

COVID-19 Weekly Epidemiological Update

Edition 47, published 6 July 2021

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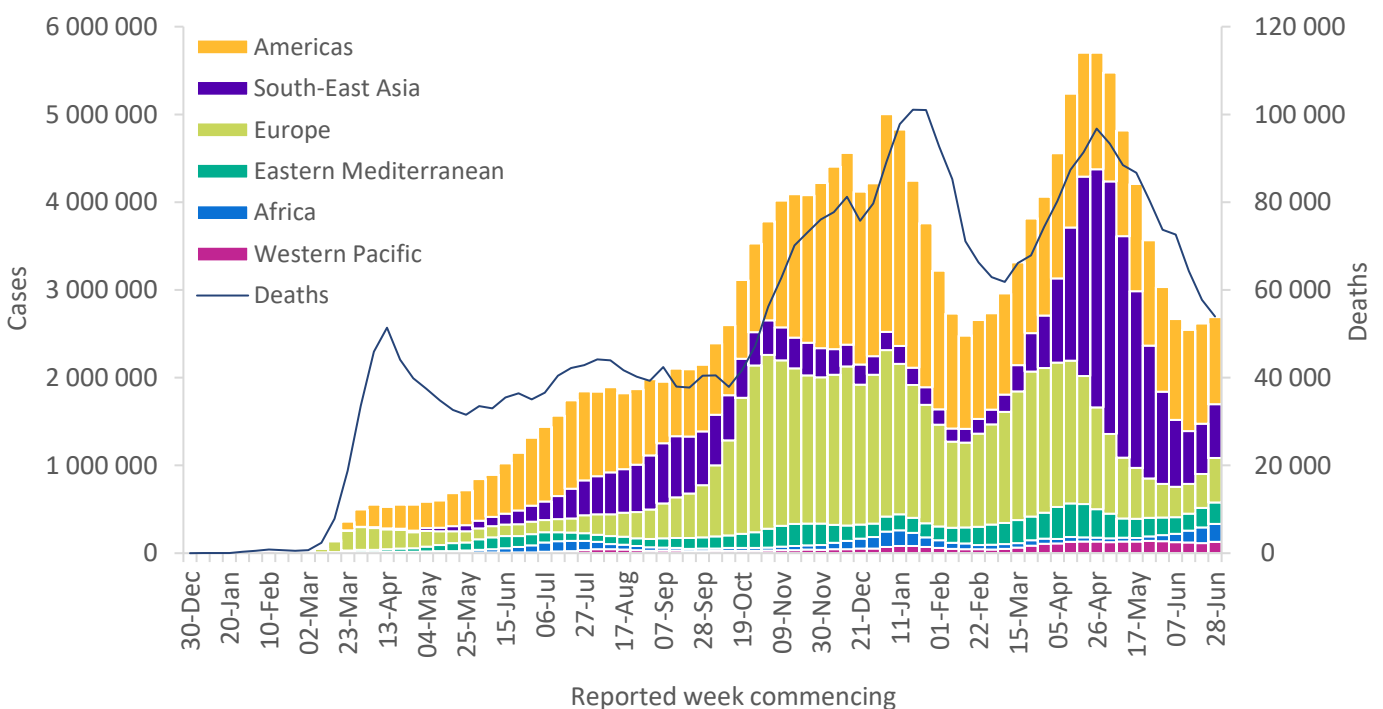
Global overview

Data as of 4 July 2021

Globally, after a decline in newly reported cases for seven consecutive weeks, there has been a slight increase in new weekly cases in the last two weeks, with over 2.6 million cases reported last week (28 June – 4 July 2021) as compared to the previous week (Figure 1). The number of weekly deaths continued to decrease, with just under 54 000 deaths reported in the past week, a 7% decrease as compared to the previous week. This is the lowest weekly mortality figure since early October 2020. The cumulative number of cases reported globally now exceeds 183 million and the number of deaths is almost 4 million.

This week, all Regions except the Americas reported an increase in new cases. The European Region reported a sharp increase in incidence (30%) whereas the African region reported a sharp increase in mortality (23%) as compared to the previous week (Table 1). All Regions, with the exception of the Americas and South-East Asia Regions, reported an increase in the number of deaths in the past week.

Figure 1. COVID-19 cases reported weekly by WHO Region, and global deaths, as of 4 July 2021**



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

The highest numbers of new cases were reported from Brazil (364 709 new cases; 30% decrease), India (312 250 new cases; 11% decrease), Colombia (204 556 new cases; similar to last week), Indonesia (168 780 new cases; 35% increase), and the United Kingdom (161 805 new cases; 67% increase). Over the past week, the highest numbers of new cases per 100 000 population were reported from Seychelles (758 new cases per 100 000 population), Mongolia (472 new cases per 100 000 population), Colombia (402 new cases per 100 000 population), Namibia (367 new cases per 100 000 population) and Cyprus (324 new cases per 100 000 population).

Globally, cases of the Alpha variant have been reported in 173 countries, territories or areas (hereafter countries; one new country in the past week), Beta in 122 countries (three new countries), Gamma in 74 countries (two new countries) and Delta in 104 countries (7 new countries).

Table 1. Newly reported and cumulative COVID-19 cases and deaths, by WHO Region, as of 4 July 2021**

| WHO Region | New cases in 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 (%) |
|-----------------------|------------------------------|--------------------------------------|-------------------------------|-------------------------------|---------------------------------------|-----------------------------|
| Americas | 992 023 (37%) | -13% | 72 804 991 (40%) | 26 721 (50%) | -11% | 1 914 473 (48%) |
| Europe | 505 790 (19%) | 30% | 56 235 850 (31%) | 6 926 (13%) | 6% | 1 189 019 (30%) |
| South-East Asia | 612 933 (23%) | 7% | 35 219 144 (19%) | 11 542 (21%) | -12% | 495 939 (12%) |
| Eastern Mediterranean | 245 740 (9%) | 11% | 11 133 173 (6%) | 3 479 (6%) | 2% | 218 804 (6%) |
| Africa | 204 012 (8%) | 15% | 4 172 433 (2%) | 3 359 (6%) | 23% | 97 682 (2%) |
| Western Pacific | 128 063 (5%) | 10% | 3 631 664 (2%) | 1 931 (4%) | 7% | 55 757 (1%) |
| Global | 2 688 561 (100%) | 3% | 183 198 019 (100%) | 53 958 (100%) | -7% | 3 971 687 (100%) |

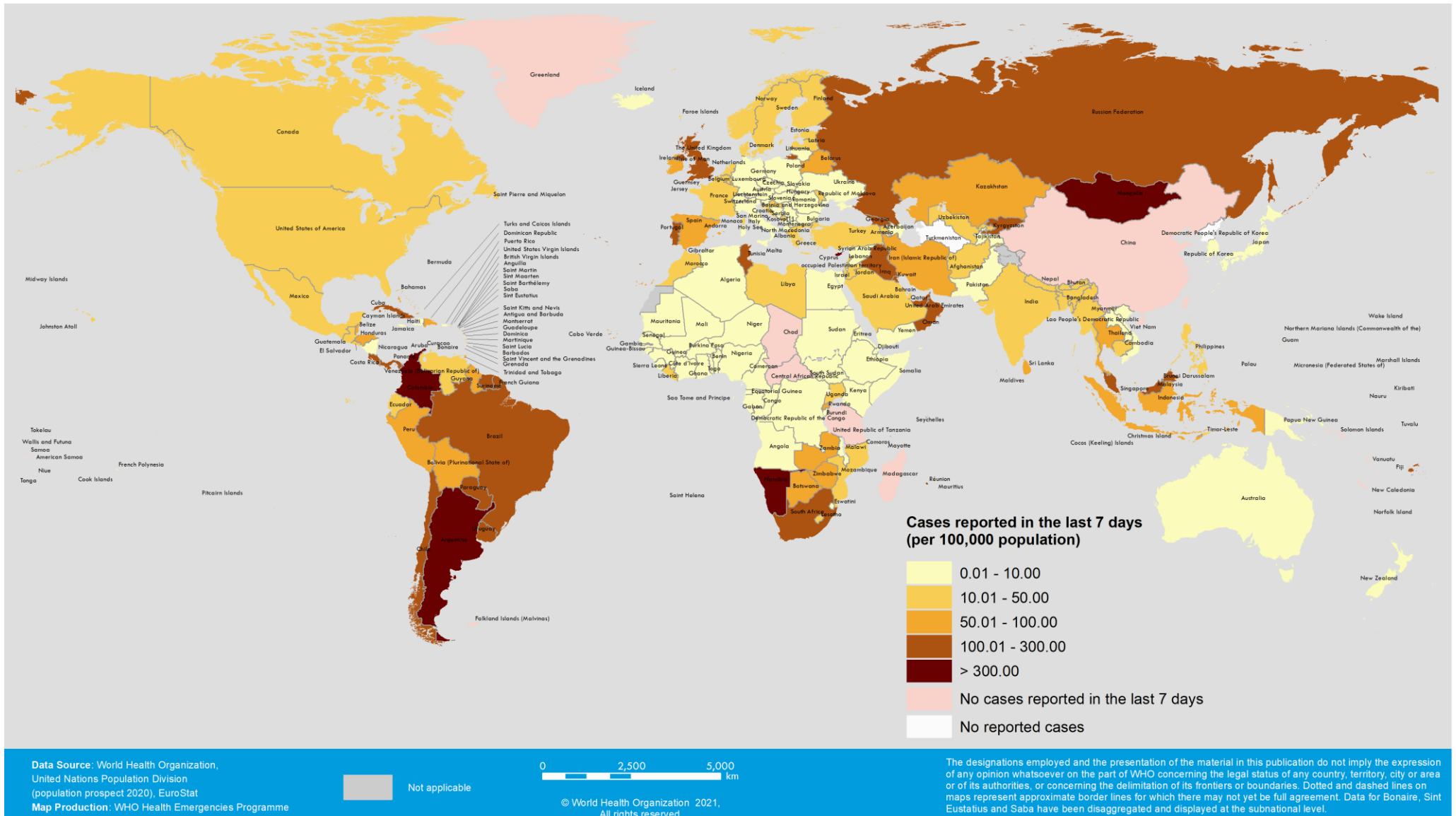
*Percent change in the number of newly confirmed cases/deaths in past seven days, compared to seven days prior

**See [Annex 2: Data, table and figure notes](#)

For the latest data and other updates on COVID-19, please see:

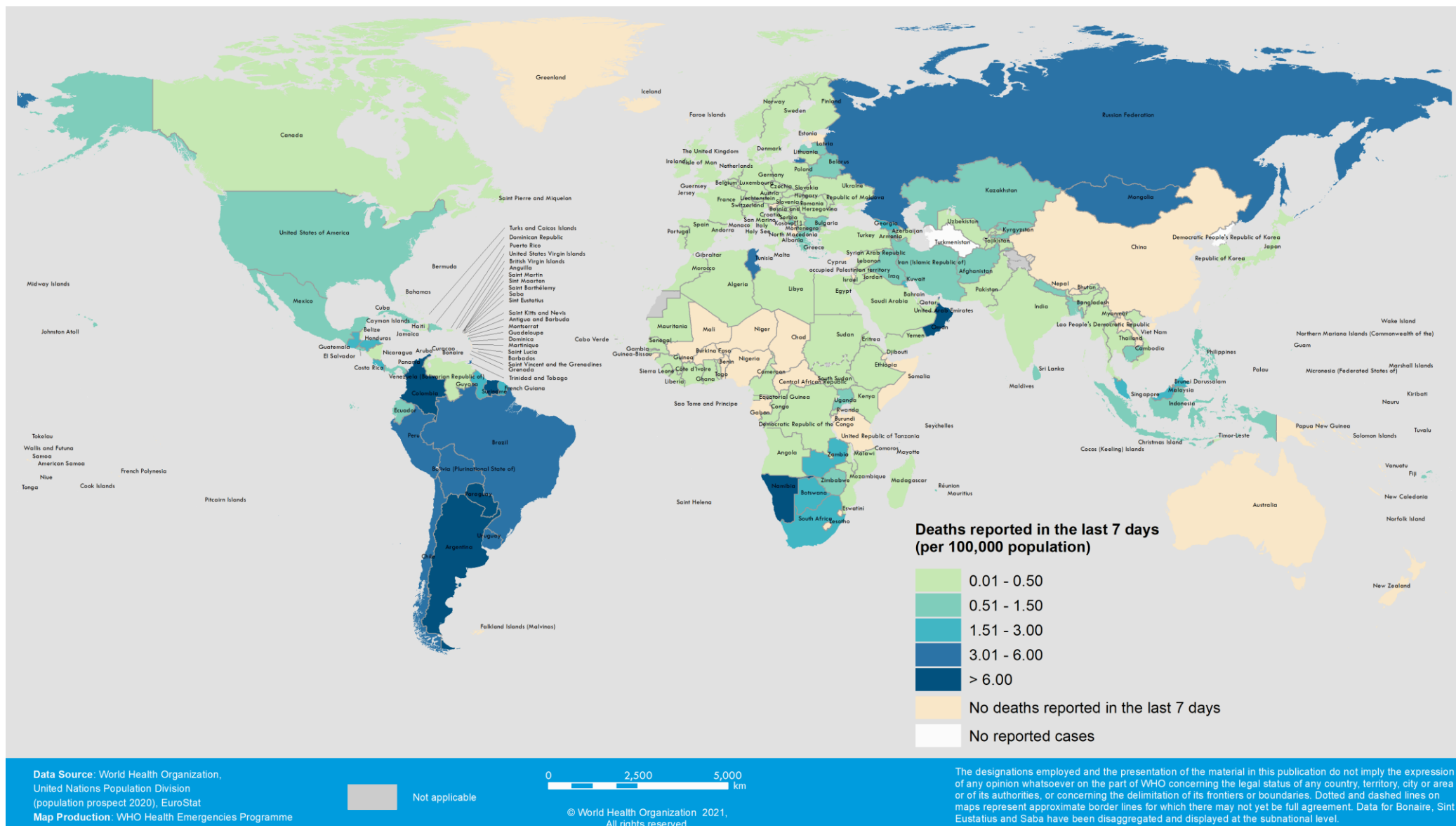
- [WHO COVID-19 Dashboard](#)
- [WHO COVID-19 Weekly Operational Update and previous editions of the Weekly Epidemiological Update](#)

Figure 2. COVID-19 cases per 100 000 population reported by countries, territories and areas, 28 June – 4 July 2021**



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

Figure 3. COVID-19 deaths per 100 000 population reported by countries, territories and areas, 28 June – 4 July 2021**



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

Special Focus: Update on SARS-CoV-2 Variants of Interest and Variants of Concern

WHO, in collaboration with national authorities, institutions and researchers, routinely assesses if variants of SARS-CoV-2 alter transmission or disease characteristics, or impact vaccine, therapeutics, diagnostics or effectiveness of public health and social measures (PHSM) applied by national authorities to control disease spread. “Signals” of potential Variants of Concern (VOCs) or Variants of Interest (VOIs) are detected and assessed based on the risk posed to global public health. National authorities may choose to designate other variants of local interest/concern and are encouraged to investigate and report on impacts of these variants. Here we provide updates on:

- Variant working definitions, and other variants and amino acid changes under monitoring
- Updates to the variant classifications
- Countries/territories/areas reporting the detection of VOCs

Variant working definitions, and other variants and amino acid changes under monitoring

Given the ongoing evolution in our understanding of the impacts of VOCs and VOIs, and the requirements for surveillance and response, WHO periodically reviews and adjusts working definitions (see Box 1 and [WHO Tracking SARS-CoV-2 Variants website](#)).

The revised set of definitions additionally formalizes a third category labelled ‘Alerts for Further Monitoring’, which includes variants with indications that they may pose a risk to global public health, depending on the evolving pandemic, but for which evidence of phenotypic or epidemiological impacts are less clear when compared to the listed VOCs or VOIs. These Alerts are reassessed regularly against criteria outlined in the VOI/VOC working definitions.

Box 1: SARS-CoV-2 Variant Working Definitions, last updated 6 July

Variant of Concern

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.

Variant of Interest

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.

Alerts for Further Monitoring

A SARS-CoV-2 variant with genetic changes that are suspected to affect virus characteristics with some indication that it may pose a future risk, but evidence of phenotypic or epidemiological impact is currently unclear, requiring enhanced monitoring and further assessment pending new evidence.

See also the [WHO Tracking SARS-CoV-2 Variants website](#) for the latest working definitions, and currently designated VOCs, VOIs and Alerts for Further Monitoring, and further information.

In addition to these alerts, reported detections of VOCs with additional amino acid changes, which may or may not carry increased risk of additional phenotypic impacts, are being regularly assessed – e.g., Delta with K417N mutation or Alpha with E484K mutation. Notably, all variants, including VOCs and VOIs, are expected to continue to evolve over time given the ongoing high rates of transmission globally. A phenomenon whereby variants independently acquire the same or similar amino acid substitutions that may offer a competitive advantage (also known as convergent evolution) has been repeatedly observed over the course of the pandemic. Where there is evidence of a common constellation of amino acid changes that have sufficiently diverged from the parent VOC lineage, such sequences may be reclassified under Pango into sublineages to support ongoing investigations, tracking and scientific discourse. While it remains important to track and better understand the impacts of these variants, to date VOCs with additional notable amino acid changes comprise a small fraction of the total number of sequenced cases, and there remains limited direct evidence of further phenotypic impacts.

It is expected that our understanding of designated ‘Alerts for Further Monitoring’, VOCs with notable amino acid changes (including established sublineages) will evolve over time, and variants may be readily added/removed from these characterizations. WHO will, therefore, not be designating labels for these two categories of variants at this time, but where appropriate refer to these cases by their parent lineages (e.g., Delta includes B.1.617.2, AY.1, and AY.2; or Alpha (Pango lineage B.1.1.7; GISAID clade GRY (formerly GR/501Y.V1); Nextstrain clade 20I (V1)) includes B.1.1.7 with E484K. If these variants demonstrate changes in virus characteristics, compared to the parent lineage, in the future, and as such, are assessed as independently meeting the VOC or VOI definitions, then labels will be assigned accordingly.

Updates to the variant classifications

As the global public health risks posed by specific SARS-CoV-2 variants becomes better understood, WHO will continue to update the list of global VOIs and VOCs (Table 2) to support setting priorities for surveillance and research, and ultimately guide response strategies. These updates reflect emergence of new variants, changing epidemiology, and our evolving understanding of the phenotypic impacts of variants as new evidence becomes available. A previously designated Variant of Interest (VOI) or Variant of Concern (VOC) which has conclusively demonstrated to no longer pose a major added risk to global public health compared to other circulating SARS-CoV-2 variants, can be reclassified.

Based upon the latest round of assessments, VOIs Epsilon (B.1.427/B.1.429), Zeta (P.2), and Theta (P.3) were reclassified as ‘Alerts for further monitoring’. While all three variants carry mutations with suspected and/or established phenotypic impacts, reported detections of these variants have decreased over time, suggesting a decline in their respective incidence worldwide, and diminishing public health risks relative to other VOCs and VOIs. Importantly, this assessment considers primarily global risks posed by these variants, and national authorities may choose to continue to designate these as variants of local interest/concern. Moreover, these variants will continue to be monitored, and if new evidence of impacts emerges, their classification will be reassessed.

Epsilon (B.1.427/B.1.429) has been associated with increased transmissibility, a modest decrease in susceptibility to some antibody treatments, and reduced neutralization by convalescent and post-vaccination sera.¹ As of 6 July, just under 50 000 sequences have been uploaded to GISAID from 45 countries.² Worldwide prevalence among sequenced samples has declined from 5% at peak in early February, to less than 0.5% of samples in recent months.³ The vast majority of worldwide sequences (98%) were reported from the United States of America, where Epsilon has been progressively displaced by the emergence of Alpha, Gamma, Delta and other variants, and contributed <0.2% of sequenced samples collected during the weeks two weeks ending 19 June.⁴ Moreover, available data suggest vaccines and treatments remain effective; prompting the Centers for Disease Prevention and Control to reclassify Epsilon from a local VOC on 29 June.¹

Zeta (P.2) harbours spike amino acid change E484K, which has been implicated in resistant to neutralizing antibodies; however, lacks the constellation of mutations synonymous with other VOCs and VOIs. It emerged during October 2020 concomitantly to an increase in case incidence in parts of South America, suggesting a potential increase risk. The global prevalence of samples sequenced as Zeta has remained relatively low and progressively declined to very low levels (<0.5%) from March 2021. As of 6 July, 4439 sequences have been uploaded to GISAID from 42 countries. Half of global sequences (52%, n=2319) originate from Brazil, where prevalence peaked at ~55% in early January 2021. Following the emergence and dominance of VOC Gamma (P.1) in Brazil, prevalence of Zeta has fell to <2% of sequenced samples during April 2021 and has continued to decline.⁵

Theta (P.3) harbours several amino acid changes suggestive of increased resistance to neutralizing antibodies and is potentially more transmissible; however, overall detections of this variant have remained relatively low to date. As to 6 July, a total of 269 sequences were uploaded to GISAID from 14 countries. Most of these sequences (71%, n=191) were reported from the Philippines; predominantly in the Central Visayas Region, where a cluster of cases was identified earlier this year.² Globally over the past 3 months, only sporadic detections or small clusters of cases have been reported.

Updated working definitions, summary table of VOCs and VOIs, and a list of Alerts for Further Monitoring, are available on the [WHO Tracking SARS-CoV-2 Variants website](#).

Geographic distribution

As surveillance activities to detect SARS-CoV-2 variants are strengthened at local and national levels, including by strategic genomic sequencing, the number of countries/areas/territories (hereafter countries) reporting VOCs continues to increase (Figure 2, Annex 1). This distribution should be interpreted with due consideration of surveillance limitations, including differences in sequencing capacities and sampling strategies between countries.

Phenotypic characteristics

Available evidence on phenotypic impacts of VOCs is summarized in Table 3, as well as in [previous editions](#) of these COVID-19 Weekly Epidemiological Updates. Since the last detailed [update](#) on 22 June, new evidence has been published on the phenotypic characteristics of the Delta variant. Based on the estimated transmission advantage of the Delta variant, it is expected that Delta will rapidly outcompete other variants and become the dominant circulating lineage over the coming months.⁶ Based on global data submitted to GISAID, the estimated effective reproductive number for the Delta variant is 55% (95%CI 43-68%) higher than the Alpha variant and 97% (95%CI 76-117%) higher relative to non-VOC/VOI.

In the European Region, based on the estimated transmission advantage of the Delta variant and using modelling forecasts, an estimated 90% of new SARS-CoV-2 infections are expected to be due to Delta by the end of August.⁷ Early data from Scotland, from individuals who tested positive from 1 April to 21 June 2021, showed an increased risk of hospitalization (hazard ratio of hospitalization 1.8; 95%CI 1.4-2.3; data adjusted for age, sex, poverty index, temporal trend, and comorbidities) among cases infected with the Delta variant (as detected by screening of PCR S-gene positive samples), compared with those infected with the Alpha variant (S-gene target failure).⁸

In regards to the Alpha variant, findings from a recent study carried out in 2147 inpatients showed no overall increase in mortality [hazard ratio (HR) 1.01; 95% CI 0.79 – 1.28] or Intensive Therapy Unit (ITU) admission (HR 1.01; 95% CI: 0.75 – 1.37) associated with the Alpha variant as compared to other lineages after adjusting for age, sex, co-morbidities, care home residence, pregnancy and ethnicity. However, an analysis of gender-specific effects of the Alpha variant suggests an increased risk of mortality (HR 1.30; 95% CI: 0.95 – 1.78) and ITU admission (HR 1.82; 95% CI: 1.15 -2.90) in females infected with this variant as compared to other lineages. Males do not show an increased risk of mortality or ITU admission

(mortality HR 0.82, 95% CI 0.61-1.10; ITU HR 0.74, 95% CI 0.52-1.04); this indicates that women may potentially be at an increased risk of admission to ITU and at modestly increased risk of mortality.⁹ Being among the largest studies of hospitalized patients, this study conducted in the United Kingdom provides useful information on disease course and progression, however, analysis of these patients may not provide information on disease severity across all SARS-CoV-2 infections in the population as a whole. Additionally, information on vaccination status for individual patients was not considered in this study.

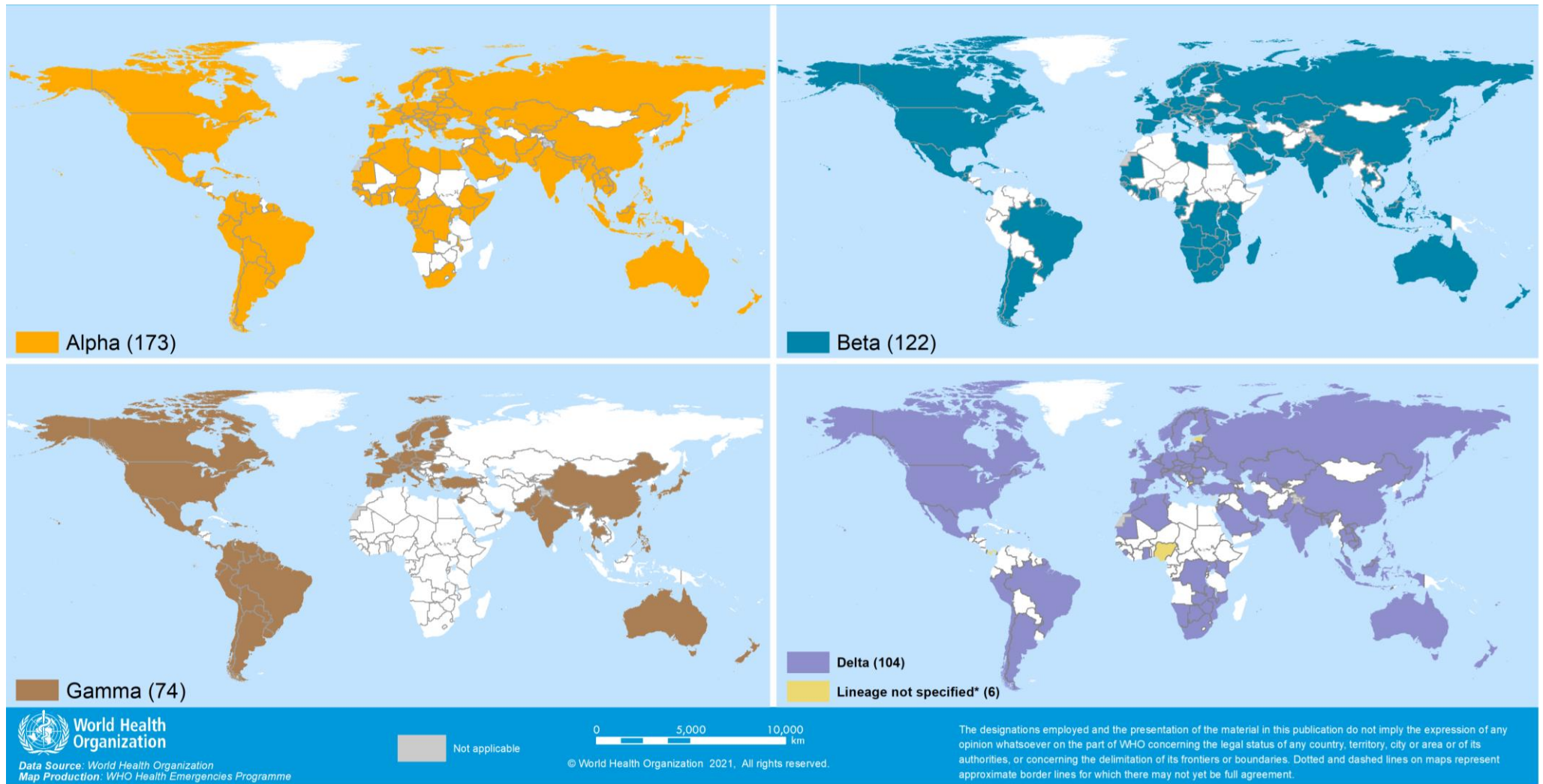
A preprint cohort study conducted in Norway analyzed 1103 unvaccinated individuals hospitalized for COVID-19 from 21 December 2020 to 25 April 2021. Among people infected with the Alpha variant, there was no difference in the length of stay in the hospital or ICU, and no significant difference in mortality up to 30 days following discharge as compared to those infected with non-VOCs.¹⁰ This suggests that, while Alpha may increase the risk of hospitalization, other characteristics such as age and underlying risk factors likely influence the hospitalized patients' clinical course and the type of healthcare required.^{10,11}

Table 3: Summary of phenotypic impacts* of Variants of Concern

| WHO label | Alpha | Beta | Gamma | Delta |
|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------|-------------------------------------------------------------------------|
| Transmissibility | Increased transmissibility and secondary attack rate ¹² | Increased transmissibility ¹³ | Increased transmissibility ¹⁴ | Increased transmissibility and secondary attack rate ^{6,15,16} |
| Disease severity | Increased risk of hospitalization ¹⁷ , possible increased risk of severity and mortality ¹⁸ | Not confirmed, possible increased risk of in-hospital mortality ^{19,20} | Not confirmed, possible increased risk of hospitalization ²¹ | Not confirmed, possible increased risk of hospitalization ²² |
| Risk of reinfection | Neutralizing activity retained, ²³ risk of reinfection remains similar ^{24,25} | Reduction in neutralizing activity reported; T cell response elicited by D614G virus remains effective ²⁶⁻²⁹ | Moderate reduction in neutralizing activity reported ^{30,31} | Reduction in neutralizing activity reported ³² |
| 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 ³³ | No impact on RT-PCR or Ag RDTs observed ¹⁶ | 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.*

Figure 4. Countries, territories and areas reporting variants Alpha, Beta, Gamma and Delta, as of 6 July 2021**



*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.

VOC impacts on vaccines

Table 4 summarises the impact of variants on vaccine efficacy/effectiveness (VE) and quantifies the reduction in VE due to variants compared to VE in non-VOC settings. Of note, reductions in VE do not mean loss of protection, as indicated by the absolute VE estimate. For example, a 10 percent point reduction in VE against symptomatic disease for mRNA vaccines would still mean high vaccine effectiveness of ~85%. In addition, vaccines have shown higher VE against severe disease; thus, small reductions in VE against severe disease due to VOCs may still mean good protection, as is the case for AstraZeneca-Vaxzevria.

Since the 22 June [update](#), phase 3 trial results for Bharat-Covaxin (not yet peer-reviewed) have been made available. This double-blind, randomized control trial included 25 798 participants aged 18 years and older, randomized to receive two doses of the vaccine or a placebo with 4 weeks in between doses. Overall vaccine efficacy against severe and symptomatic disease ≥ 14 days post second dose was 93.4% (95% CI: 57.1-99.8%) and 77.8% (65.2-86.4%), respectively. Among 130 SARS-CoV-2 positive samples, 79 (60.8%) were genotyped. VE against Delta symptomatic disease (65.2% (33.1-83.0%)) was lower than other typed variants; 90.1% (30.4-99.8%) against Kappa (B.1.617.1), and 73.0% (-2.2-95.2%) against all other variants, although numbers were small with overlapping confidence intervals.³⁴

A test-negative case-control study in Ontario, Canada (not yet peer reviewed) assessed the effectiveness against variants of concern among 421 073 individuals aged 16 years and older, who were tested for SARS-CoV-2. The authors used a combination of whole genome sequencing and mutation screening by PCR to classify VOC. VE of two doses of both Pfizer BioNTech-Comirnaty and Moderna-mRNA-1273 against symptomatic disease ≥ 7 days post final dose was measured. VE for Pfizer BioNTech-Comirnaty was 93% (95% CI: 88-96%), 89% (86-91%), 84% (69-92%), and 87% (64-95%) against non-VOC, Alpha, Beta/Gamma, and Delta variants, respectively. VE of Moderna-mRNA-1273 was 92% (86-96%) against Alpha as compared to 89% (65-96%) against non-VOC (VE against Beta/Gamma and Delta not measured). A single dose of AstraZeneca-Vaxzevria resulted in a VE of 64-67% for non-VOC, Alpha and Delta, and a VE of 48% against Beta/Gamma. Two dose VE estimates for AstraZeneca-Vaxzevria were not provided due to insufficient numbers. The study also found two doses of Pfizer BioNTech-Comirnaty and Moderna-mRNA-1273 vaccines to provide very good protection against hospitalization or death due to Alpha and non-VOC (VE estimates of 94-96%), and two doses of Pfizer BioNTech-Comirnaty also had high VE against Beta/Gamma (95%); no data for Moderna-mRNA-1273 against Beta/Gamma. A single dose of Pfizer BioNTech-Comirnaty, Moderna-mRNA-1273 and AstraZeneca-Vaxzevria prevented 78%, 96% and 88% of hospitalizations/deaths due to Delta, respectively.³⁵

Another study (not yet peer-reviewed) reported on the effectiveness of Sinovac-CoronaVac in Manaus, Brazil, during a time when the predominant circulating strain was Gamma (86% of genotyped SARS-CoV-2 were the Gamma variant during the peak of the epidemic in Manaus). The study used a test-negative case-control design to estimate VE among ~400 case-control pairs of health care workers. VE of two doses of the vaccine against symptomatic disease and against infection 14+ days post final dose was 36.8% (95% CI: -54.9-74.2%) and 37.9% (95% CI: -46.4 to 73.6%), respectively. Authors note the low VE estimate likely reflect a bias towards the null hypothesis as suggested by the finding that vaccinated individuals were much more likely to be infected than unvaccinated individuals in the period 0-13 days after receipt of the first dose (aOR 2.11, 95% CI 1.36-3.27). Authors also note that the analysis may have been underpowered to be able to detect a VE of lower than 70%.³⁶

Four new studies (not yet peer reviewed) have evaluated the ability of vaccine sera to neutralize the Delta variant. While these four studies found relatively modest reductions in neutralization of the Delta variant by AstraZeneca-Vaxzevria (4.0-fold reduction), SII-Covishield (3.2-fold reduction), Moderna-mRNA-1273 (2.1-fold reduction), and Janssen-Ad26.COV 2.5 (1.6-fold reduction) relative to the reference strain, a larger reduction was found for the Pfizer BioNTech-Comirnaty (11.3-fold reduction) in one of the studies.³⁷⁻⁴⁰ To date, five studies have evaluated neutralization of the Delta variant by Pfizer BioNTech-Comirnaty and report fold-reductions ranging from 1.4 to 11.3; two studies evaluating AstraZeneca-Vaxzevria have both reported an approximate 4-fold reduction; and single studies have found ~2-3-fold reductions by sera from individuals who had received Janssen-Ad26.COV 2.5, Moderna-mRNA-1273, Bharat-Covaxin, and SII-Covishield vaccines.³⁷⁻⁴⁶

Table 4. Summary of vaccine performance against Variants of Concern

| Alpha | Beta | Gamma | Delta |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Efficacy/effectiveness against disease or infection (full vaccination), see key below table | | | |
| Protection retained against all outcomes | Reduced protection against symptomatic disease, but retained against severe disease; limited evidence | Unclear impact; very limited evidence | Protection retained against severe disease; possible reduced protection against symptomatic disease and infection |
| Severe disease | | | |
| <ul style="list-style-type: none"> ↔ to ↓: Moderna-mRNA-1273 (1), Pfizer BioNTech-Comirnaty (3), Moderna-mRNA-1273/Pfizer BioNTech-Comirnaty (1)^{35,47-49} ↓: AstraZeneca- Vaxzevria (1)⁴⁹ | <ul style="list-style-type: none"> ↔: Janssen Ad26.COV 2.5 (1), Pfizer BioNTech-Comirnaty (1)^{48,50} | <ul style="list-style-type: none"> No evidence | <ul style="list-style-type: none"> ↔: AstraZeneca- Vaxzevria (1), Pfizer BioNTech-Comirnaty (1)⁴⁹ |
| Symptomatic disease | | | |
| <ul style="list-style-type: none"> ↔: Moderna-mRNA-1273/Pfizer BioNTech-Comirnaty (2), Pfizer BioNTech-Comirnaty (3)^{35,47,51,52} ↔ to ↓: AstraZeneca-Vaxzevria (3)⁵¹⁻⁵³ ↓: Novavax-Covavax (1)⁵⁴ | <ul style="list-style-type: none"> ↔: Janssen-Ad26. COV 2.5 (1)⁵⁰ ↓↓↓: AstraZeneca-Vaxzevria (1), Novavax-Covavax (1)^{55,56} | <ul style="list-style-type: none"> ↔ to ↓: Sinovac-CoronaVac (1)^{36,57} | <ul style="list-style-type: none"> ↔ to ↓: Pfizer BioNTech-Comirnaty (3)^{35,51,52} ↓: Bharat-Covaxin (1)³⁴ ↓↓: AstraZeneca- Vaxzevria (2)^{51,52} |
| Infection | | | |
| <ul style="list-style-type: none"> ↔: Pfizer BioNTech-Comirnaty (3)^{52,58} ↔ to ↓: AstraZeneca-Vaxzevria (2)^{52,53} | <ul style="list-style-type: none"> ↓: PfizerBioNTech-Comirnaty (1)⁴⁸ | <ul style="list-style-type: none"> No evidence | <ul style="list-style-type: none"> ↓: AstraZeneca-Vaxzevria (1), Pfizer BioNTech-Comirnaty (1)⁵² |
| Neutralization (full vaccination), see key below table | | | |
| <ul style="list-style-type: none"> ↔: Beijing CNBG-BBIBP-CorV (1), Bharat-Covaxin (1), Gamaleya-Sputnik V (1), Novavax-Covavax (1), Sinovac-CoronaVac (2)⁵⁹⁻⁶³ ↔ to ↓: Janssen-Ad26.COV 2.5 (2), Moderna- mRNA-1273 (9), Pfizer BioNTech-Comirnaty (26)^{29,37,38,41,63-90} ↓ to ↓↓: AstraZeneca-Vaxzevria (2)^{53,68} | <ul style="list-style-type: none"> ↔ to ↓: Anhui ZL-Recombinant (2), Beijing CNBG-BBIBP-CorV (2)^{59,91,92} ↓: Bharat-Covaxin (1)⁴² ↓ to ↓↓: Pfizer BioNTech-Comirnaty (27), Sinovac-CoronaVac (3)^{29,39,41,59,62,64,65,68,70-74,76,77,80-82,86-89,91,93-97} ↓ to ↓↓↓: Janssen-Ad26.COV 2.5 (3)^{38,90,98} ↓↓: AstraZeneca-Vaxzevria (3), Gamaleya-Sputnik V (1), Moderna-mRNA-1273 (10)^{37,39,55,61,68,70,76,79,81,85,96,97,99-101} ↓↓ to ↓↓↓: Janssen-Ad26.COV 2.5 (3)^{38,90,98} ↓↓↓: Novavax-Covavax (1)⁵⁹ | <ul style="list-style-type: none"> ↔: Sinovac-CoronaVac (1)¹⁰² ↔ to ↓: Pfizer BioNTech-Comirnaty (11)^{43,64,68,70,72,74,77,86,93,103} ↓: AstraZeneca-Vaxzevria (1), Janssen-Ad26.COV 2.5 (2), Moderna-mRNA-1273 (4)^{37,38,68,70,85,90,103} | <ul style="list-style-type: none"> ↔: Janssen-Ad.COV 2.5 (1)³⁸ ↓: AstraZeneca-Vaxzevria (2), Bharat-Covaxin (1), Moderna-mRNA-1273 (1)^{37,39,42,44} ↓ to ↓↓: Pfizer BioNTech-Comirnaty (5)^{39,41,43-45} |

Arrows generalize the magnitude of reduction in VE or neutralization: “↔” <10% reduction in VE, or VE >90% with no comparator, or that there was a <2-fold reduction in neutralization; “↓” 10 to <20% reduction in VE, or 2 to <5-fold reduction in neutralization; “↓↓” 20 to <30% reduction in VE, or 5 to <10-fold reduction in neutralization; “↓↓↓” ≥30% reduction in VE, or ≥10-fold reduction in neutralization. When more than one neutralization study is available, the interquartile range (25th and 75th percentiles) of fold-reductions across all studies for specific vaccine/variant was used.

The number of studies is shown in parentheses.

“Moderna-mRNA-1273/Pfizer BioNTech-Comirnaty” indicates that both vaccines were evaluated together in study.

Additional resources

- [Tracking SARS-CoV-2 variants](#)
- [COVID-19 new variants: Knowledge gaps and research](#)
- [Genomic sequencing of SARS-CoV-2: a guide to implementation for maximum impact on public health](#)
- [Considerations for implementing and adjusting public health and social measures in the context of COVID-19](#)

Additional notes on VOC impacts on vaccines

- Studies presenting VOC specific VE estimates are assessed against a comparator VE estimate to determine level of reduction in VE. For symptomatic disease, VOC VE is compared against phase 3 randomised RCT results from non-VOC settings. For severe disease and infection, VOC VE is compared to non-VOC VE estimates from the same study when available (or to Alpha VE from same study when assessing Beta, Gamma, or Delta); with an exception for AstraZeneca Vaxzevria for severe disease (phase 3 RCT efficacy estimates against severe disease are used as comparator since within study comparator is unavailable) and for infection (phase 3 estimate of VE against infection due to non-VOC is available and used as comparator). In some instances, a study may be included for severe disease or infection even without a comparator if very high VE estimate against a VOC is reported (i.e., >90%).
- It is also important to note that studies vary in population, outcome definitions, study design and other methodological considerations, which may in part explain differences when comparing VE estimates between different studies. In addition, the reductions presented consider VE point estimates only and do not take into account the uncertainty around these estimates. The reductions in VE noted should be interpreted with these limitations in mind.

References

1. United States Centers for Disease Control and Prevention. SARS-CoV-2 Variant Classifications and Definitions. Centers for Disease Control and Prevention. Published February 11, 2020. Accessed July 6, 2021. <https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-info.html>
2. GISAID. GISAID Tracking of SARS-CoV-2 Variants. GISAID: Global initiative on sharing all influenza data. Accessed July 6, 2021. <https://www.gisaid.org/hcov19-variants/>
3. Outbreak info. Outbreak info B.1.427/429 Lineage Report. outbreak.info. Accessed July 6, 2021. <https://outbreak.info/>
4. United States Centers for Disease Control and Prevention. *COVID Data Tracker, Variant Proportions*. <https://covid.cdc.gov/covid-data-tracker/#variant-proportions>
5. Outbreak info. Outbreak info P.2 Lineage Report. outbreak.info. Accessed July 6, 2021. <https://outbreak.info/>
6. Campbell F, Archer B, Laurenson-Schafer H, et al. Increased transmissibility and global spread of SARS-CoV-2 variants of concern as at June 2021. *Eurosurveillance*. 2021;26(24):2100509. <https://www.eurosurveillance.org/content/10.2807/1560-7917.ES.2021.26.24.2100509>
7. *Implications for the EU/EEA on the Spread of the SARS-CoV-2 Delta (B.1.617.2) Variant of Concern*. ECDC; 2021. https://www.ecdc.europa.eu/sites/default/files/documents/Implications-for-the-EU-EEA-on-the-spread-of-SARS-CoV-2-Delta-VOC-23-June-2021_2.pdf
8. Public Health England. *SARS-CoV-2 Variants of Concern and Variants under Investigation in England- Technical Briefing 17*. Public Health England (PHE); 2021. https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/997418/Variants_of_Concern_VOC_Technical_Briefing_17.pdf
9. Stirrup OT, Boshier FAT, Venturini C, et al. SARS-CoV-2 lineage B.1.1.7 is associated with greater disease severity among hospitalised women but not men. *medRxiv*. Published online June 28, 2021:2021.06.24.21259107. doi:10.1101/2021.06.24.21259107
10. Whittaker R, Kristofferson AB, Seppälä E, et al. Trajectories of hospitalisation for patients infected with SARS-CoV-2 variant B.1.1.7 in Norway, December 2020 – April 2021. *medRxiv*. Published online July 2, 2021:2021.06.28.21259380. doi:10.1101/2021.06.28.21259380
11. Nyberg T, Twhohig KA, Harris RJ, et al. Risk of hospital admission for patients with SARS-CoV-2 variant B.1.1.7: cohort analysis. *BMJ*. 2021;373:n1412. doi:10.1136/bmj.n1412
12. Buchan SA, Tibebe S, Daneman N, et al. Increased household secondary attacks rates with Variant of Concern SARS-CoV-2 index cases. *Clinical Infectious Diseases*. 2021;(ciab496). doi:10.1093/cid/ciab496
13. Tegally H, Wilkinson E, Giovanetti M, et al. Emergence of a SARS-CoV-2 variant of concern with mutations in spike glycoprotein. *Nature*. Published online 2021. <https://doi.org/10.1038/s41586-021-03402-9>
14. Curran J, Dol J, Boulos L, et al. Transmission characteristics of SARS-CoV-2 variants of concern Rapid Scoping Review. *medRxiv*. Published online January 1, 2021:2021.04.23.21255515. doi:10.1101/2021.04.23.21255515
15. Cherian S, Potdar V, Jadhav S, et al. Convergent evolution of SARS-CoV-2 spike mutations, L452R, E484Q and P681R, in the second wave of COVID-19 in Maharashtra, India. *bioRxiv*. Published online January 1, 2021:2021.04.22.440932. doi:10.1101/2021.04.22.440932
16. Public Health England. *SARS-CoV-2 Variants of Concern and Variants under Investigation in England Technical Briefing 16*.; 2021. https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/994839/Variants_of_Concern_VOC_Technical_Briefing_16.pdf
17. Bager P, Wohlfahrt J, Fonager J, Albertsen. Increased Risk of Hospitalisation Associated with Infection with SARS-CoV-2 Lineage B.1.1.7 in Denmark. doi:Bager, Peter and Wohlfahrt, Jan and Fonager, Jannik and Albertsen, Mads and Yssing Michaelsen, Thomas and Holten Møller, Camilla and Ethelberg, Steen and Legarth, Rebecca and Fischer Button, Mia Sara and Gubbels, Sophie Madeleine and Voldstedlund, Marianne and Mølbak, Kåre and Skov, Robert Leo and Fomsgaard, Anders and Grove Krause, Tyra, Increased Risk of Hospitalisation Associated with Infection with SARS-CoV-2 Lineage B.1.1.7 in Denmark. Available at SSRN: <https://ssrn.com/abstract=3792894> or <http://dx.doi.org/10.2139/ssrn.3792894>
18. NERVTAG paper on COVID-19 variant of concern B.1.1.7. *GOV.UK*. Published online 2021. <https://www.gov.uk/government/publications/nervtag-paper-on-covid-19-variant-of-concern-b117>, <http://files/64/nervtag-paper-on-covid-19-variant-of-concern-b117.html> [2021/02/08/18:37:19
19. Pearson CA, Eggo. Estimates of severity and transmissibility of novel South Africa SARS-CoV-2 variant 501Y.V2. https://cmmid.github.io/topics/covid19/reports/sa-novel-variant/2021_01_11_Transmissibility_and_severity_of_501Y_V2_in_SA.pdf
20. Jassat W MC. *Increased Mortality among Individuals Hospitalised with COVID-19 during the Second Wave in South Africa*.; 2021. <https://www.medrxiv.org/content/10.1101/2021.03.09.21253184v1>
21. Funk T, Pharris A, Spiteri G, et al. Characteristics of SARS-CoV-2 variants of concern B.1.1.7, B.1.351 or P.1: data from seven EU/EEA countries, weeks 38/2020 to 10/2021. *Eurosurveillance*. 2021;26(16). doi:https://doi.org/10.2807/1560-7917.ES.2021.26.16.2100348
22. Public Health England. *SARS-CoV-2 Variants of Concern and Variants under Investigation in England Technical Briefing 14*.; 2021. https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/991343/Variants_of_Concern_VOC_Technical_Briefing_14.pdf
23. Muik A, Wallisch A-K, Sängler B, et al. Neutralization of SARS-CoV-2 lineage B.1.1.7 pseudovirus by BNT162b2 vaccine-elicited human sera. *Science*. Published online 2021:eabg6105. <https://science.sciencemag.org/content/sci/early/2021/01/28/science.abg6105.full.pdf>
24. Gallais F, Gantner P, Bruel T, et al. Anti-SARS-CoV-2 Antibodies Persist for up to 13 Months and Reduce Risk of Reinfection. *medRxiv*. Published online January 1, 2021:2021.05.07.21256823. doi:10.1101/2021.05.07.21256823
25. Graham MS, Sudre CH, May A, et al. Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study. *Lancet Public Health*. 2021;6(5):e335-e345. doi:10.1016/S2468-2667(21)00055-4
26. Wibmer CK, Ayres F, Hermanus T, et al. SARS-CoV-2 501Y.V2 escapes neutralization by South African COVID-19 donor plasma. *Nat Med*. Published online March 2021. <https://www.ncbi.nlm.nih.gov/pubmed/33654292>
27. Li R, Ma X, Deng J, et al. Differential efficiencies to neutralize the novel mutants B.1.1.7 and 501Y.V2 by collected sera from convalescent COVID-19 patients and RBD nanoparticle-vaccinated rhesus macaques. *Cell Mol Immunol*. Published online February 2021. <https://www.ncbi.nlm.nih.gov/pubmed/33580167>
28. Cele S, Gazy I, Jackson L, et al. Escape of SARS-CoV-2 501Y.V2 variants from neutralization by convalescent plasma. :19. <https://www.medrxiv.org/content/10.1101/2021.01.26.21250224v1>
29. Caniels TG, Bontjer I, Straten K van der, et al. Emerging SARS-CoV-2 variants of concern evade humoral immune responses from infection and vaccination. *medRxiv*. Published online June 1, 2021:2021.05.26.21257441. doi:10.1101/2021.05.26.21257441
30. Sabino EC, Buss LF, Carvalho MPS, et al. Resurgence of COVID-19 in Manaus, Brazil, despite high seroprevalence. *The Lancet*. 2021;397(10273):452-455. <https://linkinghub.elsevier.com/retrieve/pii/S0140673621001835>
31. Naveca F, Nascimento V, Souza V, et al. Phylogenetic relationship of SARS-CoV-2 sequences from Amazonas with emerging Brazilian variants harboring mutations E484K and N501Y in the Spike protein. *Virological*. Published online 2021. <https://virological.org/t/phylogenetic-relationship-of-sars-cov-2-sequences-from-amazonas-with-emerging-brazilian-variants-harboring-mutations-e484k-and-n501y-in-the-spike-protein/585>
32. Planas D, Veyer D, Baidaliuk A, et al. *Reduced Sensitivity of Infectious SARS-CoV-2 Variant B.1.617.2 to Monoclonal Antibodies and Sera from Convalescent and Vaccinated Individuals*. Microbiology; 2021. doi:10.1101/2021.05.26.445838

33. SARS-CoV-2 lateral flow antigen tests: evaluation of VUI-202012/01. *GOV.UK*. <https://www.gov.uk/government/publications/sars-cov-2-lateral-flow-antigen-tests-evaluation-of-vui-20201201/sars-cov-2-lateral-flow-antigen-tests-evaluation-of-vui-20201201>, <http://files/62/sars-cov-2-lateral-flow-antigen-tests-evaluation-of-vui-20201201.html> [2021/02/08/16:54:26]
34. Ella R. Efficacy, safety, and lot to lot immunogenicity of an inactivated SARS-CoV-2 vaccine (BBV152): a double-blind, randomised, controlled phase 3 trial. :29.
35. Nasreen S. Effectiveness of COVID-19 vaccines against variants of concern, Canada. :27.
36. Hitchings MDT, Ranzani OT, Torres MSS, et al. Effectiveness of CoronaVac among healthcare workers in the setting of high SARS-CoV-2 Gamma variant transmission in Manaus, Brazil: A test-negative case-control study. *medRxiv*. Published online June 24, 2021:2021.04.07.21255081. doi:10.1101/2021.04.07.21255081
37. Choi A, Koch M, Wu K, et al. Serum Neutralizing Activity of mRNA-1273 against SARS-CoV-2 Variants. *bioRxiv*. Published online June 28, 2021:2021.06.28.449914. doi:10.1101/2021.06.28.449914
38. Jongeneelen M, Kaszas K, Veldman D, et al. Ad26.COV2.S elicited neutralizing activity against Delta and other SARS-CoV-2 variants of concern. *bioRxiv*. Published online July 1, 2021:2021.07.01.450707. doi:10.1101/2021.07.01.450707
39. Davis C, Logan N, Tyson G, et al. Reduced neutralisation of the Delta (B.1.617.2) SARS-CoV-2 variant of concern following vaccination. *medRxiv*. Published online June 28, 2021:2021.06.23.21259327. doi:10.1101/2021.06.23.21259327
40. Sapkal G, Yadav PD, Sahay RR, et al. Neutralization of Delta variant with sera of Covishield vaccinees and COVID-19 recovered vaccinated individuals. *bioRxiv*. Published online July 2, 2021:2021.07.01.450676. doi:10.1101/2021.07.01.450676
41. Wall EC, Wu M, Harvey R, et al. Neutralising antibody activity against SARS-CoV-2 VOCs B.1.617.2 and B.1.351 by BNT162b2 vaccination. *The Lancet*. 2021;0(0). doi:10.1016/S0140-6736(21)01290-3
42. Yadav PD, Sapkal GN, Ella R, et al. Neutralization against B.1.351 and B.1.617.2 with sera of COVID-19 recovered cases and vaccinees of BBV152. *bioRxiv*. Published online June 7, 2021:2021.06.05.447177. doi:10.1101/2021.06.05.447177
43. Liu J, Liu Y, Xia H, et al. BNT162b2-elicited neutralization of B.1.617 and other SARS-CoV-2 variants. *Nature*. Published online June 10, 2021:1-5. doi:10.1038/s41586-021-03693-y
44. Liu C, Ginn HM, Dejnirattisai W, et al. Reduced neutralization of SARS-CoV-2 B.1.617 by vaccine and convalescent serum. *Cell*. Published online June 17, 2021. doi:10.1016/j.cell.2021.06.020
45. Planas D, Veyer D, Baidaliuk A, et al. Reduced sensitivity of infectious SARS-CoV-2 variant B.1.617.2 to monoclonal antibodies and sera from convalescent and vaccinated individuals. *bioRxiv*. Published online May 27, 2021:2021.05.26.445838. doi:10.1101/2021.05.26.445838
46. Lustig Y, Zuckerman N, Nemet I, et al. Neutralising capacity against Delta (B.1.617.2) and other variants of concern following Comirnaty (BNT162b2, BioNTech/Pfizer) vaccination in health care workers, Israel. *Eurosurveillance*. 2021;26(26):2100557. doi:10.2807/1560-7917.ES.2021.26.26.2100557
47. Chung H, He S, Nasreen S, et al. Effectiveness of BNT162b2 and mRNA-1273 COVID-19 vaccines against symptomatic SARS-CoV-2 infection and severe COVID-19 outcomes in Ontario, Canada. Published online 2021:30.
48. Abu-Raddad LJ, Chemaitelly H, Butt AA, National Study Group for COVID-19 Vaccination. Effectiveness of the BNT162b2 Covid-19 Vaccine against the B.1.1.7 and B.1.351 Variants. *The New England journal of medicine*. Published online May 2021. doi:10.1056/NEJMc2104974
49. Stowe J, Andrews JR, Gower C, et al. Effectiveness of COVID-19 vaccines against hospital admission with the Delta variant - Public library - PHE national - Knowledge Hub. Accessed June 18, 2021. https://khub.net/web/phe-national/public-library/-/document_library/v2WsRK3ZIEig/view/479607266
50. Sadoff J, Gray G, Vandebosch A, et al. Safety and Efficacy of Single-Dose Ad26.COV2.S Vaccine against Covid-19. *New England Journal of Medicine*. Published online April 2021:NEJMoa2101544-NEJMoa2101544. doi:10.1056/NEJMoa2101544
51. Lopez Bernal J, Andrews N, Gower C, et al. Effectiveness of COVID-19 vaccines against the B.1.617.2 variant. doi:https://doi.org/10.1101/2021.05.22.21257658
52. Sheikh A, McMenamin J, Taylor B, Robertson C. SARS-CoV-2 Delta VOC in Scotland: demographics, risk of hospital admission, and vaccine effectiveness. *The Lancet*. 2021;0(0). doi:10.1016/S0140-6736(21)01358-1
53. Emary KRW, Golubchik T, Aley PK, et al. Efficacy of ChAdOx1 nCoV-19 (AZD1222) vaccine against SARS-CoV-2 variant of concern 202012/01 (B.1.1.7): an exploratory analysis of a randomised controlled trial. *The Lancet*. 2021;397(10282):1351-1362. doi:10.1016/S0140-6736(21)00628-0
54. Heath PT, Eva Galiza FP, David Neil Baxter M, et al. Efficacy of the NVX-CoV2373 Covid-19 Vaccine Against the B.1.1.7 Variant. *medRxiv*. Published online May 2021:2021.05.13.21256639-2021.05.13.21256639. doi:10.1101/2021.05.13.21256639
55. Madhi SA, Baillie V, Cutland CL, et al. Efficacy of the ChAdOx1 nCoV-19 Covid-19 Vaccine against the B.1.351 Variant. *New England Journal of Medicine*. Published online March 2021:NEJMoa2102214-NEJMoa2102214. doi:10.1056/NEJMoa2102214
56. Shinde V, Bhikha S, Hoosain Z, et al. Efficacy of NVX-CoV2373 Covid-19 Vaccine against the B.1.351 Variant. *New England Journal of Medicine*. Published online May 2021:NEJMoa2103055-NEJMoa2103055. doi:10.1056/NEJMoa2103055
57. Ranzani OT, Hitchings M, Neto MD, et al. Effectiveness of the CoronaVac vaccine in the elderly population during a P.1 variant-associated epidemic of COVID-19 in Brazil: A test-negative case-control study. *medRxiv*. Published online May 21, 2021:2021.05.19.21257472. doi:10.1101/2021.05.19.21257472
58. Pritchard E, Matthews PC, Stoesser N, et al. Impact of vaccination on SARS-CoV-2 cases in the community: a population-based study using the UK's COVID-19 Infection Survey. *medRxiv*. Published online April 2021:2021.04.22.21255913-2021.04.22.21255913. doi:10.1101/2021.04.22.21255913
59. Wang G-L, Wang Z-Y, Duan L-J, et al. Susceptibility of Circulating SARS-CoV-2 Variants to Neutralization. *New England Journal of Medicine*. Published online April 2021:NEJMc2103022-NEJMc2103022. doi:10.1056/nejmc2103022
60. Yadav P, Sapkal GN, Abraham P, et al. Neutralization of variant under investigation B.1.617 with sera of BBV152 vaccinees. *bioRxiv*. Published online April 2021:2021.04.23.441101-2021.04.23.441101. doi:10.1101/2021.04.23.441101
61. Ikegame S, A Siddiquey MN, Hung C-T, et al. Qualitatively distinct modes of Sputnik V vaccine-neutralization escape by SARS-CoV-2 Spike variants. *medRxiv*. Published online April 2021:2021.03.31.21254660-2021.03.31.21254660. doi:10.1101/2021.03.31.21254660
62. Chen Y, Shen H, Huang R, Tong X, Wu C. Serum neutralising activity against SARS-CoV-2 variants elicited by CoronaVac. *The Lancet Infectious Diseases*. 2021;0(0). doi:10.1016/S1473-3099(21)00287-5
63. Shen X, Tang H, McDanal C, et al. SARS-CoV-2 variant B.1.1.7 is susceptible to neutralizing antibodies elicited by ancestral spike vaccines. *Cell Host & Microbe*. 2021;29(4):529-539.e3. doi:10.1016/j.chom.2021.03.002
64. Anichini G, Terrosi C, Gori Savellini G, Gandolfo C, Franchi F, Cusi MG. Neutralizing Antibody Response of Vaccinees to SARS-CoV-2 Variants. *Vaccines*. 2021;9(5):517. doi:10.3390/vaccines9050517
65. Bates TA, Leier HC, Lyski ZL, et al. Neutralization of SARS-CoV-2 variants by convalescent and vaccinated serum. *medRxiv*. Published online April 2021:2021.04.04.21254881-2021.04.04.21254881. doi:10.1101/2021.04.04.21254881
66. Becker M, Dulovic A, Junker D, et al. Immune response to SARS-CoV-2 variants of concern in vaccinated individuals. *Nat Commun*. 2021;12(1):3109. doi:10.1038/s41467-021-23473-6
67. Collier AY, McMahan K, Yu J, et al. Immunogenicity of COVID-19 mRNA Vaccines in Pregnant and Lactating Women. Published online 2021. doi:10.1001/jama.2021.7563
68. Dejnirattisai W, Zhou D, Supasa P, et al. Antibody evasion by the P.1 strain of SARS-CoV-2. *Cell*. 2021;0(0). doi:10.1016/j.cell.2021.03.055
69. Edara VV, Floyd K, Lai L, et al. Infection and mRNA-1273 vaccine antibodies neutralize SARS-CoV-2 UK variant. *medRxiv : the preprint server for health sciences*. Published online February 2021:2021.02.02.21250799-2021.02.02.21250799. doi:10.1101/2021.02.02.21250799

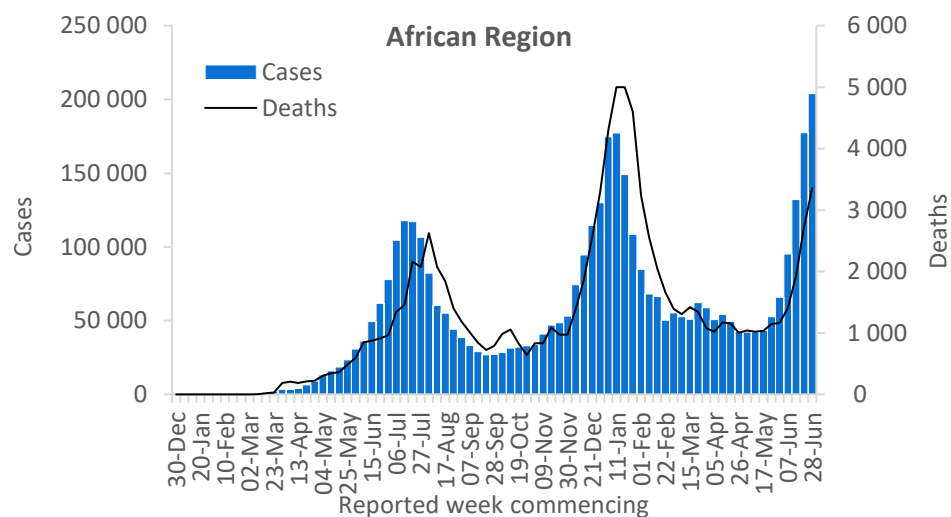
70. Garcia-Beltran WF, Lam EC, St. Denis K, et al. Multiple SARS-CoV-2 variants escape neutralization by vaccine-induced humoral immunity. *Cell*. 2021;0(0). doi:10.1016/j.cell.2021.03.013
71. Gonzalez C, Saade C, Bal A, et al. Live virus neutralisation testing in convalescent patients and subjects vaccinated 1 against 19A, 20B, 20I/501Y.V1 and 20H/501Y.V2 isolates of SARS-CoV-2 2 3. *medRxiv*. Published online May 2021:2021.05.11.21256578-2021.05.11.21256578. doi:10.1101/2021.05.11.21256578
72. Hoffmann M, Arora P, Groß R, et al. SARS-CoV-2 variants B.1.351 and P.1 escape from neutralizing antibodies. *Cell*. 2021;184(9):2384-2393.e12. doi:10.1016/j.cell.2021.03.036
73. Kuzmina A, Khalaila Y, Voloshin O, et al. SARS-CoV-2 spike variants exhibit differential infectivity and neutralization resistance to convalescent or post-vaccination sera. *Cell Host and Microbe*. 2021;29(4):522-528.e2. doi:10.1016/j.chom.2021.03.008
74. Liu Y, Liu J, Xia H, et al. Neutralizing Activity of BNT162b2-Elicited Serum. *New England Journal of Medicine*. 2021;384(15):1466-1468. doi:10.1056/nejmc2102017
75. Liu Y, Liu J, Xia H, et al. BNT162b2-Elicited Neutralization against New SARS-CoV-2 Spike Variants. *New England Journal of Medicine*. Published online May 2021:NEJMc2106083-NEJMc2106083. doi:10.1056/NEJMc2106083
76. Liu J, Bodnar BH, Wang X, et al. Correlation of vaccine-elicited antibody levels and neutralizing activities against SARS-CoV-2 and its variants. *bioRxiv*. Published online May 31, 2021:2021.05.31.445871. doi:10.1101/2021.05.31.445871
77. McCallum M, Bassi J, Marco AD, et al. SARS-CoV-2 immune evasion by the B.1.427/B.1.429 variant of concern. *Science*. Published online July 1, 2021. doi:10.1126/science.abi7994
78. Muik A, Wallisch A-K, Sängler B, et al. Neutralization of SARS-CoV-2 lineage B.1.1.7 pseudovirus by BNT162b2 vaccine-elicited human sera. *Science*. 2021;371(6534):1152-1153. doi:10.1126/science.abg6105
79. Pegu A, O'Connell S, Schmidt SD, et al. Durability of mRNA-1273-induced antibodies against SARS-CoV-2 variants. *bioRxiv*. Published online May 2021:2021.05.13.444010-2021.05.13.444010. doi:10.1101/2021.05.13.444010
80. Planas D, Bruel T, Grzelak L, et al. Sensitivity of infectious SARS-CoV-2 B.1.1.7 and B.1.351 variants to neutralizing antibodies. *Nature Medicine*. Published online March 2021:1-8. doi:10.1038/s41591-021-01318-5
81. Zhou D, Dejnirattisai W, Supasa P, et al. Evidence of escape of SARS-CoV-2 variant B.1.351 from natural and vaccine-induced sera. *Cell*. 2021;189(0):1-14. doi:10.1016/j.cell.2021.02.037
82. Tada T, Dcosta BM, Samanovic-Golden M, et al. Neutralization of viruses with European, South African, and United States SARS-CoV-2 variant spike proteins by convalescent sera and BNT162b2 mRNA vaccine-elicited antibodies. *bioRxiv : the preprint server for biology*. Published online February 2021:2021.02.05.430003-2021.02.05.430003. doi:10.1101/2021.02.05.430003
83. Trinité B, Pradenas E, Marfil S, et al. Previous SARS-CoV-2 infection increases B.1.1.7 cross-neutralization by vaccinated individuals. Equal contribution. *bioRxiv*. Published online March 2021:2021.03.05.433800-2021.03.05.433800. doi:10.1101/2021.03.05.433800
84. Wang Z, Schmidt F, Weisblum Y, et al. mRNA vaccine-elicited antibodies to SARS-CoV-2 and circulating variants. *Nature*. 2021;592(7855):616-616. doi:10.1038/s41586-021-03324-6
85. Wu K, Werner AP, Koch M, et al. Serum Neutralizing Activity Elicited by mRNA-1273 Vaccine. *New England Journal of Medicine*. 2021;384(15):1468-1470. doi:10.1056/NEJMc2102179
86. Zani A, Caccuri F, Messali S, Bonfanti C, Caruso A. Serosurvey in BNT162b2 vaccine-elicited neutralizing antibodies against authentic B.1, B.1.1.7, B.1.351, B.1.525 and P.1 SARS-CoV-2 variants. *Emerging Microbes & Infections*. 2021;0(ja):1-6. doi:10.1080/22221751.2021.1940305
87. Geers D, Shamier MC, Bogers S, et al. SARS-CoV-2 variants of concern partially escape humoral but not T-cell responses in COVID-19 convalescent donors and vaccinees. *Science Immunology*. 2021;6(59). doi:10.1126/sciimmunol.abj1750
88. Marot S, Malet I, Leducq V, et al. Neutralization heterogeneity of United Kingdom and South-African SARS-CoV-2 variants in BNT162b2-vaccinated or convalescent COVID-19 healthcare workers. *Clinical Infectious Diseases*. 2021;(ciab492). doi:10.1093/cid/ciab492
89. Xie X, Liu Y, Liu J, et al. Neutralization of SARS-CoV-2 spike 69/70 deletion, E484K and N501Y variants by BNT162b2 vaccine-elicited sera. *Nat Med*. 2021;27(4):620-621. doi:10.1038/s41591-021-01270-4
90. Alter G, Yu J, Liu J, et al. Immunogenicity of Ad26.COV2.S vaccine against SARS-CoV-2 variants in humans. *Nature*. Published online June 9, 2021:1-9. doi:10.1038/s41586-021-03681-2
91. Cao Y, Yisimayi A, Bai Y, et al. Humoral immune response to circulating SARS-CoV-2 variants elicited by inactivated and RBD-subunit vaccines. *Cell Research*. Published online May 21, 2021:1-10. doi:10.1038/s41422-021-00514-9
92. Huang B, Dai L, Wang H, et al. Neutralization of SARS-CoV-2 VOC 501Y.V2 by human antisera elicited by both 1 inactivated BBIBP-CorV and recombinant dimeric RBD ZF2001 vaccines 2 3 Authors. *bioRxiv*. Published online February 2021:2021.02.01.429069-2021.02.01.429069. doi:10.1101/2021.02.01.429069
93. Chang X, Sousa Augusto G, Liu X, et al. BNT162b2 mRNA COVID-19 vaccine induces antibodies of broader cross-reactivity than natural infection but recognition of mutant viruses is up to 10-fold reduced. *bioRxiv*. Published online March 2021:2021.03.13.435222-2021.03.13.435222. doi:10.1101/2021.03.13.435222
94. Hoffmann M, Hofmann-Winkler H, Krüger N, et al. SARS-CoV-2 variant B.1.617 is resistant to Bamnanimab and evades antibodies induced by infection and vaccination. *bioRxiv*. Published online May 5, 2021:2021.05.04.442663. doi:10.1101/2021.05.04.442663
95. Sahin U, Muik A, Vogler I, et al. BNT162b2 vaccine induces neutralizing antibodies and poly-specific T cells in humans. *Nature*. Published online May 27, 2021. doi:10.1038/s41586-021-03653-6
96. Stamatatos L, Czartoski J, Wan Y-H, et al. mRNA vaccination boosts cross-variant neutralizing antibodies elicited by SARS-CoV-2 infection. *Science*. Published online March 2021:eabg9175-eabg9175. doi:10.1126/science.abg9175
97. Wang P, Nair MS, Liu L, et al. Antibody resistance of SARS-CoV-2 variants B.1.351 and B.1.1.7. *Nature*. 2021;593(7857):130-135. doi:10.1038/s41586-021-03398-2
98. COVID-19 vaccinesWHO Meeting on correlates of protection. Accessed June 4, 2021. <https://www.who.int/news-room/events/detail/2021/06/01/default-calendar/covid-19-vaccineswho-meeting-on-correlates-of-protection>
99. Edara VV, Norwood C, Floyd K, et al. Infection- and vaccine-induced antibody binding and neutralization of the B.1.351 SARS-CoV-2 variant. *Cell Host and Microbe*. 2021;29(4):516-521.e3. doi:10.1016/j.chom.2021.03.009
100. Zhou H, Dcosta BM, Samanovic MI, Mulligan MJ, Landau NR, Tada T. B.1.526 SARS-CoV-2 variants identified in New York City are neutralized by vaccine-elicited and therapeutic monoclonal antibodies. *bioRxiv*. Published online March 24, 2021:2021.03.24.436620. doi:10.1101/2021.03.24.436620
101. Shen X, Tang H, Pajon R, et al. Neutralization of SARS-CoV-2 Variants B.1.429 and B.1.351. *New England Journal of Medicine*. Published online April 2021:NEJMc2103740-NEJMc2103740. doi:10.1056/nejmc2103740
102. Palacios R, Batista AP, Albuquerque CSN, et al. Efficacy and Safety of a COVID-19 Inactivated Vaccine in Healthcare Professionals in Brazil: The PROFISCOV Study. *SSRN Electronic Journal*. Published online April 2021. doi:10.2139/ssrn.3822780
103. Wang P, Casner RG, Nair MS, et al. Increased Resistance of SARS-CoV-2 Variant P.1 to Antibody Neutralization. *bioRxiv*. Published online April 9, 2021:2021.03.01.433466. doi:10.1101/2021.03.01.433466

WHO regional overviews - Epidemiological week 28 June-4 July 2021

African Region

The African Region reported over 204 000 new cases and over 3300 new deaths, a 15% and a 23% increase respectively as compared to the previous week. For the sixth consecutive week, the region continues to show a marked increase in weekly case incidence and mortality; the Southern and Eastern parts of Africa remain the most affected areas on the continent. The highest numbers of new cases were reported from South Africa (132 450 new cases; 223.3 new cases per 100 000 population; a 28% increase), Zambia (16 456 new cases; 89.5 new cases per 100 000; a 14% decrease), and Namibia (9342 new cases; 367.7 new cases per 100 000; a 28% decrease).

The highest numbers of new deaths were reported from South Africa (1729 new deaths; 2.9 new deaths per 100 000 population; a 46% increase), Zambia (430 new deaths; 2.3 new deaths per 100 000; a 16% increase), and Uganda (325 new deaths; <1 new deaths per 100 000; a 34% increase).

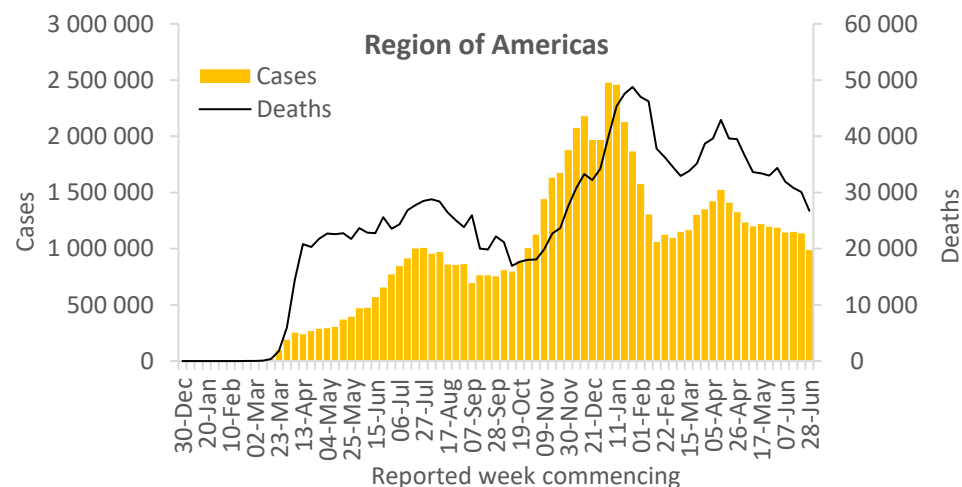


Updates from the [African Region](#)

Region of the Americas

The Region of the Americas reported over 992 000 new cases and over 26 000 new deaths, a 13% and an 11% decrease respectively compared to the previous week. The Americas is the only region showing a decrease in both weekly case incidence and mortality. For the first time since October 2020, the region reported under 1 million weekly cases. However, several countries from South America, Central America and the Caribbean are still reporting high case incidence and mortality over the past weeks. The highest numbers of new cases were reported from Brazil (364 709 new cases; 171.6 new cases per 100 000; a 30% decrease), Colombia (204 556 new cases; 402.0 new cases per 100 000; similar to the previous week), and Argentina (137 852 new cases; 305.0 new cases per 100 000; a 5% increase).

The highest numbers of new deaths were reported from Brazil (10 810 new deaths; 5.1 new deaths per 100 000; a 14% decrease), Colombia (4402 new deaths; 8.7 new deaths per 100 000; a 4% decrease), and Argentina (3403 new deaths; 7.5 new deaths per 100 000; a 9% decrease).

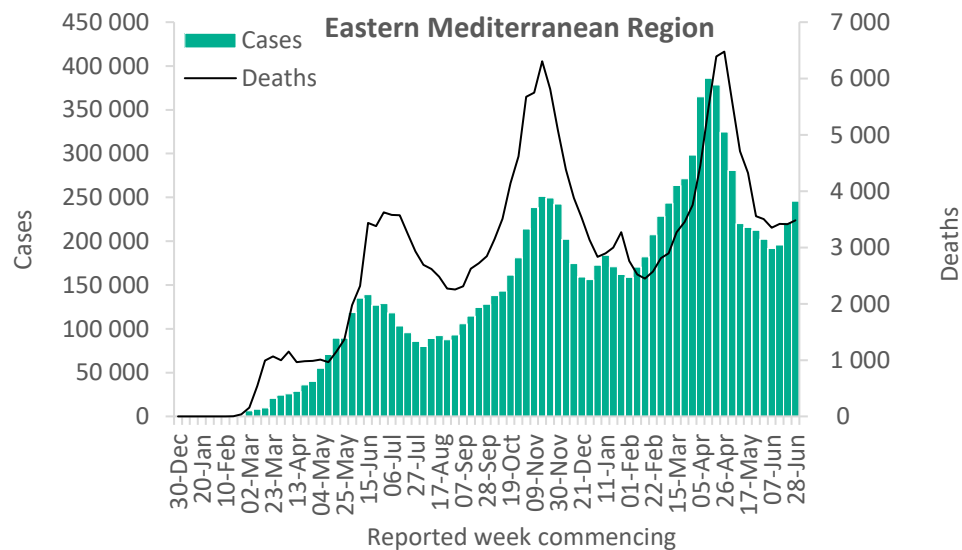


Updates from the [Region of the Americas](#)

Eastern Mediterranean Region

The Eastern Mediterranean Region reported over 245 000 new cases and over 3400 new deaths, an 11% and a 2% increase respectively as compared to the previous week. Following more than two months of decrease in weekly case incidence, for the third consecutive week the region showed an increase of case incidence, while mortality remained relatively stable for the past month. The highest numbers of new cases were reported from the Islamic Republic of Iran (83 054 new cases; 98.9 new cases per 100 000; a 17% increase), Iraq (43 979 new cases; 109.3 new cases per 100 000; a 16% increase), and Tunisia (35 452 new cases; 300.0 new cases per 100 000; a 59% increase).

The highest numbers of new deaths were reported from the Islamic Republic of Iran (916 new deaths; 1.1 new deaths per 100 000; a 7% increase), Tunisia (682 new deaths; 5.8 new deaths per 100 000; a 10% increase), and Afghanistan (549 new deaths; 1.4 new deaths per 100 000; a 4% increase).

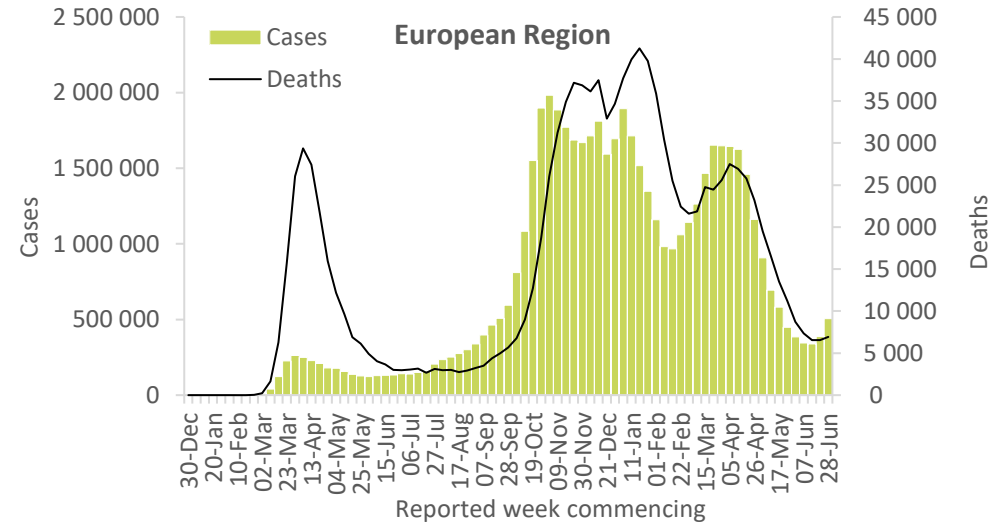


Updates from the [Eastern Mediterranean Region](#)

European Region

The European Region reported over 505 000 new cases and over 6900 new deaths. Following almost three months of declining trends, the region showed for the second consecutive week an increase in the number of new weekly cases and deaths, a 30% and a 6% increase respectively as compared to the previous week. The highest numbers of new cases were reported from the United Kingdom (161 805 new cases; 238.3 new cases per 100 000; a 67% increase), the Russian Federation (159 650 new cases; 109.4 new cases per 100 000; a 19% increase), and Turkey (36 224 new cases; 43.0 new cases per 100 000; a 7% decrease).

The highest numbers of new deaths were reported from the Russian Federation (4643 new deaths; 3.2 new deaths per 100 000; an 18% increase), Turkey (350 new deaths; <1 new deaths per 100 000; a 13% decrease), and Germany (276 new deaths; <1 new deaths per 100 000; a 25% decrease).

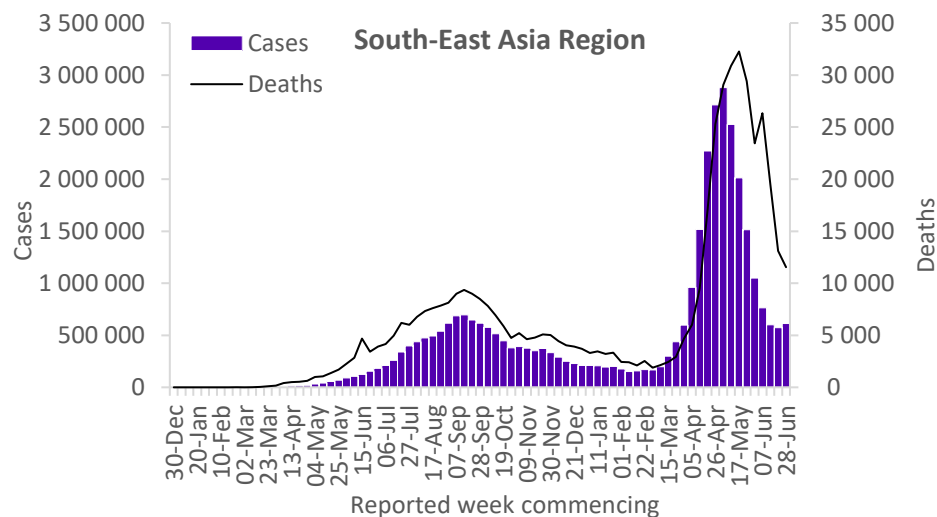


Updates from the [European Region](#)

South-East Asia Region

The South-East Asia Region reported just under 613 000 new cases and over 11 000 new deaths, a 7% increase and a 12% decrease respectively as compared to the previous week. Following a decreasing trend in weekly case incidence for almost two months, mostly driven by the decrease in cases reported in India, the region showed a slight increase of cases this week. Bangladesh, Indonesia, Myanmar and Thailand continue to report large increases in the number of newly reported cases and deaths for this week.

The highest numbers of new cases were reported from India (312 250 new cases; 22.6 new cases per 100 000; an 11% decrease), Indonesia (168 780 new cases; 61.7 new cases per 100 000; a 35% increase), and Bangladesh (56 511 new cases; 34.3 new cases per 100 000; a 54% increase). The highest numbers of new deaths were reported from India (6254 new deaths; 0.5 new deaths per 100 000; a 31% decrease), Indonesia (3444 new deaths; 1.3 new deaths per 100 000; a 39% increase), and Bangladesh (893 new deaths; 0.5 new deaths per 100 000; a 43% increase).



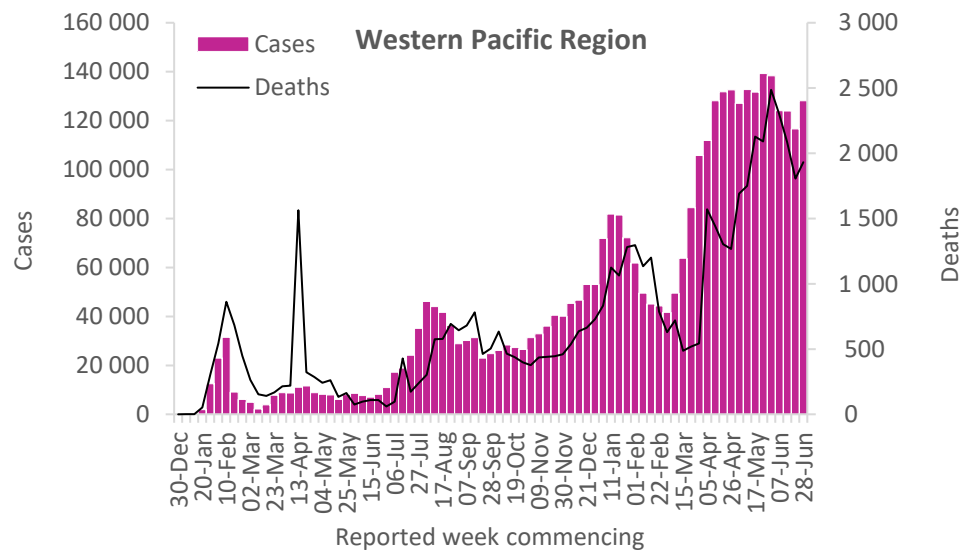
Updates from the [South-East Asia Region](#)

Western Pacific Region

The Western Pacific Region reported over 128 000 new cases and over 1900 new deaths, a 10% and a 7% increase respectively. Cambodia, Fiji and Malaysia, continue to report increases in both weekly cases and deaths.

The highest numbers of new cases were reported from Malaysia (44 145 new cases; 136.4 new cases per 100 000; an 18% increase), the Philippines (38 507 new cases; 35.1 new cases per 100 000; similar to last week), and Mongolia (15 478 new cases; 472.1 new cases per 100 000; a 4% decrease).

The highest numbers of new deaths were reported from the Philippines (819 new deaths; <1 new deaths per 100 000; a 16% increase), Malaysia (550 new deaths; 1.7 new deaths per 100 000; a 3% increase), and Japan (185 new deaths; <1 new deaths per 100 000; a 28% decrease).



Updates from the [Western Pacific Region](#)

Key weekly updates

WHO Director-General's key messages

- In his [opening remarks at the media briefing on COVID-19 – 2 July 2021](#), the Director-General highlighted two ways for countries to push back against COVID-19 surges. These include:
 - **Strengthening public health and social measures (PHSM)**- including strong surveillance, strategic testing, early case detection, isolation and clinical care- remains critical. Additionally, masking, physical distance, avoiding crowded places and keeping indoor areas well ventilated remain the basis for the response.
 - **Equitable distribution or sharing of resources** such as protective gear, medical oxygen, tests, treatments and vaccines.
- In [his introductory remarks at the event: Gender Equal Health and Care Workforce Initiative - 1 July 2021](#), the Director-General emphasized the need to address gender inequalities as a priority especially when majority of the world's health workers - almost 70% - are women. WHO is committed to advocating for decent and safe work conditions for all health and care workers.

Updates and publications

- **COVID-19 Vaccines and Vaccine Safety**
 - [Ethical Framework for WHO's work in the ACT-Accelerator](#)
 - [Observational Study Protocol Template for sentinel surveillance of adverse events of special interest \(AESIs\) after vaccination with COVID-19 vaccines](#)
- **International Travel**
 - [Technical considerations for implementing a risk-based approach to international travel in the context of COVID-19: Interim guidance, 2 July 2021](#)
 - [Policy considerations for implementing a risk-based approach to international travel in the context of COVID-19, 2 July 2021](#)
- **Essential Health Services**
 - [Implementation guidance for assessments of frontline service readiness: strengthening real-time monitoring of health services in the context of the COVID-19 pandemic, 1 July 2021](#)

Annex

COVID-19 confirmed cases and deaths reported in the last seven days by countries, territories and areas, and WHO Region (reported in previous issues) are now available at: <https://covid19.who.int/table>

Annex 1. List of countries/territories/areas reporting Variants of Concern as of 6 July 2021**

| Country/Territory/Area | Alpha | Beta | Gamma | Delta | Unspecified B.1.617 |
|----------------------------------|-------|------|-------|-------|---------------------|
| Afghanistan | ● | - | - | - | - |
| Albania | ● | - | - | - | - |
| Algeria | ● | - | - | ● | - |
| Angola | ● | ● | - | - | - |
| Antigua and Barbuda | ●* | ●* | - | - | - |
| Argentina | ● | ● | ● | ● | - |
| Armenia | ○ | - | - | - | - |
| Aruba | ● | ● | ● | ● | - |
| Australia | ● | ● | ● | ● | - |
| Austria | ● | ● | ● | ● | - |
| Azerbaijan | ● | - | - | - | - |
| Bahrain | ● | ● | - | ● | - |
| Bangladesh | ● | ● | - | ● | - |
| Barbados | ● | - | ● | ● | - |
| Belarus | ● | - | - | ○ | - |
| Belgium | ● | ● | ● | ● | - |
| Belize | ● | - | - | - | - |
| Bermuda | ● | ● | - | - | - |
| Bhutan | ● | ● | - | ● | - |
| Bolivia (Plurinational State of) | ● | - | ● | - | - |
| Bonaire | ● | - | - | - | - |
| Bosnia and Herzegovina | ○ | - | - | - | - |
| Botswana | - | ● | - | ● | - |
| Brazil | ● | ● | ● | ● | - |
| British Virgin Islands | ● | - | ● | - | - |

| Country/Territory/Area | Alpha | Beta | Gamma | Delta | Unspecified B.1.617 |
|----------------------------------|-------|------|-------|-------|---------------------|
| Brunei Darussalam | ● | ● | - | - | - |
| Bulgaria | ● | ● | - | ● | - |
| Burkina Faso | ● | - | - | - | - |
| Cabo Verde | ● | - | - | - | - |
| Cambodia | ● | - | - | ● | - |
| Cameroon | ● | ● | - | - | - |
| Canada | ● | ● | ● | ● | - |
| Cayman Islands | ● | - | - | - | - |
| Central African Republic | ● | - | - | - | - |
| Chile | ● | ● | ● | ● | - |
| China | ● | ● | ● | ○ | - |
| Colombia | ● | - | ● | - | - |
| Comoros | - | ● | - | - | - |
| Congo | ● | - | - | - | - |
| Costa Rica | ● | ● | ● | - | - |
| Croatia | ● | ● | ○* | ○ | - |
| Cuba | ● | ● | - | - | - |
| Curaçao | ● | - | ● | - | ● |
| Cyprus | ● | ● | - | - | ● |
| Czechia | ● | ● | ● | ● | - |
| Côte d'Ivoire | ● | ● | - | - | - |
| Democratic Republic of the Congo | ● | ● | - | ● | - |
| Denmark | ● | ● | ● | ● | - |
| Djibouti | ● | ● | - | - | - |

| Country/Territory/Area | Alpha | Beta | Gamma | Delta | Unspecified B.1.617 |
|------------------------|-------|------|-------|-------|---------------------|
| Dominica | ● | - | - | - | - |
| Dominican Republic | ● | - | ● | - | - |
| Ecuador | ● | - | ● | - | - |
| Egypt | ● | - | - | - | - |
| Equatorial Guinea | ● | ● | - | - | - |
| Estonia | ● | ● | ○ | - | ○ |
| Eswatini | - | ● | - | - | - |
| Ethiopia | ○ | - | - | - | - |
| Faroe Islands | ● | - | ● | - | - |
| Fiji | - | - | - | ● | - |
| Finland | ● | ● | ● | ● | - |
| France | ● | ● | ● | ● | - |
| French Guiana | ● | ● | ● | ● | - |
| French Polynesia | ● | ● | ● | ● | - |
| Gabon | ● | ○ | - | - | - |
| Gambia | ● | - | - | ● | - |
| Georgia | ● | ○ | - | ● | - |
| Germany | ● | ● | ● | ● | - |
| Ghana | ● | ● | - | ● | - |
| Gibraltar | ● | - | - | - | - |
| Greece | ● | ● | ● | ● | - |
| Grenada | ● | - | - | - | - |
| Guadeloupe | ● | ● | ● | ● | - |
| Guam | ● | ● | ● | ● | - |
| Guatemala | ● | ●* | ●* | - | - |

| Country/Territory/Area | Alpha | Beta | Gamma | Delta | Unspecified B.1.617 |
|----------------------------------|-------|------|-------|-------|---------------------|
| Guinea | ● | ● | - | - | - |
| Guinea-Bissau | ● | ● | - | - | - |
| Guyana | - | - | ● | - | - |
| Haiti | ● | - | ● | - | - |
| Honduras | ● | - | - | - | - |
| Hungary | ● | ○ | - | ○ | - |
| Iceland | ● | - | - | - | - |
| India | ● | ● | ● | ● | - |
| Indonesia | ● | ● | - | ● | - |
| Iran (Islamic Republic of) | ● | ● | - | ● | - |
| Iraq | ● | ● | - | - | - |
| Ireland | ● | ● | ● | ● | - |
| Israel | ● | ● | ● | ● | - |
| Italy | ● | ● | ● | ● | - |
| Jamaica | ● | - | - | - | - |
| Japan | ● | ● | ● | ● | - |
| Jordan | ● | ● | ● | ● | - |
| Kazakhstan | ○ | ○ | - | ●* | - |
| Kenya | ● | ● | - | ● | - |
| Kosovo[1] | ● | ○ | - | ○ | - |
| Kuwait | ● | - | - | ● | - |
| Kyrgyzstan | ● | - | - | - | - |
| Lao People's Democratic Republic | ● | - | - | ●* | - |
| Latvia | ● | ● | ● | ○* | - |
| Lebanon | ● | - | - | ●* | - |
| Lesotho | - | ● | - | - | - |
| Liberia | ● | - | - | - | - |
| Libya | ● | ● | - | - | - |
| Liechtenstein | ● | - | - | - | - |
| Lithuania | ● | ● | ● | ○ | - |
| Luxembourg | ● | ● | ● | ● | - |

| Country/Territory/Area | Alpha | Beta | Gamma | Delta | Unspecified B.1.617 |
|--------------------------------|-------|------|-------|-------|---------------------|
| Madagascar | - | ● | - | - | - |
| Malawi | ● | ● | - | ● | - |
| Malaysia | ● | ● | - | ● | - |
| Maldives | ● | - | - | ● | - |
| Malta | ● | ○ | ● | ○ | - |
| Martinique | ● | ● | ● | ● | - |
| Mauritania | ● | ● | - | ● | - |
| Mauritius | ○ | ● | - | ● | - |
| Mayotte | ● | ● | - | - | - |
| Mexico | ● | ● | ● | ● | - |
| Monaco | ● | ○ | - | - | - |
| Montenegro | ● | - | - | - | - |
| Montserrat | ● | - | - | - | - |
| Morocco | ● | - | - | ● | - |
| Mozambique | - | ● | - | ● | - |
| Myanmar | ● | - | - | - | - |
| Namibia | - | ● | - | ○* | - |
| Nepal | ● | - | - | ● | - |
| Netherlands | ● | ● | ● | ● | - |
| New Caledonia | ● | - | - | - | - |
| New Zealand | ● | ● | ○ | ○ | - |
| Niger | ● | - | - | - | - |
| Nigeria | ● | - | - | - | ● |
| North Macedonia | ● | ● | - | - | ● |
| Norway | ● | ● | ● | ● | - |
| Occupied Palestinian Territory | ● | ● | - | ● | - |
| Oman | ● | ●* | - | ●* | - |
| Pakistan | ● | ● | ● | ● | - |
| Panama | ● | ● | ● | - | ● |
| Paraguay | ● | - | ● | - | - |
| Peru | ● | - | ● | ● | - |

| Country/Territory/Area | Alpha | Beta | Gamma | Delta | Unspecified B.1.617 |
|------------------------|-------|------|-------|-------|---------------------|
| Philippines | ● | ● | ● | ● | - |
| Poland | ● | ○ | ● | ● | - |
| Portugal | ● | ● | ● | ● | - |
| Puerto Rico | ● | ● | ● | ● | - |
| Qatar | ● | ● | - | ● | - |
| Republic of Korea | ● | ● | ● | ● | - |
| Republic of Moldova | ○ | - | - | - | - |
| Romania | ● | ● | ● | ● | - |
| Russian Federation | ● | ● | - | ● | - |
| Rwanda | ● | ○ | - | - | - |
| Réunion | ● | ● | ● | ○ | - |
| Saba | - | - | - | ● | - |
| Saint Barthélemy | ● | - | - | - | - |
| Saint Lucia | ● | - | - | - | - |
| Saint Martin | ● | ● | - | - | - |
| Sao Tome and Principe | ● | - | - | - | - |
| Saudi Arabia | ● | ● | - | ● | - |
| Senegal | ● | ● | - | - | - |
| Serbia | ● | - | - | - | - |
| Seychelles | - | ● | - | - | - |
| Sierra Leone | - | - | - | ○* | - |
| Singapore | ● | ● | ● | ● | - |
| Sint Maarten | ● | ● | - | ● | - |
| Slovakia | ● | ● | - | ● | - |
| Slovenia | ● | ● | ● | ● | - |
| Somalia | ● | - | - | - | - |
| South Africa | ● | ● | - | ● | - |
| Spain | ● | ● | ● | ● | - |
| Sri Lanka | ● | ● | - | ● | - |
| Suriname | ● | ● | ● | - | - |
| Sweden | ● | ● | ● | ● | - |

| Country/Territory/Area | Alpha | Beta | Gamma | Delta | Unspecified B.1.617 |
|--------------------------|-------|------|-------|-------|---------------------|
| Switzerland | ● | ● | ○ | ● | - |
| Thailand | ● | ● | ● | ● | - |
| Timor-Leste | ● | - | - | - | - |
| Togo | ● | ● | - | - | - |
| Trinidad and Tobago | ● | - | ● | - | - |
| Tunisia | ● | ● | - | ● | - |
| Turkey | ● | ● | ● | ● | - |
| Turks and Caicos Islands | ● | - | ● | - | - |

| Country/Territory/Area | Alpha | Beta | Gamma | Delta | Unspecified B.1.617 |
|-----------------------------|-------|------|-------|-------|---------------------|
| Uganda | ● | ● | - | ● | - |
| Ukraine | ● | ○ | - | ○ | - |
| United Arab Emirates | ● | ● | ● | ● | - |
| United Kingdom | ● | ● | ● | ● | - |
| United Republic of Tanzania | - | ● | - | - | - |
| United States of America | ● | ● | ● | ● | - |
| Uruguay | ● | - | ● | - | - |
| Uzbekistan | ● | ● | - | ○ | - |

| Country/Territory/Area | Alpha | Beta | Gamma | Delta | Unspecified B.1.617 |
|------------------------------------|-------|------|-------|-------|---------------------|
| Venezuela (Bolivarian Republic of) | ● | - | ● | - | - |
| Viet Nam | ● | ● | - | ● | - |
| Wallis and Futuna | ● | - | - | - | - |
| Zambia | - | ● | - | ● | - |
| Zimbabwe | - | ○ | - | ● | - |

*Newly reported in this update.

“Unspecified B.1.617” reflects countries/territories/areas reporting detection of B.1.617 without further specification of lineage at this time. These will be reallocated as further details become available.

“●” indicates that information for this variant was received by WHO from official sources.

“○” indicates that information for this variant was received by WHO from unofficial sources and will be reviewed as more information become available.

**Variant Beta for Kyrgyzstan and unspecified B.1.617 for Latvia were excluded this week based on further information received.

***Includes countries/territories/areas reporting the detection of VOCs among travelers (e.g., imported cases detected at points of entry), or local cases (detected in the community). Efforts are ongoing to differentiate these in future reports. Excludes countries, territories, and areas that have never reported the detection of a variant of concern.

See also [Annex 2: Data, table and figure notes](#).

Annex 2. Data, table and figure notes

Data presented are based on official laboratory-confirmed COVID-19 case and deaths reported to WHO by country/territories/areas, largely based upon WHO [case definitions](#) and [surveillance guidance](#). While steps are taken to ensure accuracy and reliability, all data are subject to continuous verification and change, and caution must be taken when interpreting these data as several factors influence the counts presented, with variable underestimation of true case and death incidence, and variable delays to reflecting these data at global level. Case detection, inclusion criteria, testing strategies, reporting practices, and data cut-off and lag times differ between countries/territories/areas. A small number of countries/territories/areas report combined probable and laboratory-confirmed cases. Differences are to be expected between information products published by WHO, national public health authorities, and other sources. Due to public health authorities conducting data reconciliation exercises which remove large numbers of cases or deaths from their total counts, negative numbers may be displayed in the new cases/deaths columns as appropriate. When additional details become available that allow the subtractions to be suitably apportioned to previous days, graphics will be updated accordingly.

A record of historic data adjustment made is available upon request by emailing epi-data-support@who.int. Please specify the country(ies) of interest, time period(s), and purpose of the request/intended usage. Prior situation reports will not be edited; see covid19.who.int for the most up-to-date data.

The designations employed, and the presentation of these materials do not imply the expression of any opinion whatsoever on the part of WHO concerning the legal status of any country, territory 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. Countries, territories and areas are arranged under the administering WHO region. The mention of specific companies or of certain manufacturers' products does not imply that they are endorsed or recommended by WHO in preference to others of a similar nature that are not mentioned. Errors and omissions excepted, the names of proprietary products are distinguished by initial capital letters.

^[1] All references to Kosovo should be understood to be in the context of the United Nations Security Council resolution 1244 (1999). In the map, number of cases of Serbia and Kosovo (UNSCR 1244, 1999) have been aggregated for visualization purposes.

Technical guidance and other resources

- [WHO technical guidance](#)
- [WHO COVID-19 Dashboard](#)
- [WHO Weekly Operational Updates on COVID-19](#)
- [WHO COVID-19 case definitions](#)
- [COVID-19 Supply Chain Inter-Agency Coordination Cell Weekly Situational Update](#)
- [Research and Development](#)
- [OpenWHO courses on COVID-19](#) in official UN languages and in [additional national languages](#)
- [WHO Academy COVID-19 mobile learning app](#)
- [The Strategic Preparedness and Response Plan](#) (SPRP) outlining the support the international community can provide to all countries to prepare and respond to the virus
- Recommendations and advice for the public:
 - [Protect yourself](#)
 - [Questions and answers](#)
 - [Travel advice](#)
- [EPI-WIN: tailored information for individuals, organizations and communities](#)