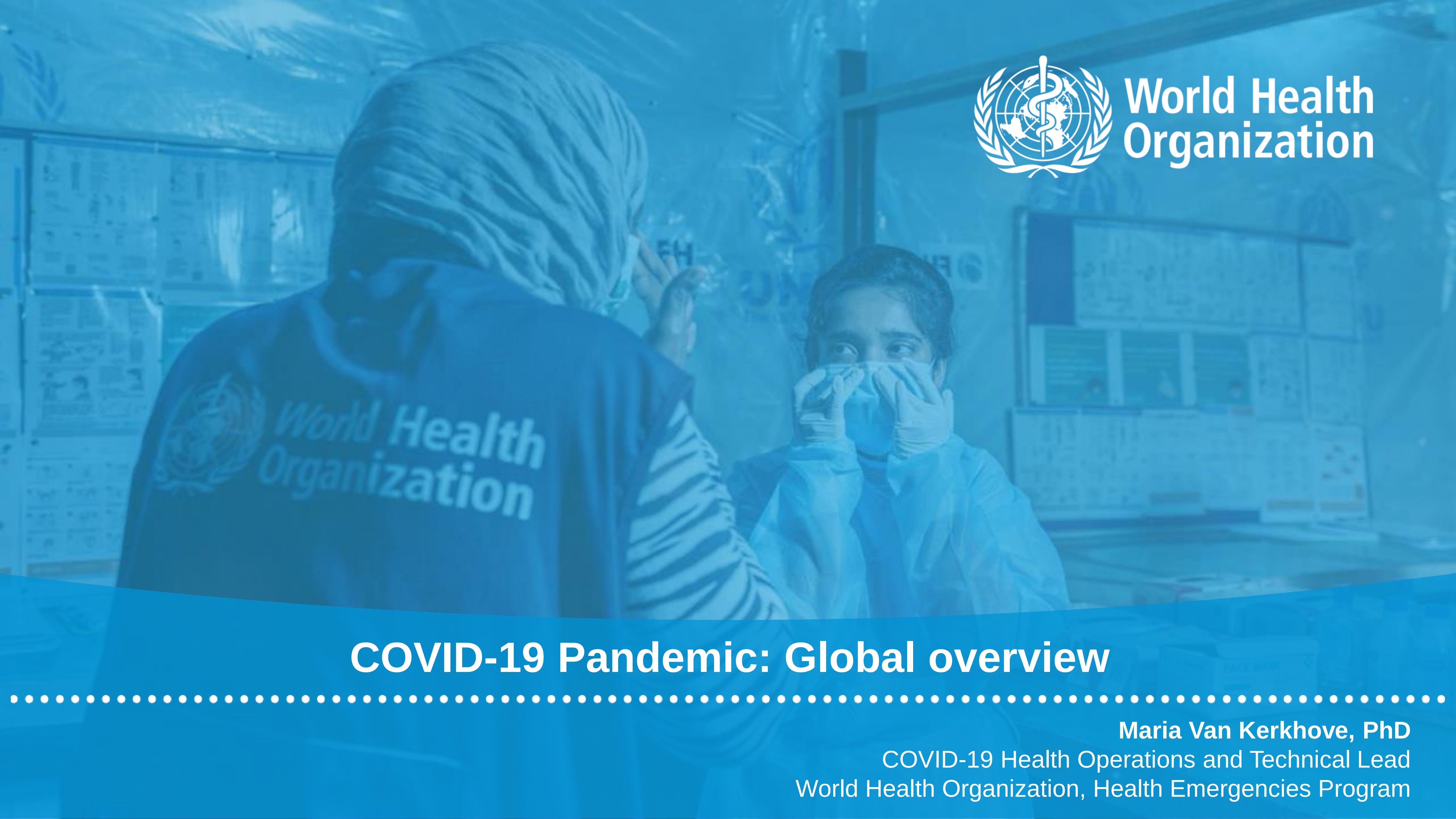
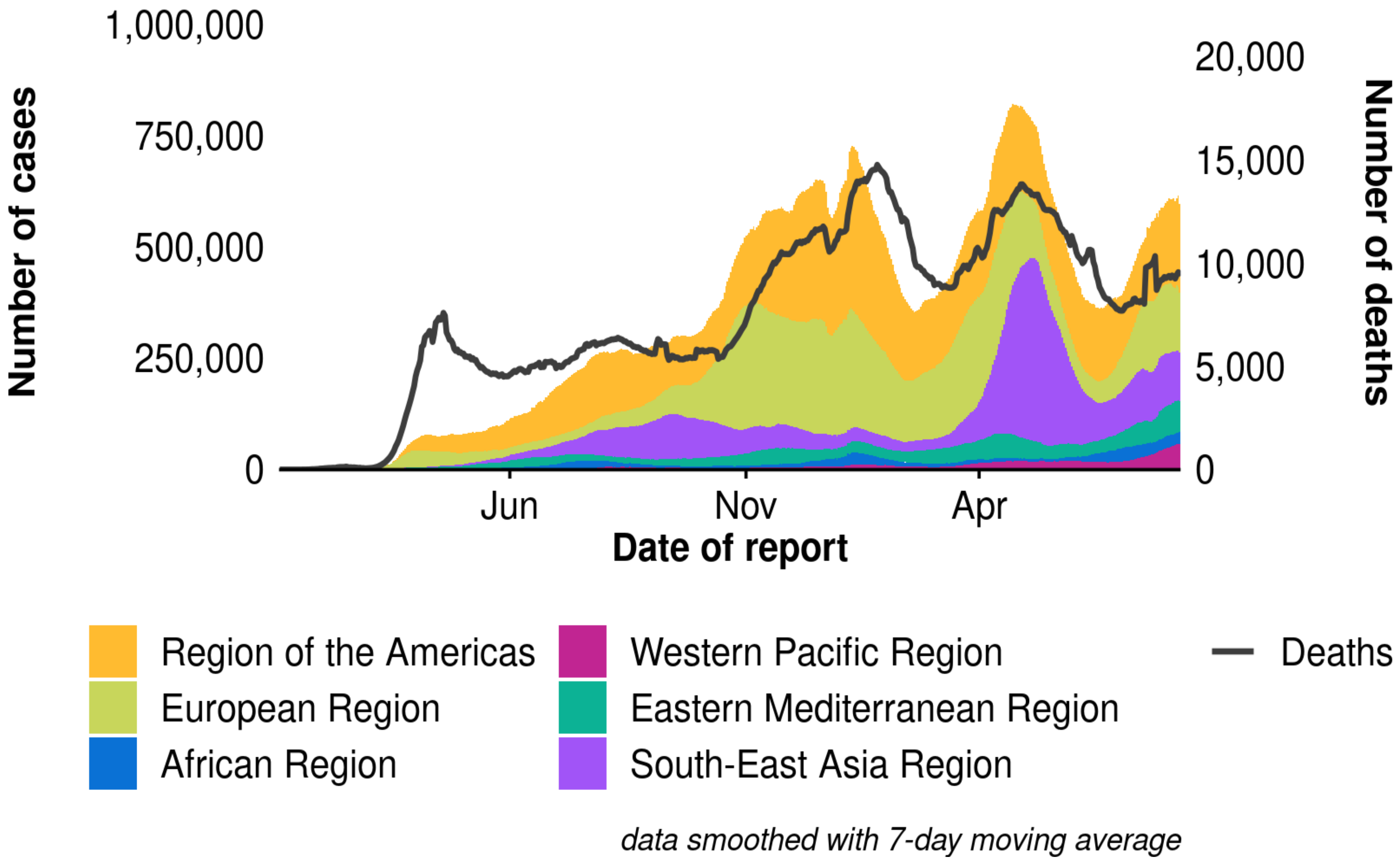


COVID-19 Pandemic: Global overview

Maria Van Kerkhove, PhD
COVID-19 Health Operations and Technical Lead
World Health Organization, Health Emergencies Program

Global epidemiological trends



data smoothed with 7-day moving average

Previous week

>4.2 million confirmed cases

>65,000 deaths

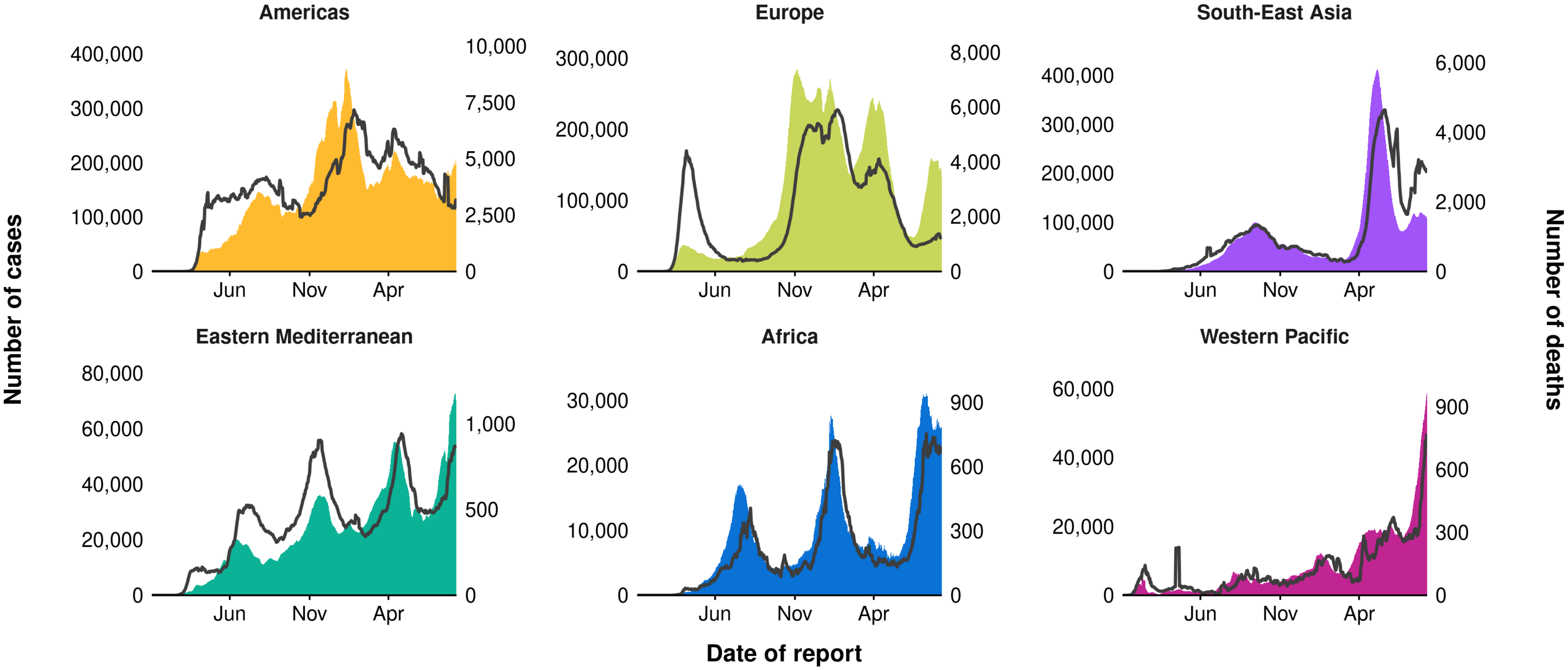
Cumulative as of 12 August 2021

204,644,849 confirmed cases

4,428,759 deaths

Regional epidemiological trends

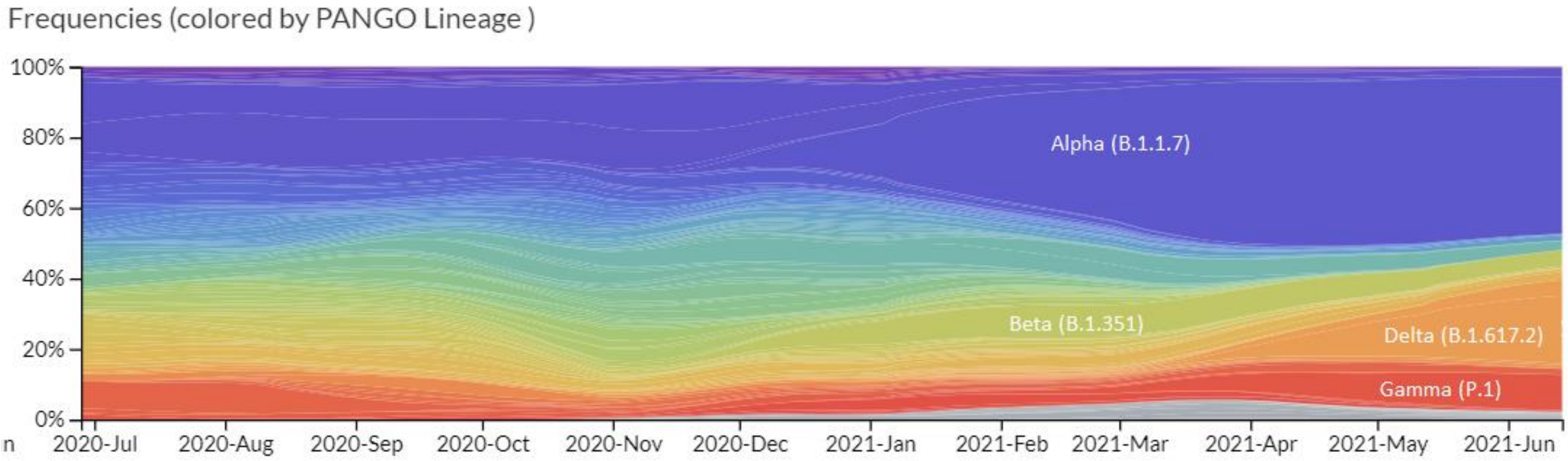
As of 9 August 2021 10h CET



Cases depicted by bars; deaths depicted by line. Data smoothed with 7-day moving average. Note different scales for y-axes.

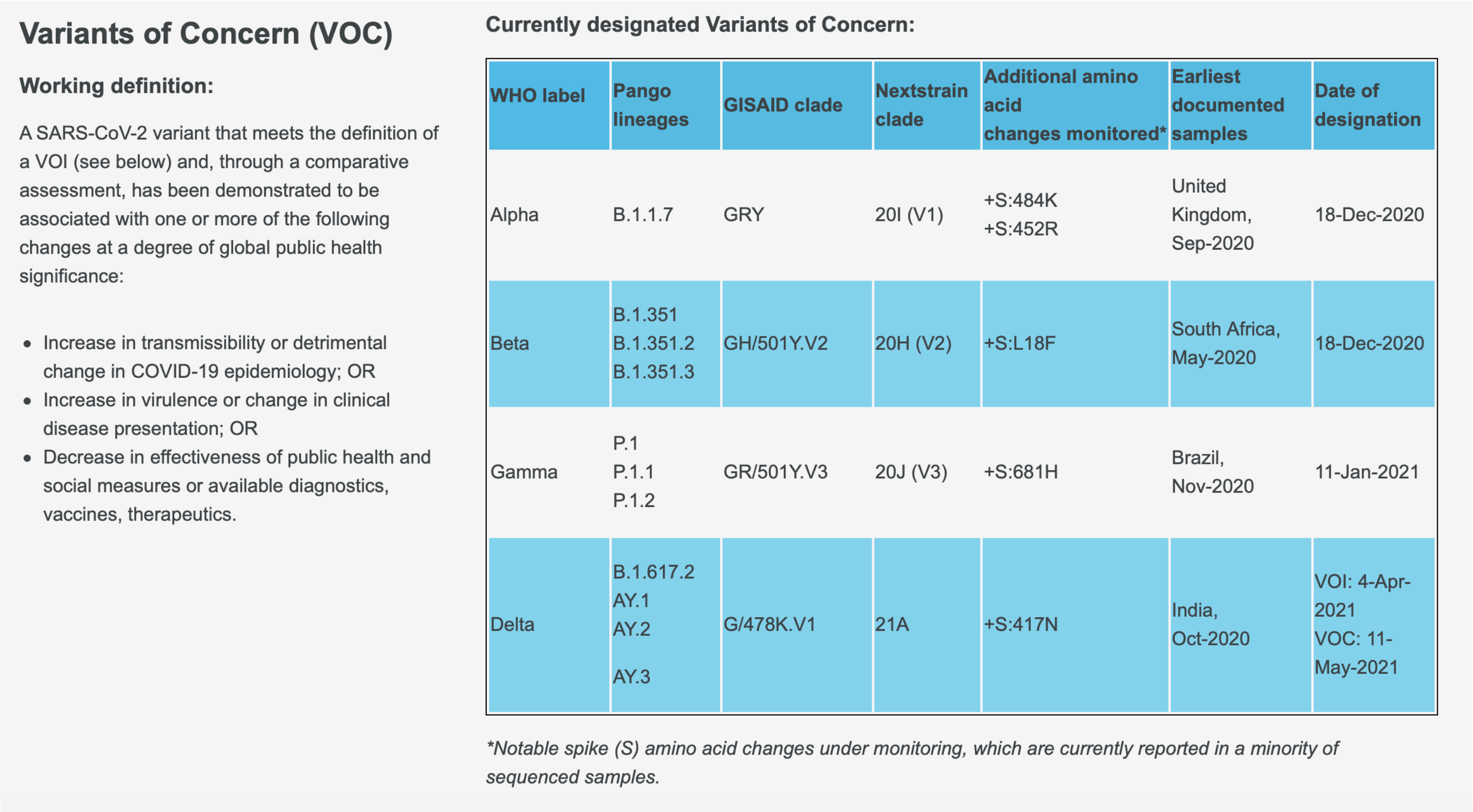
Continuous virus evolution

Genomic spread of SARS-CoV-2 variants of concern



Source: Nextstrain based on GISAID data nextstrain.org/ncov/global

Continuous virus evolution: Variants of Concern



Variants of Concern (VOC)

Working definition:

A SARS-CoV-2 variant that meets the definition of a VOI (see below) and, through a comparative assessment, has been demonstrated to be associated with one or more of the following changes at a degree of global public health significance:

- Increase in transmissibility or detrimental change in COVID-19 epidemiology; OR
- Increase in virulence or change in clinical disease presentation; OR
- Decrease in effectiveness of public health and social measures or available diagnostics, vaccines, therapeutics.

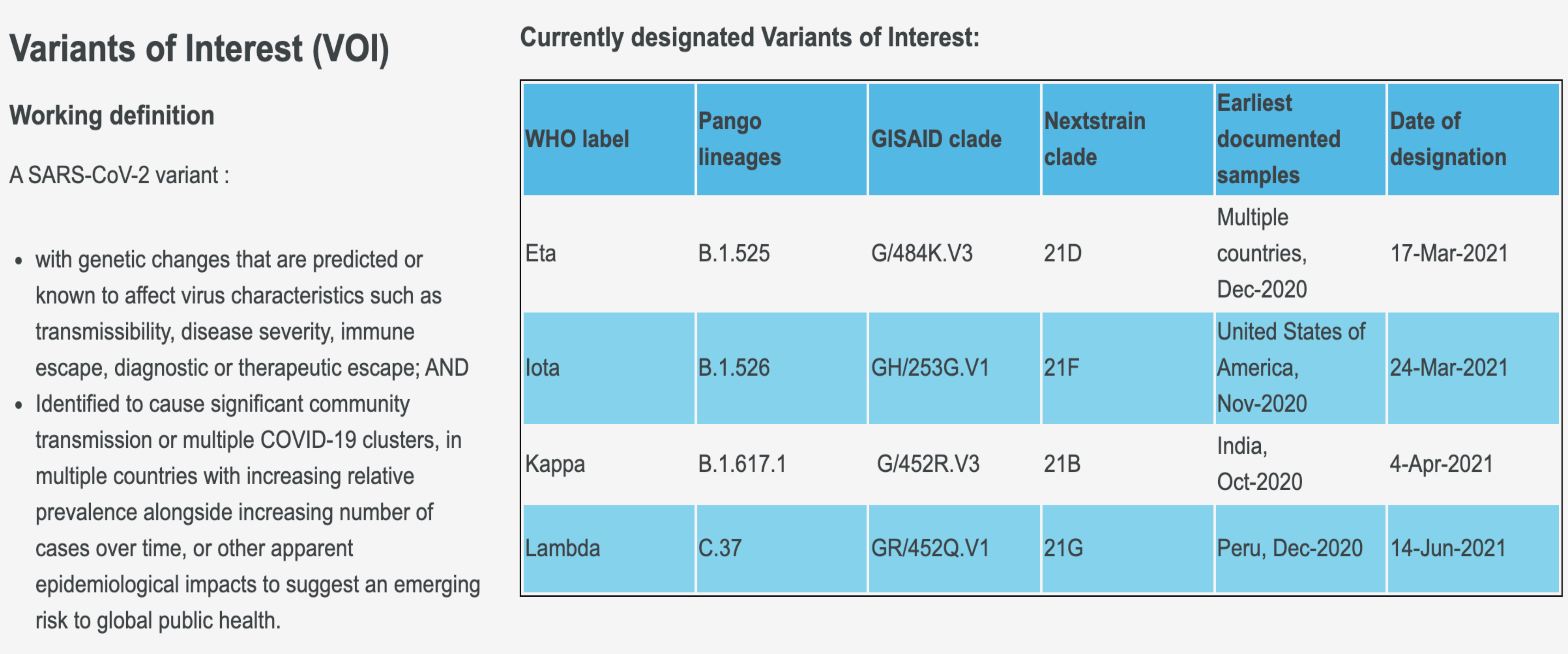
Currently designated Variants of Concern:

WHO label	Pango lineages	GISAID clade	Nextstrain clade	Additional amino acid changes monitored*	Earliest documented samples	Date of designation
Alpha	B.1.1.7	GRY	20I (V1)	+S:484K +S:452R	United Kingdom, Sep-2020	18-Dec-2020
Beta	B.1.351 B.1.351.2 B.1.351.3	GH/501Y.V2	20H (V2)	+S:L18F	South Africa, May-2020	18-Dec-2020
Gamma	P.1 P.1.1 P.1.2	GR/501Y.V3	20J (V3)	+S:681H	Brazil, Nov-2020	11-Jan-2021
Delta	B.1.617.2 AY.1 AY.2 AY.3	G/478K.V1	21A	+S:417N	India, Oct-2020	VOI: 4-Apr-2021 VOC: 11-May-2021

**Notable spike (S) amino acid changes under monitoring, which are currently reported in a minority of sequenced samples.*

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/

Continuous virus evolution: Variants of Interest



Variants of Interest (VOI)

Working definition

A SARS-CoV-2 variant :

- with genetic changes that are predicted or known to affect virus characteristics such as transmissibility, disease severity, immune escape, diagnostic or therapeutic escape; AND
- Identified to cause significant community transmission or multiple COVID-19 clusters, in multiple countries with increasing relative prevalence alongside increasing number of cases over time, or other apparent epidemiological impacts to suggest an emerging risk to global public health.

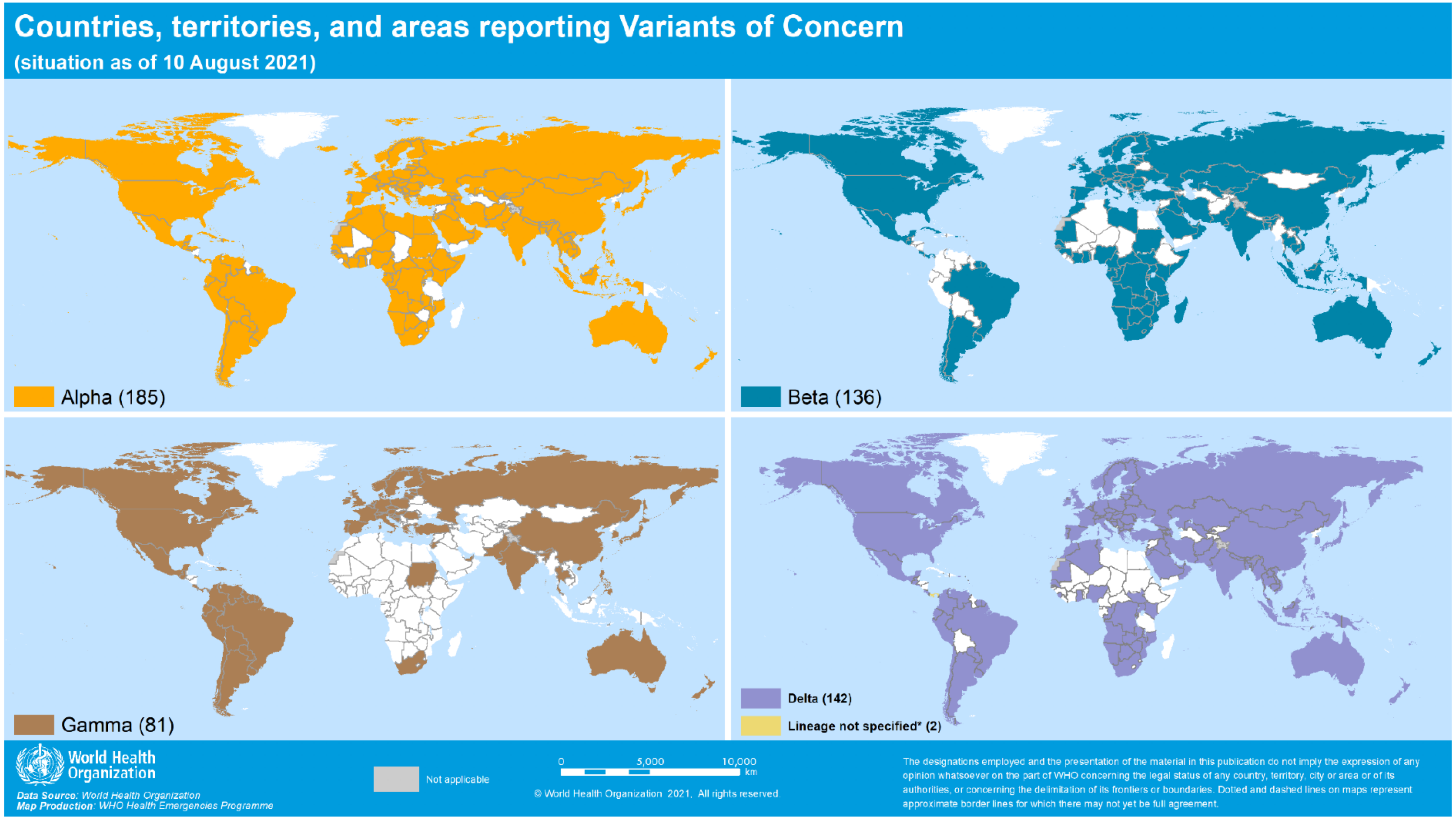
Currently designated Variants of Interest:

WHO label	Pango lineages	GISAID clade	Nextstrain clade	Earliest documented samples	Date of designation
Eta	B.1.525	G/484K.V3	21D	Multiple countries, Dec-2020	17-Mar-2021
Iota	B.1.526	GH/253G.V1	21F	United States of America, Nov-2020	24-Mar-2021
Kappa	B.1.617.1	G/452R.V3	21B	India, Oct-2020	4-Apr-2021
Lambda	C.37	GR/452Q.V1	21G	Peru, Dec-2020	14-Jun-2021

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/

World Health Organization

Continuous virus evolution: Variants of Concern



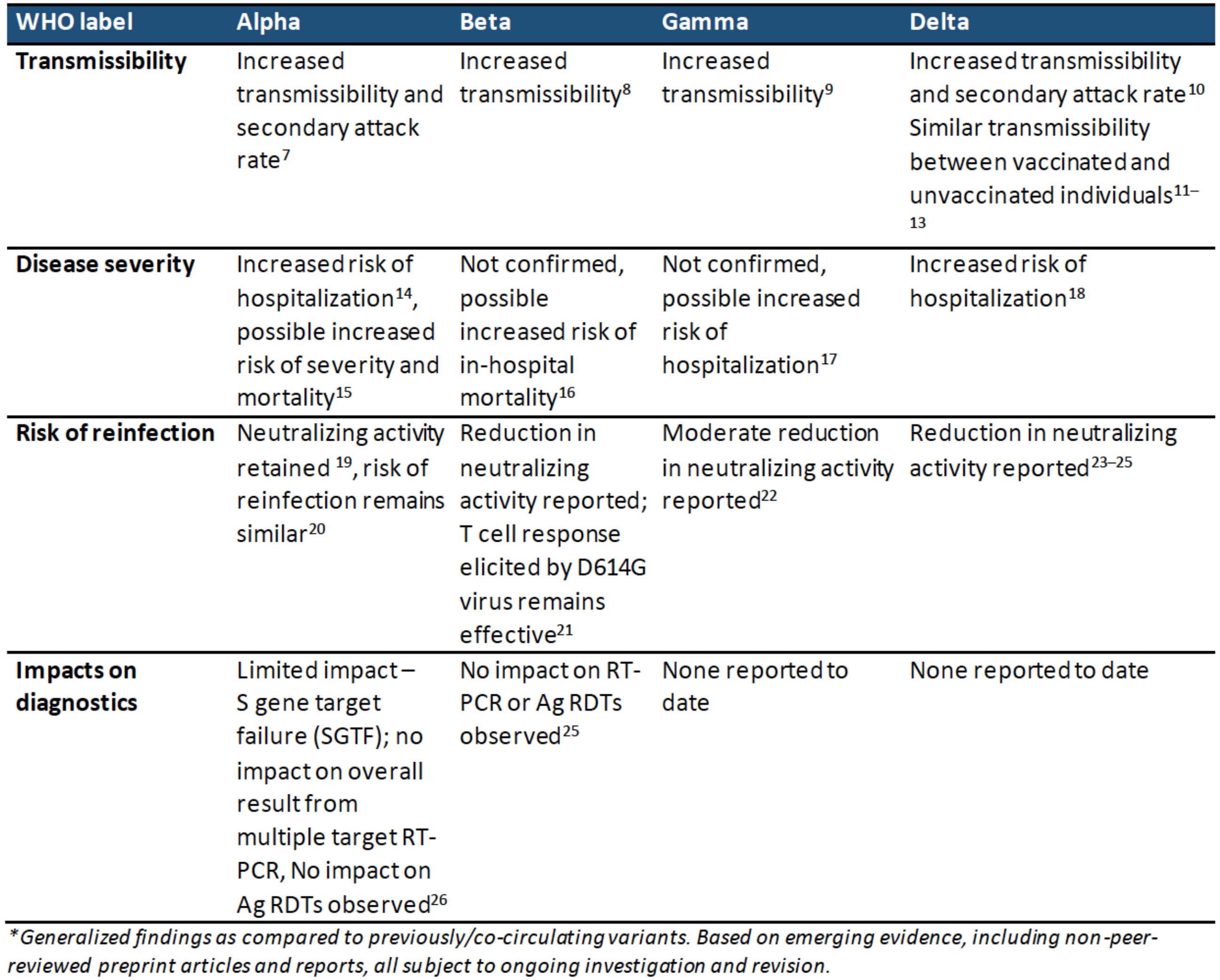
**Includes countries/territories/areas reporting the detection of B.1.617 without further specification of lineage at this time. These will be reallocated as further details become available.*

***Countries/territories/areas highlighted include both official and unofficial reports of VOC detections, and do not presently differentiate between detections among travellers (e.g., at Points of Entry) or local community cases. Please see Annex 2 for further details.*

WHO Weekly Epidemiological Update on COVID-19: 10 August 2021
https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-reports

Continuous virus evolution: Variants of Concern

Summary of phenotypic impacts* of Variants of Concern (as of 10 August 2021)



WHO label	Alpha	Beta	Gamma	Delta
Transmissibility	Increased transmissibility and secondary attack rate[7]	Increased transmissibility[8]	Increased transmissibility[9]	Increased transmissibility and secondary attack rate[10] Similar transmissibility between vaccinated and unvaccinated individuals[11–13]
Disease severity	Increased risk of hospitalization[14], possible increased risk of severity and mortality[15]	Not confirmed, possible increased risk of in-hospital mortality[16]	Not confirmed, possible increased risk of hospitalization[17]	Increased risk of hospitalization[18]
Risk of reinfection	Neutralizing activity retained [19], risk of reinfection remains similar[20]	Reduction in neutralizing activity reported; T cell response elicited by D614G virus remains effective[21]	Moderate reduction in neutralizing activity reported[22]	Reduction in neutralizing activity reported[23–25]
Impacts on diagnostics	Limited impact – S gene target failure (SGTF); no impact on overall result from multiple target RT-PCR, No impact on Ag RDTs observed[26]	No impact on RT-PCR or Ag RDTs observed[25]	None reported to date	None reported to date

**Generalized findings as compared to previously/co-circulating variants. Based on emerging evidence, including non-peer-reviewed preprint articles and reports, all subject to ongoing investigation and revision.*

WHO Weekly Epidemiological Update on COVID-19: 10 August 2021
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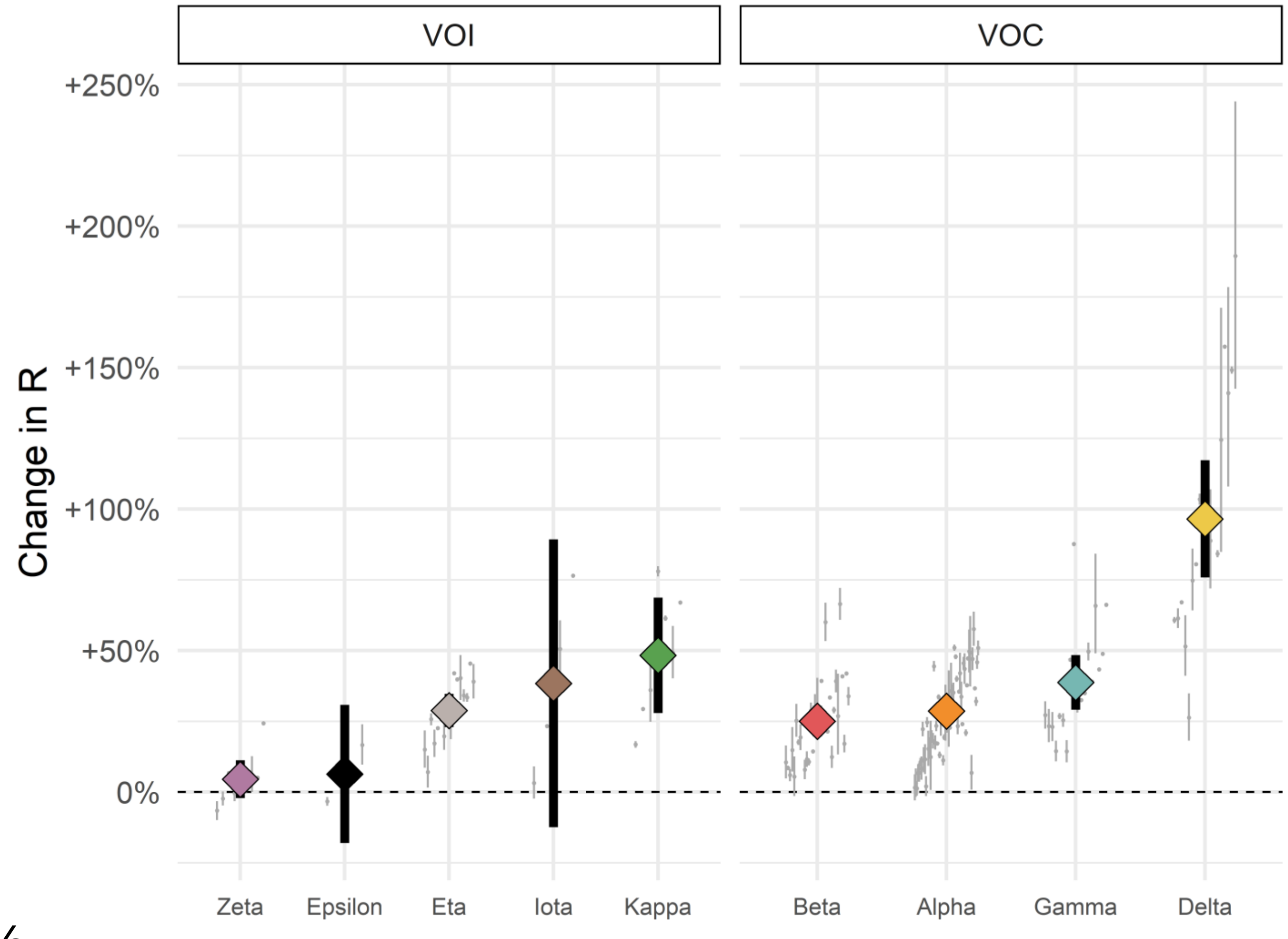
B.1.617.2 Delta variant

Delta has the highest estimated transmissibility of all variants

All VOCs and some VOIs demonstrate increased effective R

- Beta: 25% (20% – 30%)
- Alpha: 29% (24% – 33%)
- Gamma: 38% (29% – 48%)
- **Delta:* 97% (76% – 117%)**

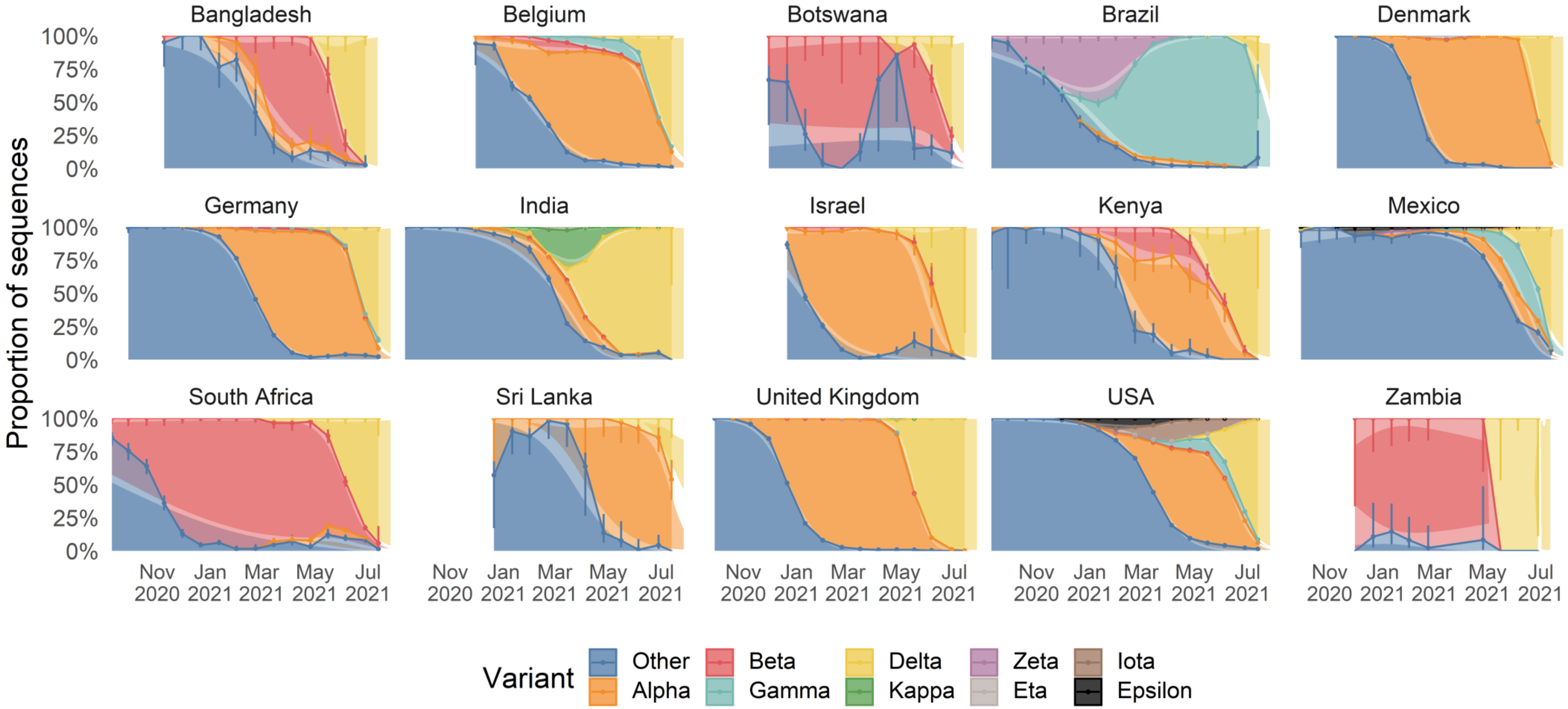
*Estimate subsequently revised to 75% based on shorter serial interval



Campbell F et al. Increased transmissibility and global spread of SARS-CoV-2 variants of concern as at June 2021. Euro Surveill; 2021;26(24):pii=2100509

B.1.617.2 Delta variant

Replacement effect of Delta

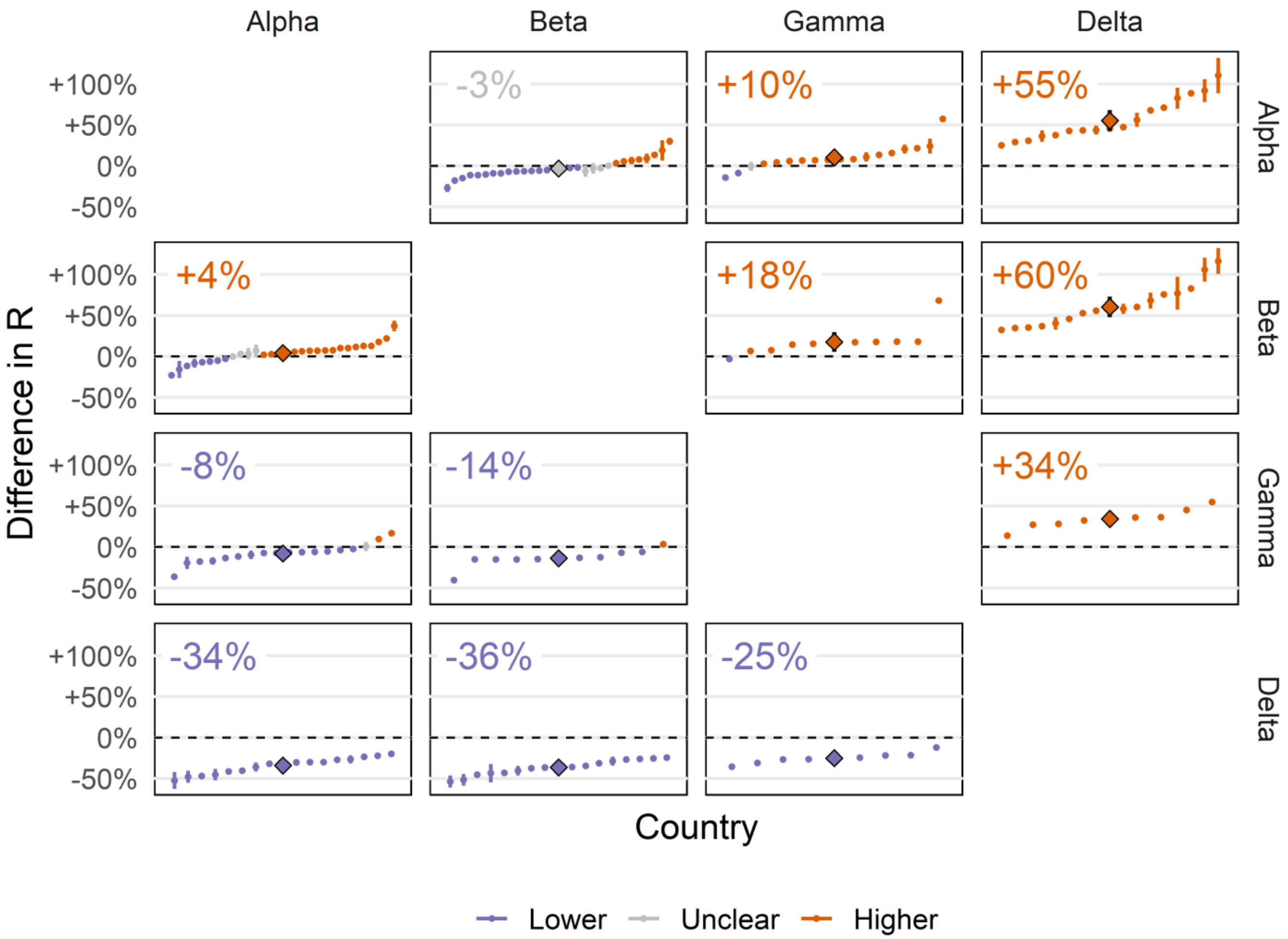


Source: WHO Epi Analytics Group

B.1.617.2 Delta variant

Delta is outcompeting all variants in all countries with data

- Delta has significantly higher effective R than other VOCs
- Expected to become dominant lineage in coming months if trends continue



Source: WHO Epi Analytics Group

B.1.617.2 Delta variant

- Increased transmissibility – R_0 likely around 5
- Higher transmissibility for both very close (e.g. household) and more casual contacts (community SAR)
- Lower Ct values/higher viral load, potentially for earlier/longer period
- Decreased latent period and shorter serial interval
- Limited data on contact events and duration of infectiousness
- Healthcare outbreaks noted to be smaller and shorter in duration

World Health Organization