

World Health Organization, Health Emergencies Program

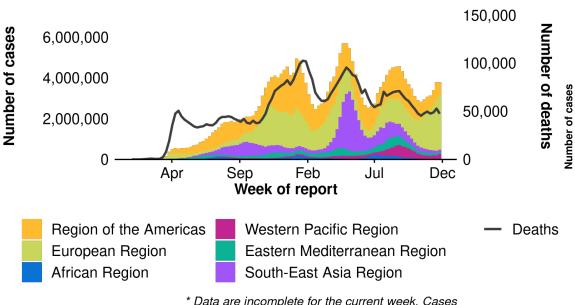


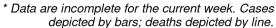
Previous week:

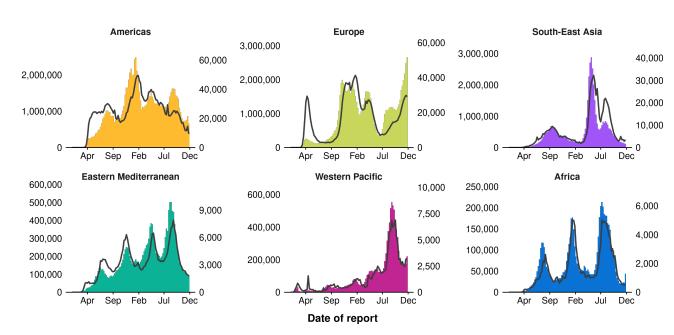
3,799,878 new confirmed cases 47,524 new deaths

Cumulative:

260,493,573 confirmed cases 5,195,354 deaths







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



EURO: Current epidemiological situation



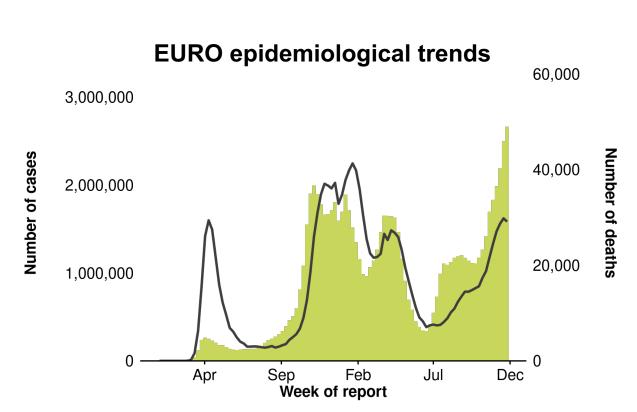
Infections, test positivity, hospitalizations and ICU admissions continue to rise across Europe

Reported COVID-19 cases and deaths have doubled in Europe over the past 2+ months

Last week, >2.6 million new cases reported and over 29,000 new deaths reported

There are many factors contributing to the current increase in cases in the EURO region, including:

- 99% prevalence of Delta variant
- Relaxation of PHSM over many months
- Slow/light re-introduction of PHSM
- Low vaccination coverage (in some areas/countries) especially among vulnerable populations

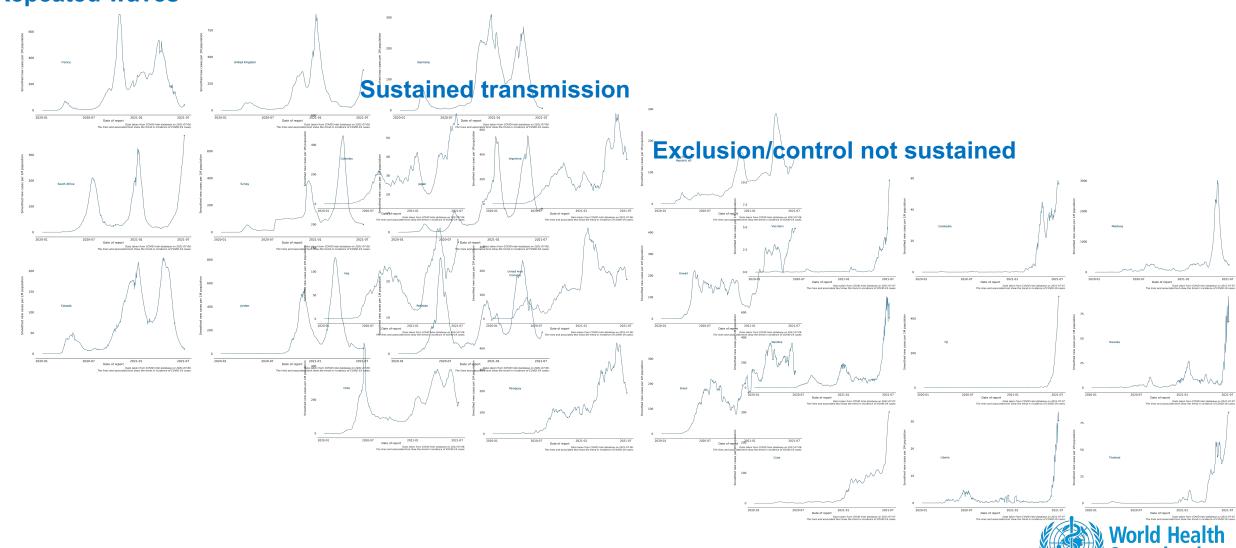




Epidemic curves



Repeated waves



Factors driving transmission



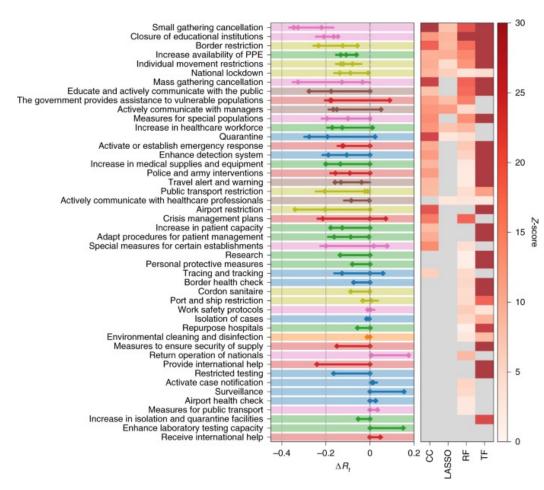
- The virus continues to evolve resulting in more transmissible variants
- Highly susceptible population: Driven by unequal vaccine distribution & access to live saving tools, a large proportion of the world population remains susceptible to infection & at increased risk of severe disease and death
- Increased social mobility and social mixing provides increases exposure to the virus, combined with Inappropriate, inconsistent use of proven Public Health and Social Measures
- Misinformation, disinformation, conflicting messaging, politicization



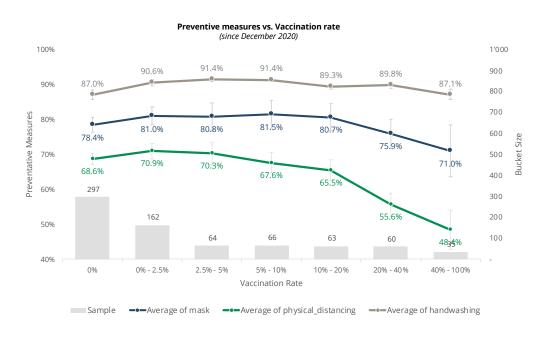


Use of PHSM in the context of increasing social mobility

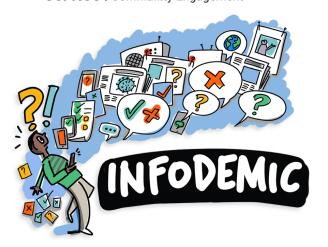




Haug N et al, Nat Hum Behav. 2020



Collective | Risk Communication and Service | Community Engagement



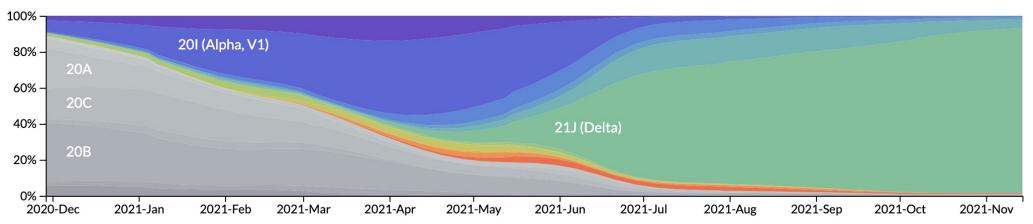


Virus evolution - Genomic spread of SARS-CoV-2 VOCs



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





Variants of Interest

WHO label	Pango lineage*	GISAID clade	Nextstrain clade	Earliest documented samples	Date of designation
Lambda	C.37	GR/452Q.V1	21G	Peru, Dec-2020	14-Jun-2021
Mu	B.1.621	GH	21H	Colombia, Jan- 2021	30-Aug-2021

Currently designated Variants Under Monitoring

Pango lineage*	GISAID clade	Nextstrain clade	Earliest documented samples	Date of designation
AZ.5 [#]	GR		Multiple countries, Jan-2021	VUM: 02-Jun-2021
C.1.2	GR		South Africa, May 2021	01-Sep-2021
B.1.617.1 [§]	G/452R.V3	21B	India, Oct-2020	VOI: 4-Apr-2021 VUM: 20-Sep-2021
B.1.526 [§]	GH/253G.V1	21F	United States of America, Nov-2020	VOI: 24-Mar-2021 VUM: 20-Sep-2021
B.1.525 [§]	G/484K.V3	21D	Multiple countries, Dec-2020	VOI:17-Mar-2021 VUM: 20-Sep-2021
B.1.630	GH	-	Dominican Republic, Mar- 2021	12-Oct-2021
B.1.640	GH/490R		Republic of Congo, Sep- 2021	22-Nov-2021

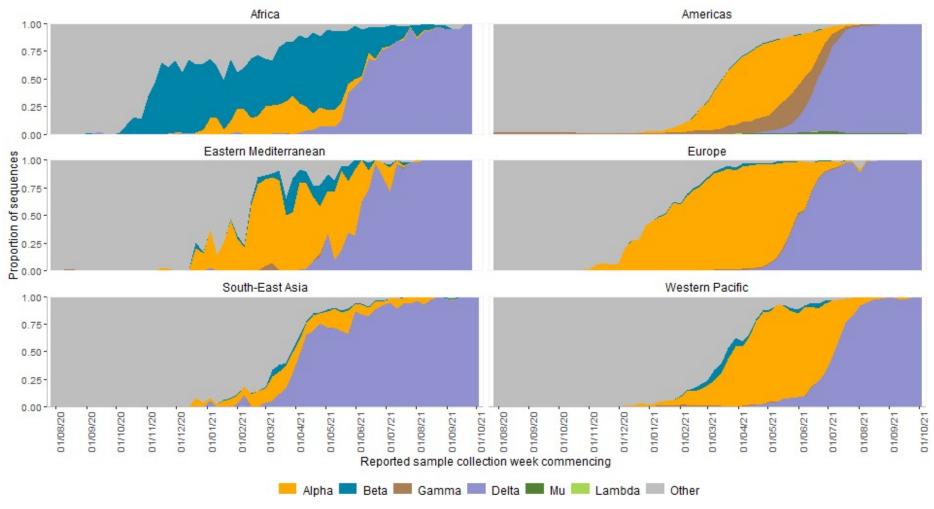
Variants under Monitoring



Virus evolution - VOC/VOIs over time by WHO Region



Proportion of VOC or VOI sequences reported among total sequences submitted over time, by WHO Region, 1 August 2020 – 15 October 2021

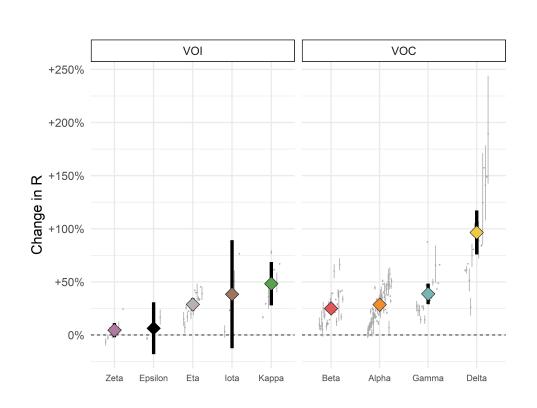


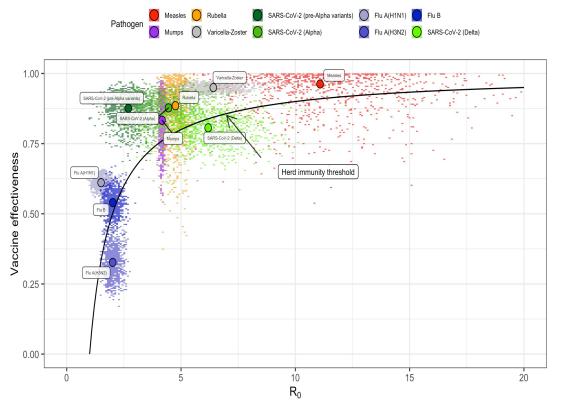
*Data source: GISAID Initiative



Delta variant: Transmissibility and impact on herd immunity







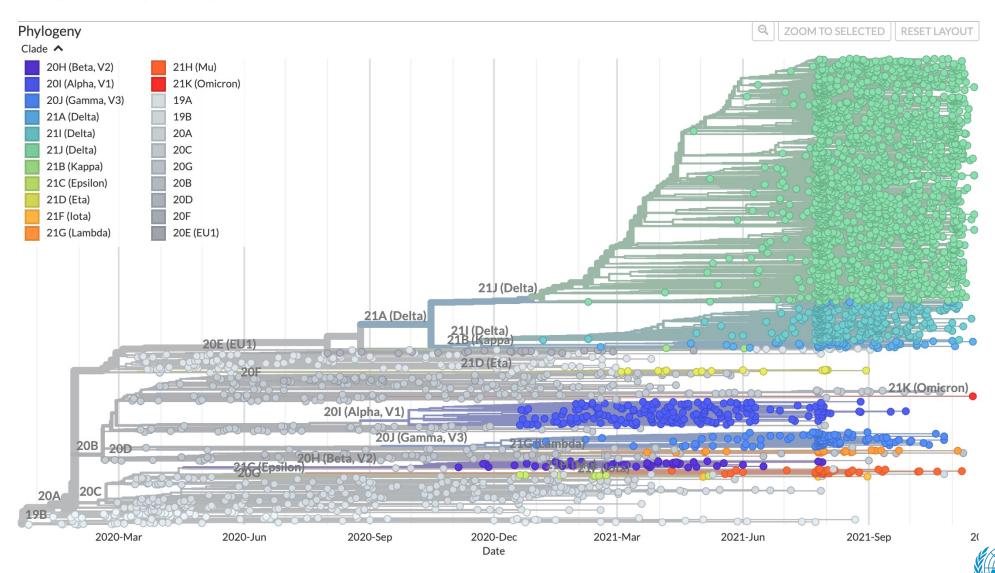
- Even with whole population vaccination coverage (100% of all ages), unlikely to achieving herd immunity threshold with a vaccine with high VE against infection (assumption here is 80%) given the properties of
- → Whole population immunization will not fully interrupt transmission; continued transmission is likely with variants



Personal communication Adam Kucharski, updated with Delta from Hodgson et al.

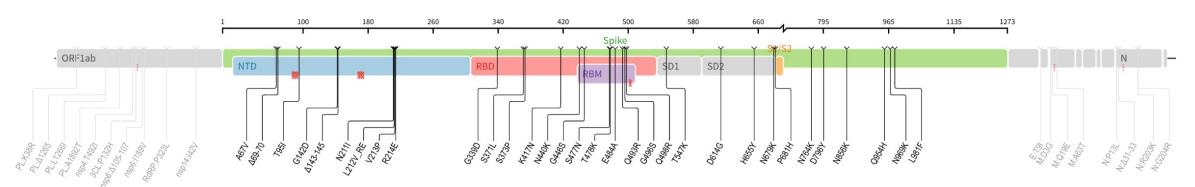


Showing 3434 of 3434 genomes sampled between Dec 2019 and Nov 2021.





Mutational profile



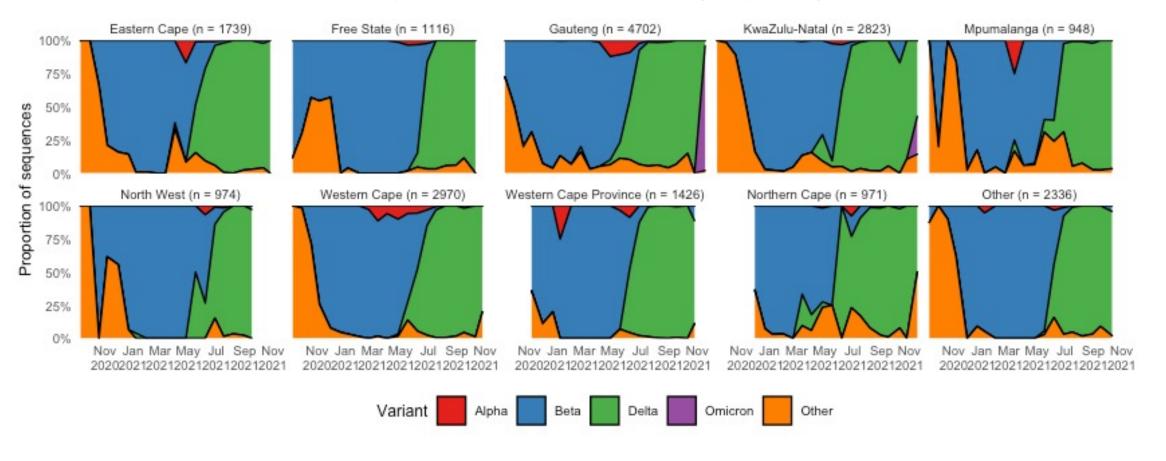
Courtesy of Tulio de Oliveira, Stellenbosch University

- Large number of mutations
 - 45-52 amino acid changes (including deletions) across the whole genome; 26-32 changes in Spike
- Some mutations are also present in Alpha, Beta, Gamma & Delta VOCs
 (Δ69-70; T95I; G142D/Δ143-145; K417N; T478K; N501Y; N655Y; N679K; P681H)
- Some mutations previously associated with:
 - impact on one specific PCR test by S-gene target failure
 - increase transmissibility
 - improve binding affinity make it easier for virus to attach to cells
 - enable the virus to partially escape antibodies





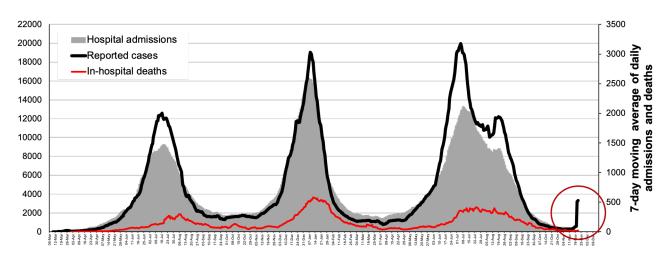
Raw proportions of sequences by province in South Africa (early data)



Source: Analysis by WHO HQ COVID-19 analytics team | Data downloaded from GISAID on 30 Nov 2021 | Latest date of collected Omicron sample in dataset 22 Nov 2021







Courtesy of Lucille Blumberg, Richard Welch and Waasila Jassat - DATCOV, NICD, South Africa

Transmission

- Early data suggest an increased growth rate, but not yet know if Omicron is more transmissible compared to other VOCs, including Delta.
- Sequencing efforts have been enhanced across the region.

Severity

- Reports of cases of Omicron range from mild to severe disease
- Too early to assess whether infection causes more or less severe disease compared to infections with other variants, including Delta.
- Preliminary data suggests that there are increasing rates of hospitalization in South Africa, but this may reflect the force of infection, rather than increased virulence.

Omicron: impact on countermeasures



	Potential impact	Studies to be conducted (in progress)	
Public Health and Social Measures	Current public health measures such as wearing well-fitting masks, hand hygiene, physical distancing, improving ventilation of indoor spaces, avoiding crowded spaces, and getting vaccinated remain effective against all VOCs.	Household transmission studies	
Diagnostics	PCR diagnostics continue to detect SARS-CoV-2 infection, including Omicron infection. S-gene target failure on PCR assay can be used a a proxy marker for Omicron, pending sequencing.	Evaluations of rapid antigen detection tests for Omicron infection	
Therapeutics	Clinical management for patients with severe COVID-19 remains unchanged.	In vivo antiviral resistance studies (mAb); In vitro antiviral resistance studies (polymerase, protease inhibitors); In vitro antiviral resistance studies (polymerase, protease inhibitors)	
Vaccines	Impact on vaccines is not yet known. Omicron mutational profile of Omicron suggests the virus to partially escape antibodies. While may see more mild breakthrough infections from Omicron due to antibody escape, there may not be the same impact on severe disease – mediated by T-cells.	Convalescent and vaccinated sera neutralization studies; matched test-negative case control studies; T cell assays; animal models – passive transfer and vaccination + challenge studies	
Surveilland		Informed	

Monitoring

Research Evidence

Assessment

Informed Decisions & Policy

Collaborative and Coordinated



COVID-19 advisory group pathway to informed decisions



Strong, multidisciplinary mechanism of external experts for evidence-based decision making

Aim: Monitor & assess SARS-CoV-2 variants and evaluate their impact on countermeasures, including vaccines, therapeutics, diagnostics or effectiveness of public health and social measures.





Monitoring & surveillance



TAG-VE

- determines where variants are circulating
- assesses whether variants alter
 - transmission or disease characteristics or
 - impact vaccines, therapeutics, diagnostics or
 - effectiveness of public health and social measures

Vaccine



Research, evidence & assessment



R&D Blueprint for epidemics

 COVID-19 Vaccines Research Expert Group

TAG-CO-VAC

- assesses the impact of Variants of Concern on current COVID-19 vaccines
- determines whether changes to vaccine composition are needed

Vaccine implementation



Policy



SAGE

advises on

- vaccination policies and strategies
- the delivery of immunization programmes



What will continue to drive future trends?



Frequency and magnitude of subsequent waves will depend on multiple factors:

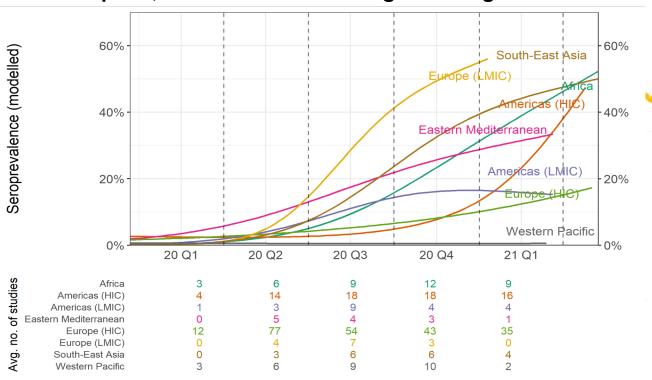
- Population level immunity from natural infection and/or vaccination, including
 - Extent of infection
 - Extent of vaccination
 - Vaccine characteristics and efficacy
 - Strategy and priority groups (e.g., at risk groups, by age group)
 - Extent of vaccination coverage/resistance
 - Duration of protection against severe disease/death and infection (vaccine, natural immunity)
- Severity of disease, access to early clinical care and availability of therapeutics
- VOCs emerging and circulating, and transmissibility of VOCs, properties of immune escape
- Use of Public Health and Social Measures, including:
 - Type of measures identify most effective measures at lowest cost (pandemic fatigue, political/economical cost)
 - Timeliness of implementation
 - Adherence to measures



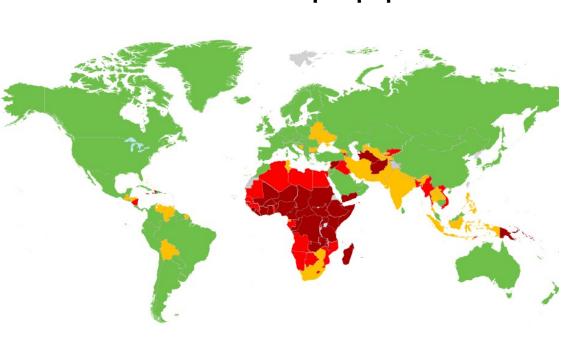
Population-level immunity



Modelled estimates of seroprevalence by WHO region, Jan 20 - Apr 21, show considerable region-to-region variation



Vaccine doses per population



Mar/Apr 2021 modelled seroprevalence ranged from 1.2% in WPR to 48.5% in AFR





Advice for all countries



Advice for all countries

- All countries should regularly to reassess and revise national plans based on current situation and national capacities
- Accelerate vaccine coverage in at risk populations identify those populations who are missed and target vaccination to those most vulnerable in country
- Intensify efforts to drive down/keep down transmission strengthen PHSM
- Strengthen surveillance, share data and samples, surge capacities
- Need collective approach to better assess Omicron

What countries should expect in the short term

- Increase incidence of infection with Delta expected where PHSMs are being relaxed, regardless of vaccination rollout: need to prepare for ongoing circulation of SARS-CoV-2 and prepare for surges
- There will be more variants, yet the impact of Omicron is not yet clear

We need to optimize our response for Delta which will benefit any future variants, including Omicron

Reduce Exposure

Suppress transmission

Protect the vulnerable

Reduce morbidity and mortality

Strengthen communities

