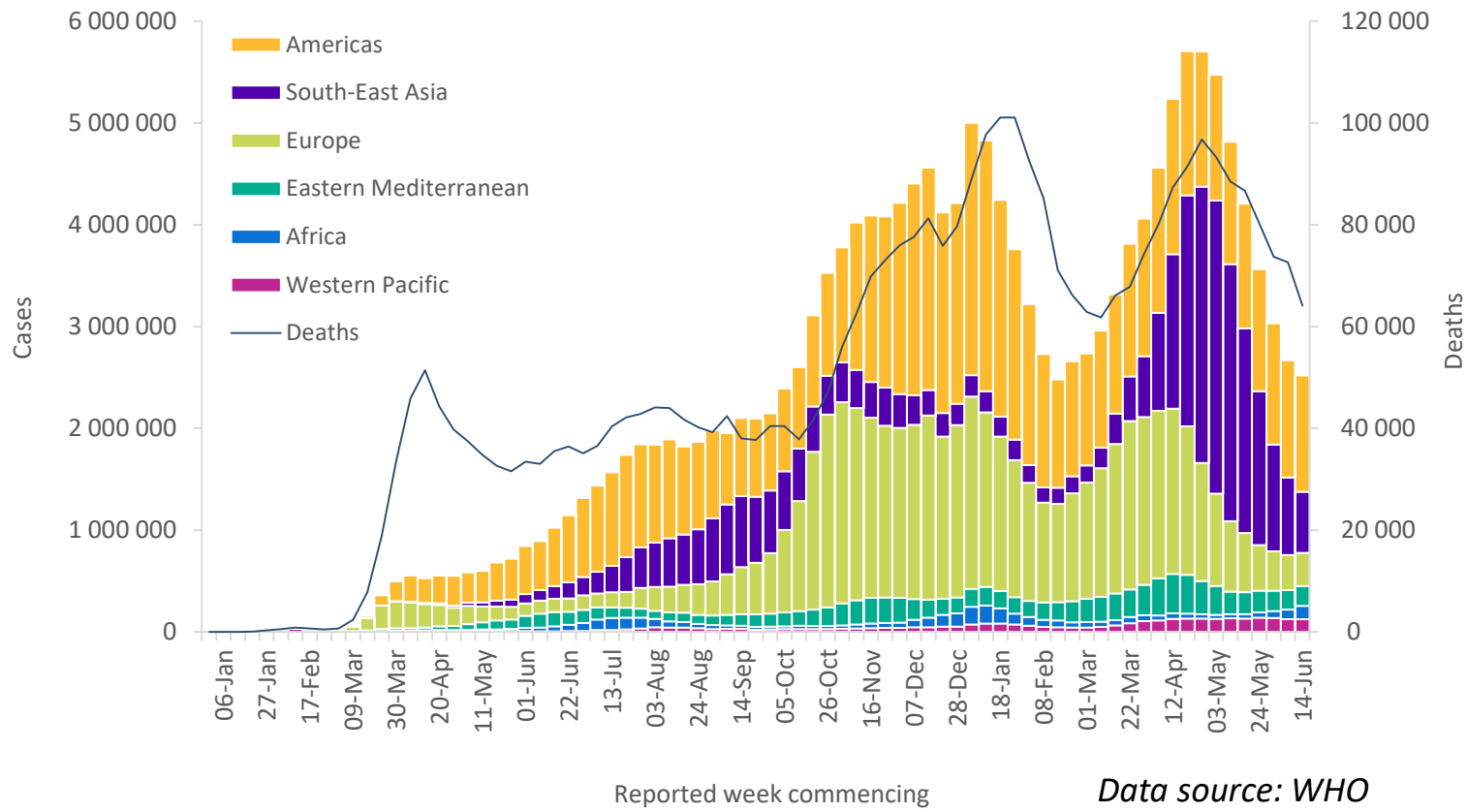
Epidemiological situation overview

- **Cumulative, as of 23 June 2021:**
  - 178 million confirmed cases
  - 3.8 million deaths
- **In the last epi week:**
  - Over 2.5 million new cases and 64,000 new deaths reported
  - Global declines primarily reflect trends in the South East Asia & European regions; declines slowing
  - 39% increase in case incidence in the African Region
- **Global public health risks remain very high**
- **Guard against complacency**

COVID-19 cases reported weekly by WHO Region, and global deaths, through week ending 20 June 2021



Data source: WHO

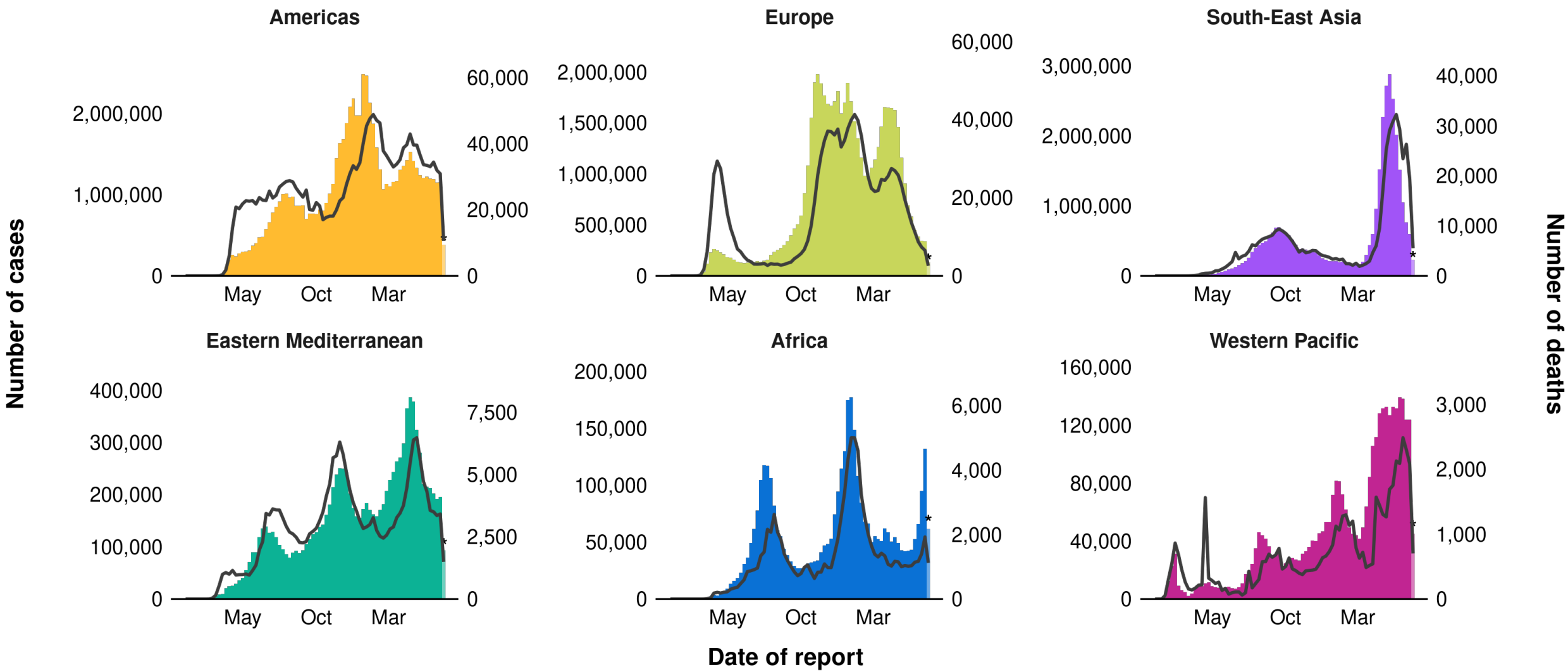
Change in cases and deaths in the last 7 days

(as of 23 June 10H CEST)

WHO Region	New cases in the last 7 days (%)	Change in new cases in last 7 days *	Cumulative cases (%)	New deaths in last 7 days (%)	Change in new deaths in last 7 days *	Cumulative deaths (%)
Africa	148,283 (5.9%)	33.1%	3,852,707 (2.15%)	2,296 (3.85%)	44.2%	92,719 (2.4%)
Eastern Mediterranean	206,355 (8.2%)	3.1%	10,759,857 (6.02%)	3,472 (5.82%)	3.5%	213,407 (5.5%)
Europe	344,259 (13.6%)	1.2%	55,473,875 (31.02%)	6,374 (10.69%)	-6.4%	1,176,552 (30.3%)
Americas	1,129,329 (44.7%)	-1.5%	71,055,452 (39.73%)	30,903 (51.82%)	-2.2%	1,868,214 (48.1%)
South-East Asia	576,964 (22.9%)	-15.2%	34,262,347 (19.16%)	14,621 (24.52%)	-49.1%	476,822 (12.3%)
Western Pacific	118,831 (4.7%)	-4.3%	3,432,202 (1.92%)	1,965 (3.30%)	-10.6%	52,723 (1.4%)
Global	2,524,021 (100%)	-3.0%	178,837,204 (100%)	59,631 (100%)	-19.7%	3,880,450 (100%)

Weekly situation by WHO region

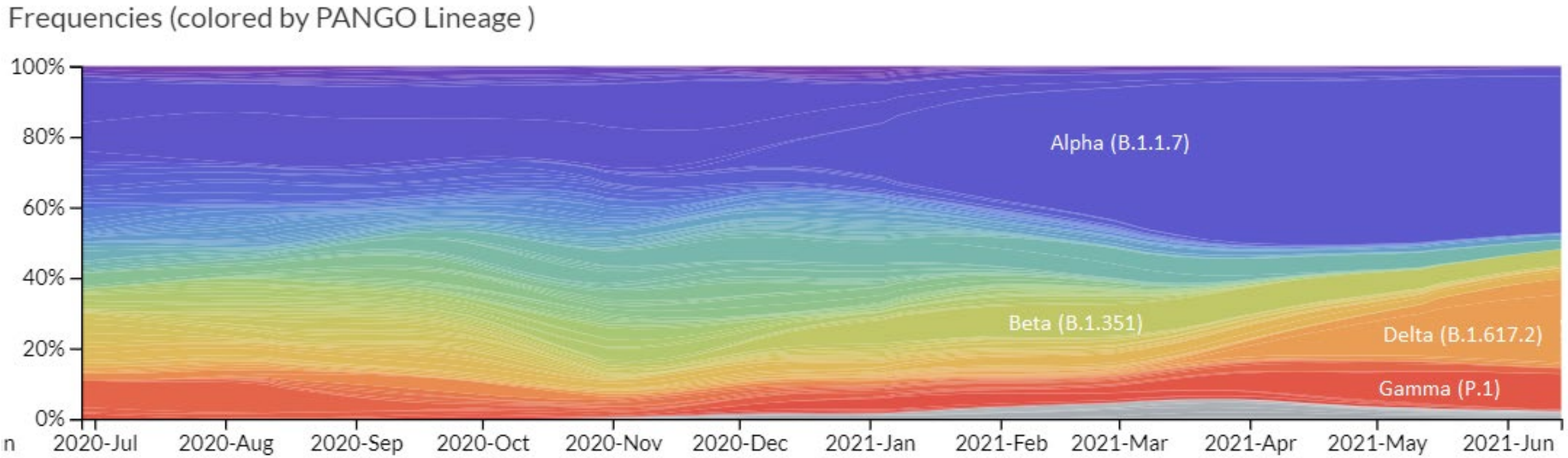
(as of 23 June 10H CEST)



** Data are incomplete for the current week. Cases depicted by bars; deaths depicted by line. Note different scales for y-axes.*

Continuous virus evolution

Genomic spread of SARS-CoV-2 variants of concern



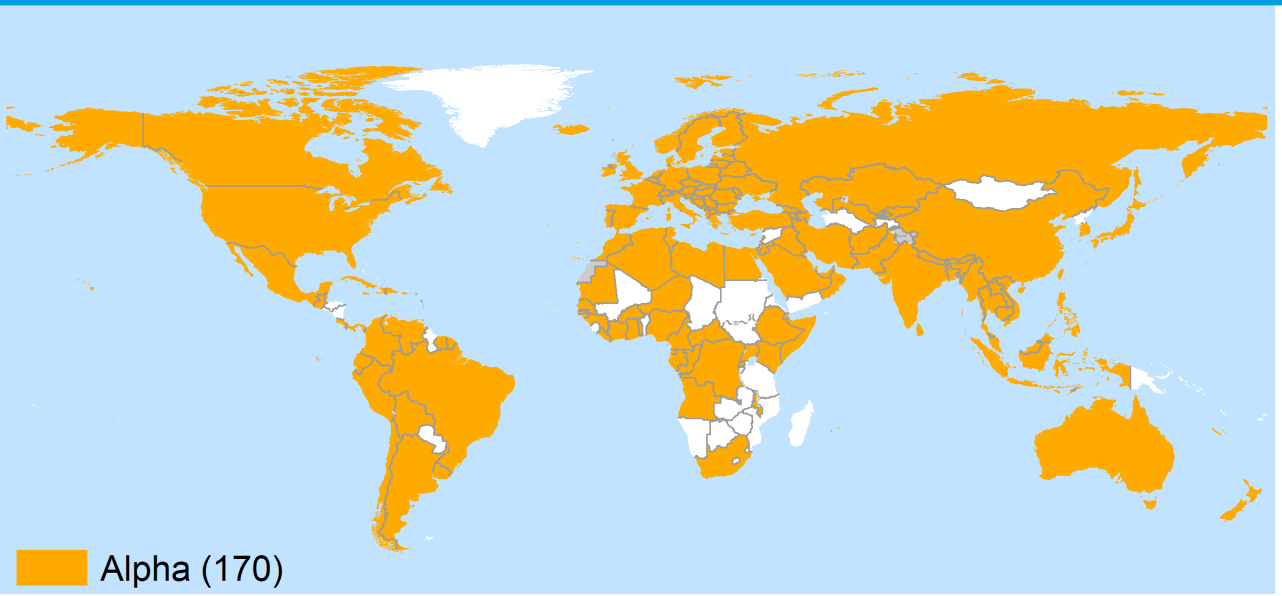
Source: Nextstrain based on GISAID data nextstrain.org/ncov/global

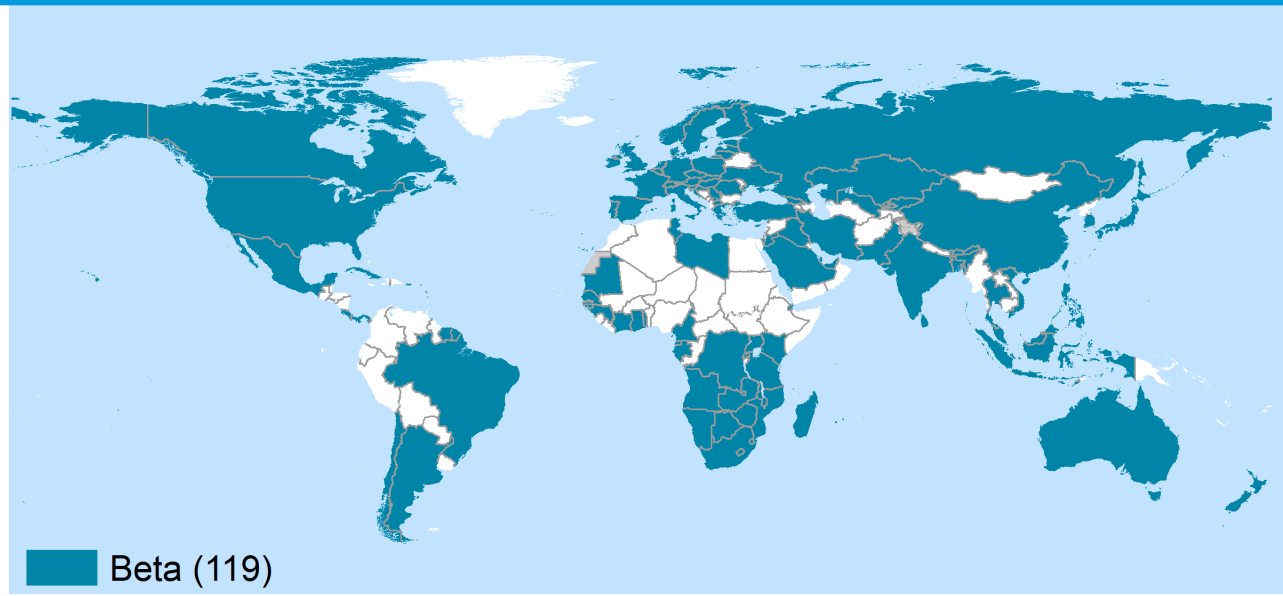
SARS-CoV-2 Variants of Concern (VOCs) and Variants of Interest (VOIs)

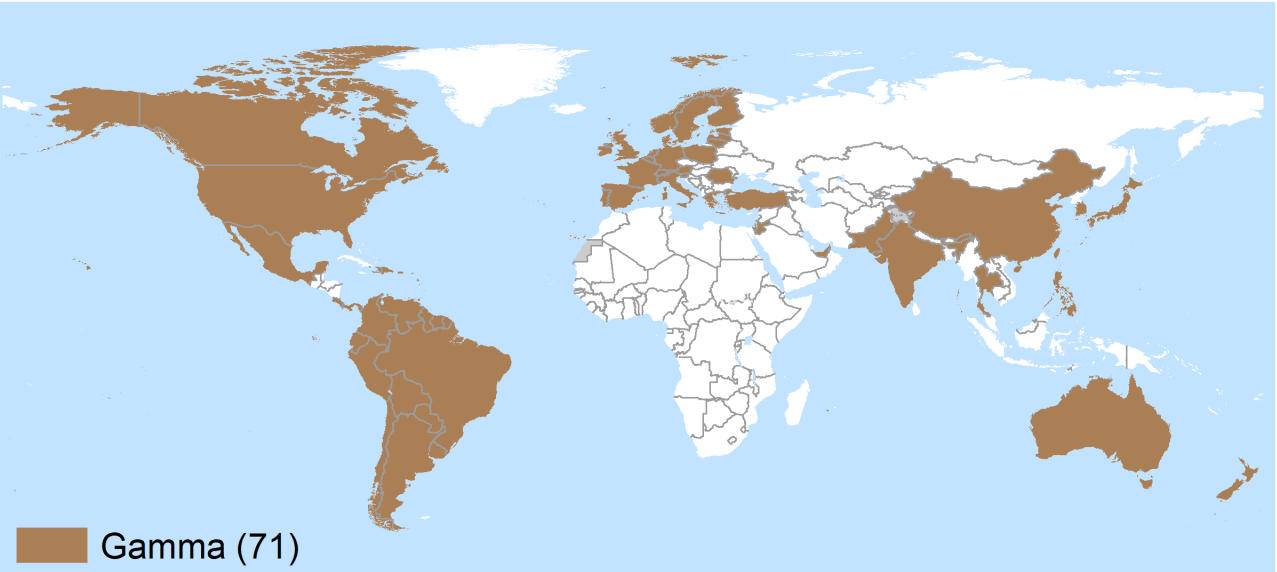
WHO label	Pango lineage	GISAID clade	Nextstrain clade	Earliest documented samples	Date of designation
Variants of Concern (VOCs):					
Alpha	B.1.1.7	GRY (formerly GR/501Y.V1)	20I (V1)	United Kingdom, Sep-2020	18-Dec-2020
Beta	B.1.351	GH/501Y.V2	20H (V2)	South Africa, May-2020	18-Dec-2020
Gamma	P.1	GR/501Y.V3	20J (V3)	Brazil, Nov-2020	11-Jan-2021
Delta	B.1.617.2	G/478K.V1	21A	India, Oct-2020	VOI: 4-Apr-2021 VOC: 11-May-2021
Variants of Interest (VOIs):					
Epsilon	B.1.427/ B.1.429	GH/452R.V1	21C	United States of America, Mar-2020	5-Mar-2021
Zeta	P.2	GR/484K.V2	20B/S.484K	Brazil, Apr-2020	17-Mar-2021
Eta	B.1.525	G/484K.V3	21D	Multiple countries,Dec-2020	17-Mar-2021
Theta	P.3	GR/1092K.V1	21E	Philippines, Jan-2021	24-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	20D	Peru, Aug-2020	14-Jun-2021

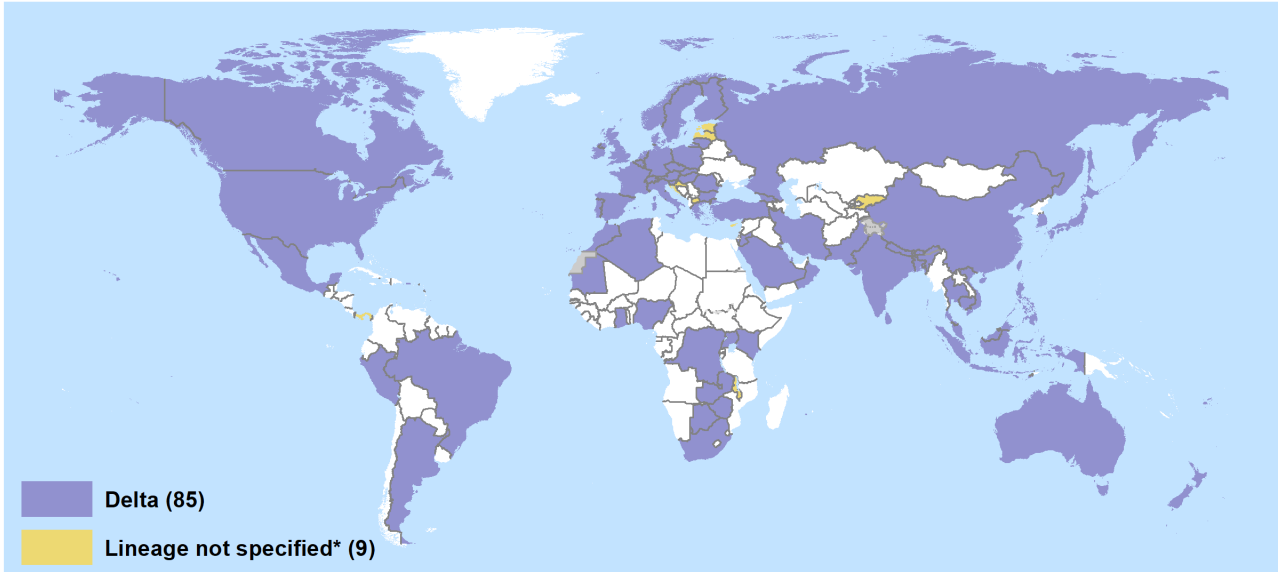
Countries, territories, and areas reporting Variants of Concern

(situation as of 22 June 2021)









World Health Organization

***Data Source**: World Health Organization*
***Map Production**: WHO Health Emergencies Programme*

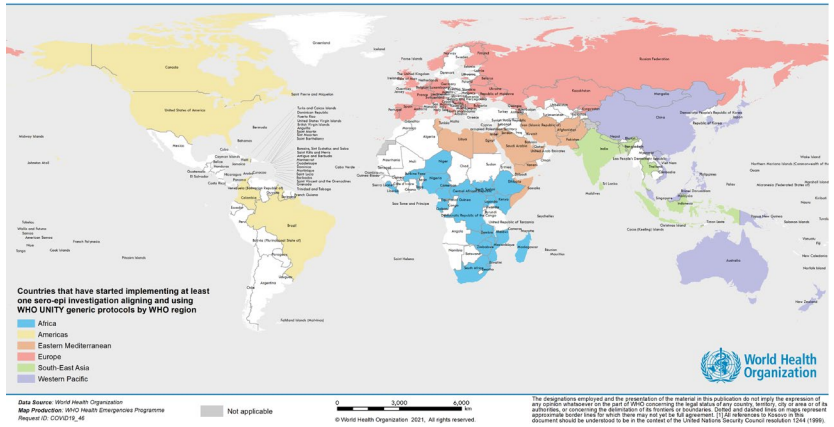
Not applicable

0 5,000 10,000 km

The designations employed and the presentation of the material in this publication do not imply the expression of any opinion whatsoever on the part of WHO concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement.

Transmission & population Immunity

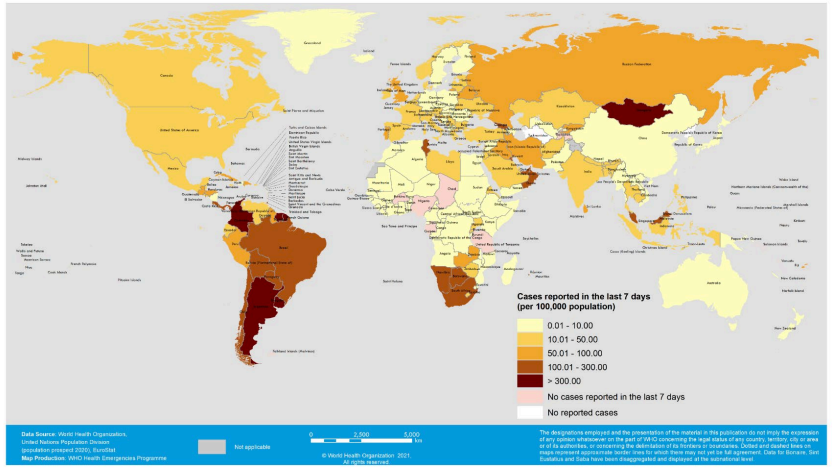
SARS-CoV-2 Seroprevalence



COVID-19 "UNITY" STUDIES: early sero-epi investigations

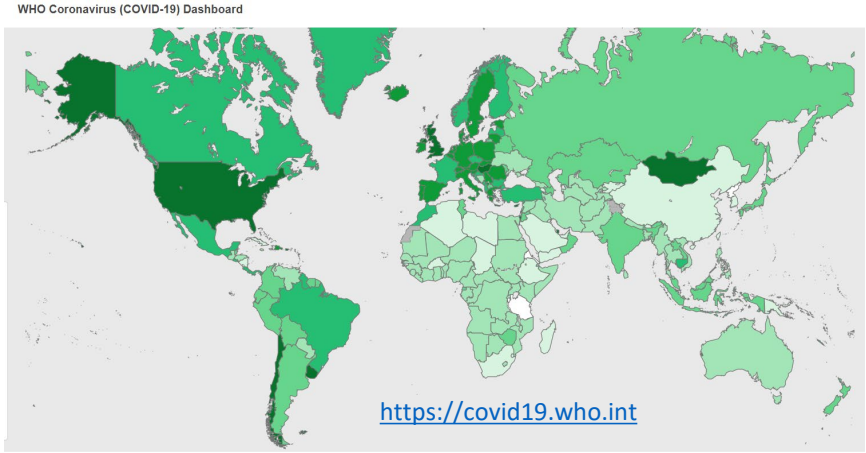
SeroTracker

SARS-CoV-2 Transmission Intensity



**See *Annex 2: Data, table and figure notes*

Persons fully vaccinated per 100 population



2,625m doses administered (as of 21 June 2021)

World Health Organization

SARS-CoV-2 Variants of Interest & Variants of Concern

(working definitions – under revision)

Variant of Interest (VOI)

A SARS-CoV-2 isolate is a Variant of Interest (VOI) if, compared to a reference isolate, its genome has mutations with established or suspected phenotypic implications, and either:

- has been identified to cause community transmission/multiple COVID-19 cases/clusters, or has been detected in multiple countries; OR
- is otherwise assessed to be a VOI by WHO in consultation with the WHO SARS-CoV-2 Virus Evolution Working Group.

Variant of Concern (VOC)

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.

From Signal to VOI/VOC

Detection

Surveillance

using EBS, global databases and IHR notifications

Review information, verify signals, share with technical teams, enter information in the variant database

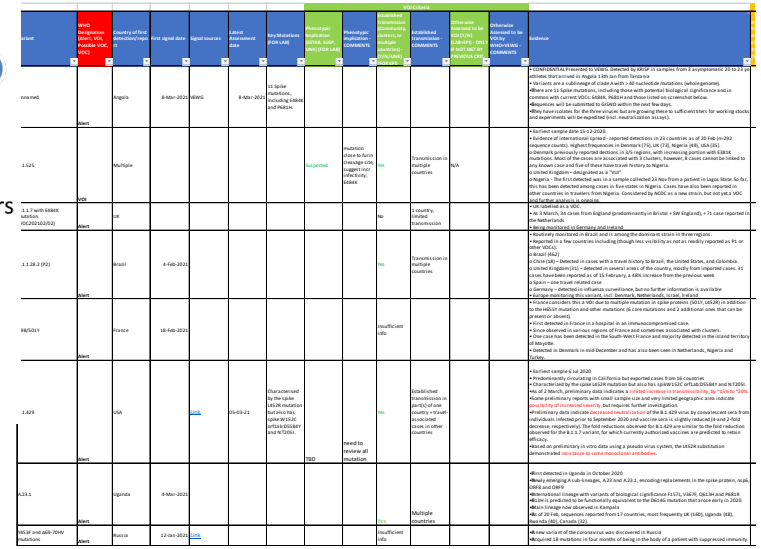
Collaboration:

Share with RO's for verification, collaborate with other public health partners

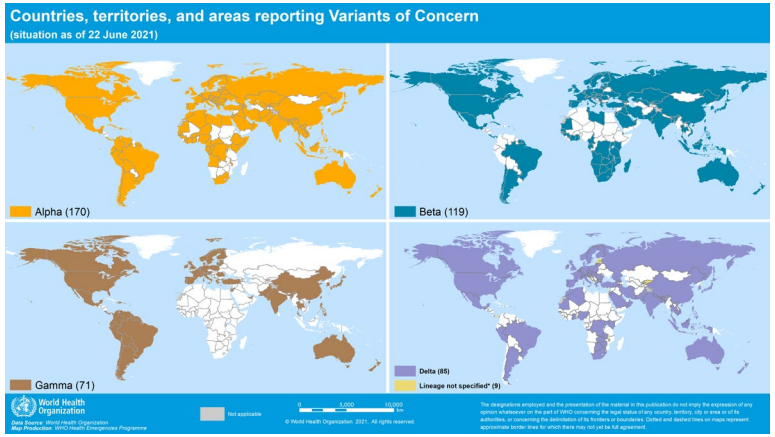
Analysis, interpretation and generation of outputs

Assessment:

By Lab + Epi Pillars,
with input from the VEWG



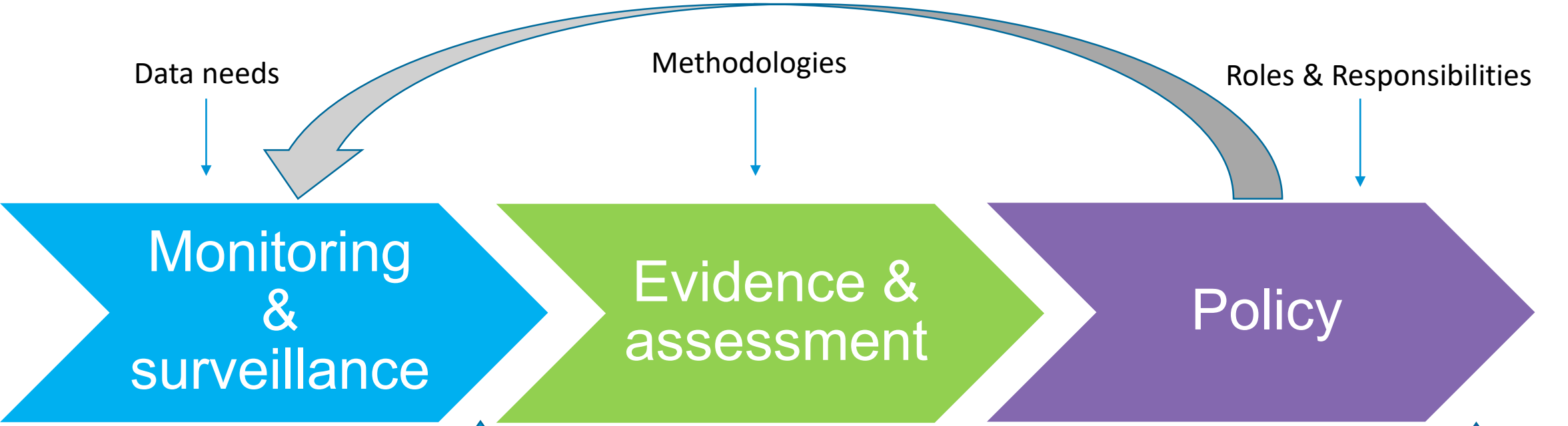
Global tracking, Investigate of phenotypic impacts, Communication



World Health Organization

HEALTH EMERGENCIES programme

Overarching aim: an integrated approach to monitor & assess SARS-CoV-2 variants



World Health Organization

Phenotypic impacts* of VOCs

	Alpha (B.1.1.7)	Beta (B.1.351)	Gamma (P.1)	Delta (B.1.617.2)
Increased transmissibility risk (change in R or secondary attack rate)	Yes	Yes	Yes	Yes ++
Increased severity (risk of hospitalization/death)	Possible	Possible	Possible	Possible
Increased reinfection risk (following natural infection by other variants)	No change	Possible	Possible	Possible
Impacts on diagnostics (PCR or Ag RDTs)	Limited, largely negated by standard assays	None reported	None reported	None reported
Impact on vaccine efficacy/effectiveness	Protection retained against disease, no/minimal loss against infection	Protection retained against severe disease, potentially reduced against mild-moderate disease or infection; limited evidence	Protection likely against disease; very limited evidence	Protection against severe disease; possible reduced protection against mild-moderate disease or infection, limited evidence

- Impacts detailed in the WHO COVID-19 Weekly Epidemiological Updates

**Generalized findings as compared to other previously/cocirculating variants. Based on emerging evidence from multiple countries, including preprint articles and preliminary reports – all subject to ongoing investigation and continuous revision. See fortnightly updates in the WHO COVID-19 Weekly Epidemiological Update for references and further detail.*

WHO label	Alpha	Beta	Gamma	Delta
Transmissibility	Increased transmissibility and secondary attack rate[1]	Increased transmissibility[2]	Increased transmissibility[3]	Increased transmissibility and secondary attack rate[4,5]
Disease severity	Increased risk of hospitalization[6], possible increased risk of severity and mortality[7]	Not confirmed, possible increased risk of in-hospital mortality[8,9]	Not confirmed, possible increased risk of hospitalization[10]	Not confirmed, possible increased risk of hospitalization[11]
Risk of reinfection	Neutralizing activity retained,[12] risk of reinfection remains similar[13,14]	Reduction in neutralizing activity reported; T cell response elicited by D614G virus remains effective[15–18]	Moderate reduction in neutralizing activity reported[19,20]	Reduction in neutralizing activity reported[21]
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[22]	No impact on RT-PCR or Ag RDTs observed[16]	None reported to date	None reported to date
Impacts on vaccine efficacy/effectiveness	Protection retained against disease • Severe disease: No/minimal loss: Pfizer BioNTech-Comirnaty[23–28] • Symptomatic Disease: No/minimal loss: AstraZeneca- Vaxzevria, Novavax-Covavax, PfizerBioNTech-Comirnaty[24,25,28–31] • Infection: No/minimal loss: PfizerBioNTech-Comirnaty[32] • Asymptomatic infection: No/minimal loss: Pfizer BioNTech-Comirnaty[24,33]; inconclusive/Moderate-substantial loss, limited sample size:AstraZeneca-Vaxzevria[30]	Reduced protection against disease; limited evidence • Severe disease: No/minimal loss: Janssen Ad26.COV 2.5, Pfizer BioNTech-Comirnaty[25,34] • Mild-moderate disease: No/minimal loss: Janssen-Ad26. COV 2.5[34]; Moderate loss: Novavax-Covavax[35]; Inconclusive/substantial loss, limited sample size: AstraZeneca-Vaxzevria[36] • Infection: Moderate loss: Pfizer BioNTech-Comirnaty[25] • Asymptomatic infection: no evidence	Protection likely against disease; very limited evidence on three vaccines • Symptomatic disease: No/minimal loss: Sinovac-CoronaVac, [37,38]; no/minimal to modest loss: *single dose* of Moderna- mRNA-1273 or PfizerBioNTech-Comirnaty[39]* • Infection: No/minimal loss: Sinovac-CoronaVac[38]	Protection retained against severe disease; possible reduced protection against disease and infection; limited evidence on only two vaccines • Severe disease: No/minimal loss: PfizerBioNTech-Comirnaty, AstraZeneca-Vaxzevria[31,40] • Symptomatic disease: No/minimal to modest loss: PfizerBioNTech-Comirnaty[41,42]; no/minimal to moderate loss: AstraZeneca-Vaxzevria[41,42] • Infection: No/minimal to moderate loss: AstraZeneca-Vaxzevria, PfizerBioNTech-Comirnaty[42];
Impacts on neutralization (full vaccination) by vaccine	• No/minimal loss: Bharat-Covaxin, Gamaleya-Sputnik V, Moderna- mRNA-1273, Novavax-Covavax, Pfizer BioNTech-Comirnaty, BeijingCNBG-BBIBP-CorV, Sinovac-CoronaVac[18,41,43–67] • Minimal/moderate loss: AstraZeneca-Vaxzevria[30,57]	• Minimal/modest loss: Bharat-Covaxin, Beijing CNBG-BBIBP-CorV, Sinovac-CoronaVac, Anhui ZL - Recombinant[68–71] • Minimal to substantial loss: Moderna-mRNA-1273, Pfizer BioNTech-Comirnaty[18,44,48,50–52,54,56–58,64,66,67,72–78] • Moderate to substantial loss: AstraZeneca-Vaxzevria, Gamaleya- Sputnik V, Janssen-Ad26.COV 2.5, Novavax-Covavax[50,59,75,75,79–81]	• No/minimal loss: AstraZeneca-Vaxzevria, Sinovac-CoronaVac [57,82] • Minimal to moderate loss: Moderna-mRNA-1273, Pfizer BioNTech-Comirnaty[18,44,45,54,56,57,63,66,83,84] • Modest loss: Janssen-Ad26.COV 2.5[81]	• No/minimal loss: Bharat-Covaxin[71] • No/Minimal to moderate loss: Pfizer BioNTech Comirnaty, Bharat-Covaxin[64,85,86] • Substantial loss: *single dose* of AstraZeneca-Vaxzevria[85]

**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.*