# COVID-19 Weekly Epidemiological Update

**Edition 119 published 23 November 2022**

In this edition:



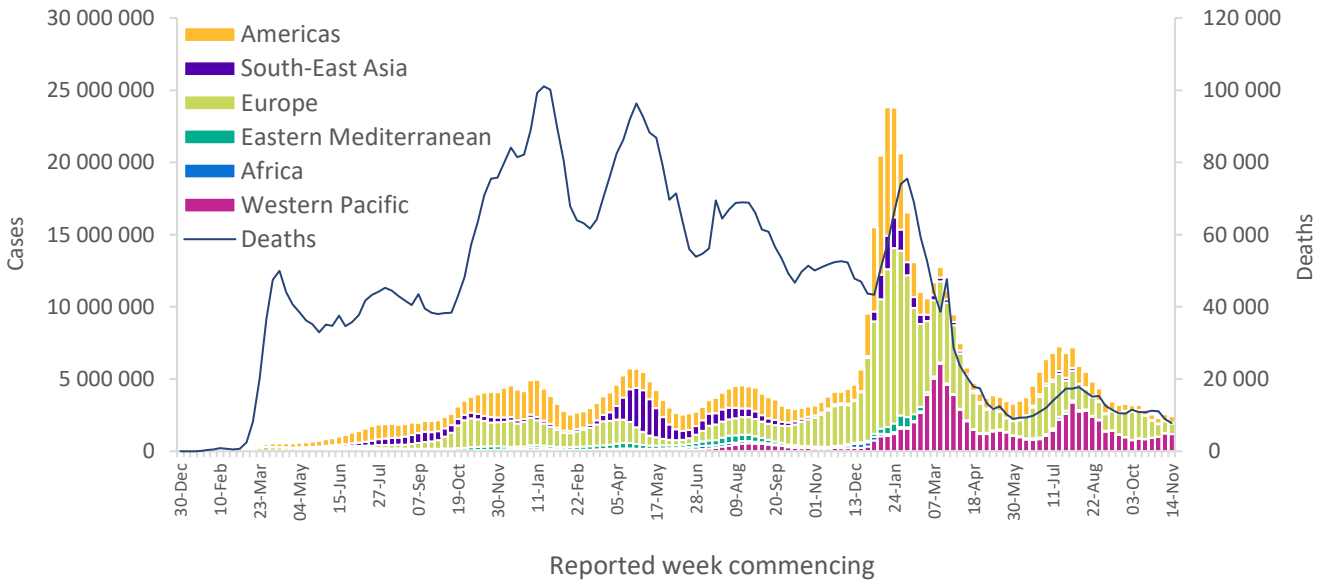
## Global overview

**Data as of 20 November 2022**

Globally, the number of new weekly cases decreased by 5% during the week of 14 to 20 November 2022 as compared to the previous week, with over 2.4 million new cases reported (Figure 1, Table 1). The number of new weekly deaths decreased by 13% as compared to the previous week, with over 7800 new fatalities reported. As of 20 November 2022, over 634 million confirmed cases and 6.6 million deaths have been reported globally.

At the regional level, the number of newly reported weekly cases decreased or remained stable across five of the six WHO regions: the Eastern Mediterranean Region (-22%), the European Region (-11%), the African Region (-9%), the Western Pacific Region (-4%) and the Region of the Americas (+3%); while case numbers increased in the South-East Asia Region (+8%). The number of newly reported weekly deaths decreased or remained stable across four regions: the European Region (-26%), the Eastern Mediterranean Region (-20%), the Region of the Americas (-11%) and the Western Pacific Region (+1%); while death numbers increased in the African Region (+124%; 38 vs eight deaths) and the South-East Asia Region (+13%).

**Figure 1. COVID-19 cases reported weekly by WHO Region, and global deaths, as of 20 November 2022****




**See *Annex 1: Data, table, and figure notes*

At the country level, the highest numbers of new weekly cases were reported from Japan (593 075 new cases; +18%), the Republic of Korea (364 536 new cases; +2%), the United States of America (274 067 new cases; -3%), France (186 446 new cases; +23%) and China (158 813 new cases; -8%). The highest numbers of new weekly deaths were reported from the United States of America (2202 new deaths; -5%), Japan (702 new deaths; +27%), China (476 new deaths; +16%), France (441 new deaths; +9%) and the Russian Federation (430 new deaths; -1%).

Current trends in reported COVID-19 cases should be interpreted with caution as several countries have been progressively changing COVID-19 testing strategies, resulting in lower overall numbers of tests performed and consequently lower numbers of cases detected. COVID-19 prevalence surveys conducted in a number of countries have found that the number of reported COVID-19 cases is an underestimate of the actual number of cases in the population [1–4]. Additionally, data from previous weeks are continuously updated to retrospectively incorporate changes in reported COVID-19 cases and deaths made by countries.

**Table 1. Newly reported and cumulative COVID-19 confirmed cases and deaths, by WHO Region, as of 20 November 2022****

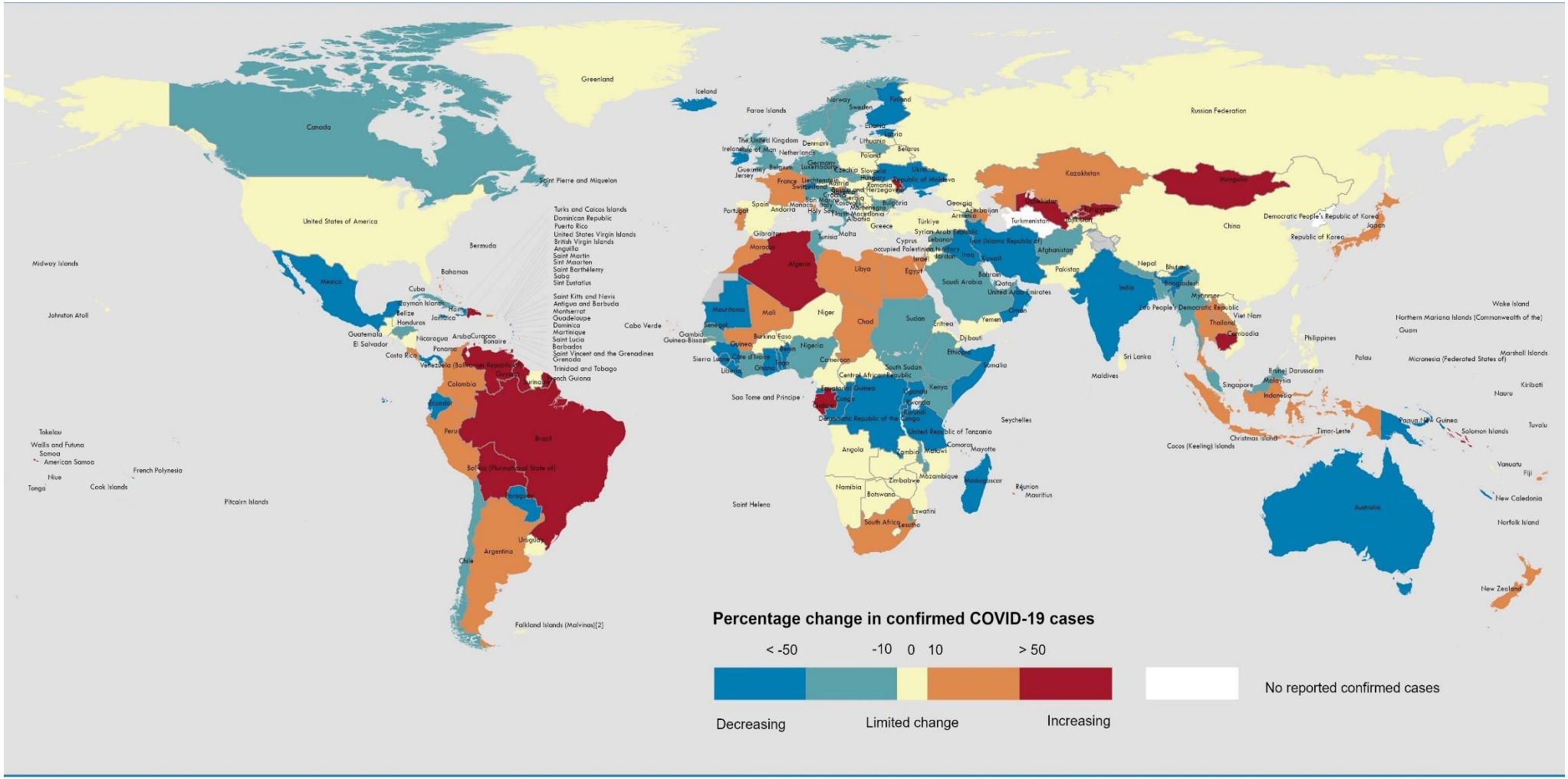
| WHO Region | New cases in last 7 days (%) | Change in new cases in last 7 days * | Cumulative cases (%) | New deaths in last 7 days (%) | Change in new deaths in last 7 days * | Cumulative deaths (%) |
|---|---|---|---|---|---|---|
| Western Pacific | 1 186 550 (49%) | -4% | 96 932 837 (15%) | 1743 (22%) | 1% | 280 651 (4%) |
| Europe | 724 002 (30%) | -11% | 263 449 995 (41%) | 2513 (32%) | -26% | 2 130 276 (32%) |
| Americas | 454 256 (19%) | 3% | 181 296 810 (29%) | 3060 (39%) | -11% | 2 865 519 (43%) |
| South-East Asia | 54 194 (2%) | 8% | 60 592 839 (10%) | 399 (5%) | 13% | 801 256 (12%) |
| Eastern Mediterranean | 8505 (<1%) | -22% | 23 183 234 (4%) | 49 (1%) | -20% | 348 854 (5%) |
| Africa | 6074 (<1%) | -9% | 9 381 403 (1%) | 38 (<1%) | 124% | 174 858 (3%) |
| **Global** | **2 433 581 (100%)** | **-5%** | **634 837 882 (100%)** | **7 802 (100%)** | **-13%** | **6 601 427 (100%)** |

**Percent change in the number of newly confirmed cases/deaths in the past seven days, compared to seven days prior. Data from previous weeks are updated continuously with adjustments received from countries.*
***See Annex 1: Data, table, and figure notes*

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

- WHO COVID-19 Dashboard
- WHO COVID-19 Monthly Operational Update and previous editions of the Weekly Epidemiological Update
- WHO COVID-19 detailed surveillance data dashboard
- WHO COVID-19 policy briefs

## Figure 2. Percentage change in confirmed COVID-19 cases over the last seven days relative to the previous seven days, 14 - 20 November 2022*



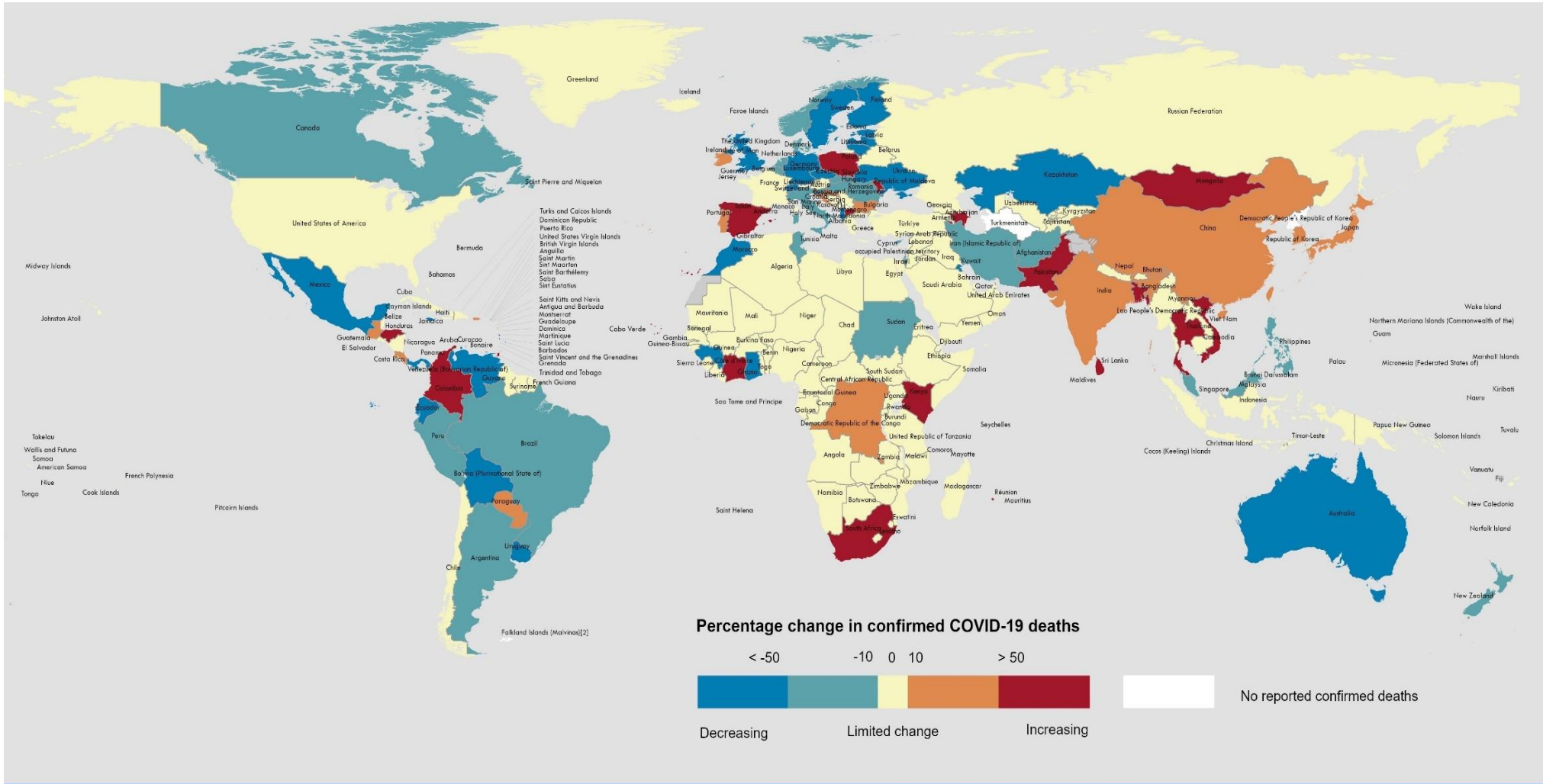

***Data Source**: World Health Organization*
***Map Production**: WHO Health Emergencies Programme*



The designations employed and the presentation of the material in this publication do not imply the expression of any opinion whatsoever on the part of WHO concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement. [1] All references to Kosovo in this document should be understood to be in the context of the United Nations Security Council resolution 1244 (1999). Number of cases of Serbia and Kosovo (UNSCR 1244, 1999) have been aggregated for visualization purposes. [2] A dispute exists between the Governments of Argentina and the United Kingdom of Great Britain and Northern Ireland concerning sovereignty over the Falkland Islands (Malvinas). Data for Bonaire, Sint Eustatius and Saba have been disaggregated and displayed at the subnational level.

**See *Annex 1: Data, table, and figure notes*

**Figure 3. Percentage change in confirmed COVID-19 deaths over the last seven days relative to the previous seven days, 14-20 November 2022****

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## SARS-CoV-2 variants of concern and Omicron subvariants under monitoring

### Geographic spread and prevalence of VOCs

Globally, from 21 October to 21 November 2022, 95 447 SARS-CoV-2 sequences were shared through GISAID. Among these, 95 322 sequences were the Omicron variant of concern (VOC), which accounted for 99.9% of sequences reported globally in the past 30 days.

During epidemiological week 44 (31 October to 6 November 2022), BA.5 descendent lineages remained dominant, with a prevalence of 72.1%; followed by BA.2 descendent lineages, with a prevalence of 9.2%, a rise from 6.4% during week 43 (24 to 30 October 2022). BA.4 descendent lineages continued to decline in prevalence, going from 3.6% to 3.0% during the same reporting period. Between weeks 43 and 44, BA.1.X had a prevalence of <1%, while BA.3.X sequences were not reported. Figure 4 and Table 2 present the global proportions and prevalence of the six variants currently classified as Omicron subvariants under monitoring, a list that is regularly updated. As of 21 November, BQ.1 and XBB (a recombinant of BA.2.10.1 and BA.2.75) and their descendent lineages have been reported from 73 and 47 countries, respectively. A comparison of sequences submitted globally during epidemiological weeks 43 and 44 show a rise in BQ.1 sequences from 19.1% to 23.1%. Similarly, the prevalence of XBB sequences also increased, rising from 2.0% in week 43 to 3.3% in week 44.

The trends describing the circulation of Omicron descendent lineages should be interpreted with due consideration of the limitations of current COVID-19 surveillance systems. These include differences in sequencing capacity and sampling strategies between countries, changes in sampling strategies over time, reductions in tests conducted and sequences shared by countries around the world, and delays in sequence submission. As of 21 November, BQ.1 and XBB (a recombinant of BA.2.10.1 and BA.2.75) and their descendent lineages have been reported from 73 and 47 countries, respectively. A comparison of sequences submitted globally during epidemiological weeks 43 and 44 show a rise in BQ.1 sequences from 19.1% to 23.1%. Similarly, the prevalence of XBB sequences also increased, rising from 2.0% in week 43 to 3.3% in week 44.

The SARS-CoV-2 pandemic can be characterized by waves of infection driven by several VOCs. Although there are variations across and within countries, globally, since January 2022, Omicron has been the dominant VOC, after replacing Delta. Several countries experienced a surge in cases driven by Omicron subvariant BA.1 and its descendent lineages. Currently, there are more than 500 sublineages of Omicron in circulation. To date, there have been more than 58 BA.1 descendent sublineages assigned a PANGO designation. Several countries across several WHO regions experienced a wave of infection due to the Omicron BA.2 sublineage, following a wave of BA.1 infection. BA.2 has over 218 descendent sublineages, including BJ.1, XBB, BA.2.75 and BA.2.3.20, which are Omicron subvariants under monitoring by WHO. BA.3 and its descendent lineage have been reported from 29 countries so far, with a global prevalence of 1% in week 41 (10 to 16 October). While there were no reports of BA.3 driven waves, the emergence of BA.3 was followed by the emergence of BA.4 and BA.5, both of which have led to a significant rise in cases and deaths globally. BA.4 and BA.5 share similar mutations in the SARS-CoV-2 spike protein but differ from one another in other parts of the proteome. Combined, they have over 260 descendent lineages. BA.5 and its descendent lineages continue to be dominant globally, with dominance differing by country. Among BA.5 descendent lineages, BA.5.2, BA.5.2.1, BF.5 (BA.5.2.1.5) and BF.7 (BA.5.2.1.7) are the most prevalent sublineages.

**Additional resources**

- Tracking SARS-CoV-2 Variants
- TAG-VE statement on Omicron sublineages BQ.1 and XBB
- COVID-19 new variants: Knowledge gaps and research
- Genomic sequencing of SARS-CoV-2: a guide to implementation for maximum impact on public health
- VIEW-hub: repository for the most relevant and recent vaccine data

## Figure 4. Panel A and B: The number and percentage of SARS-CoV-2 sequences, as of 21 November 2022

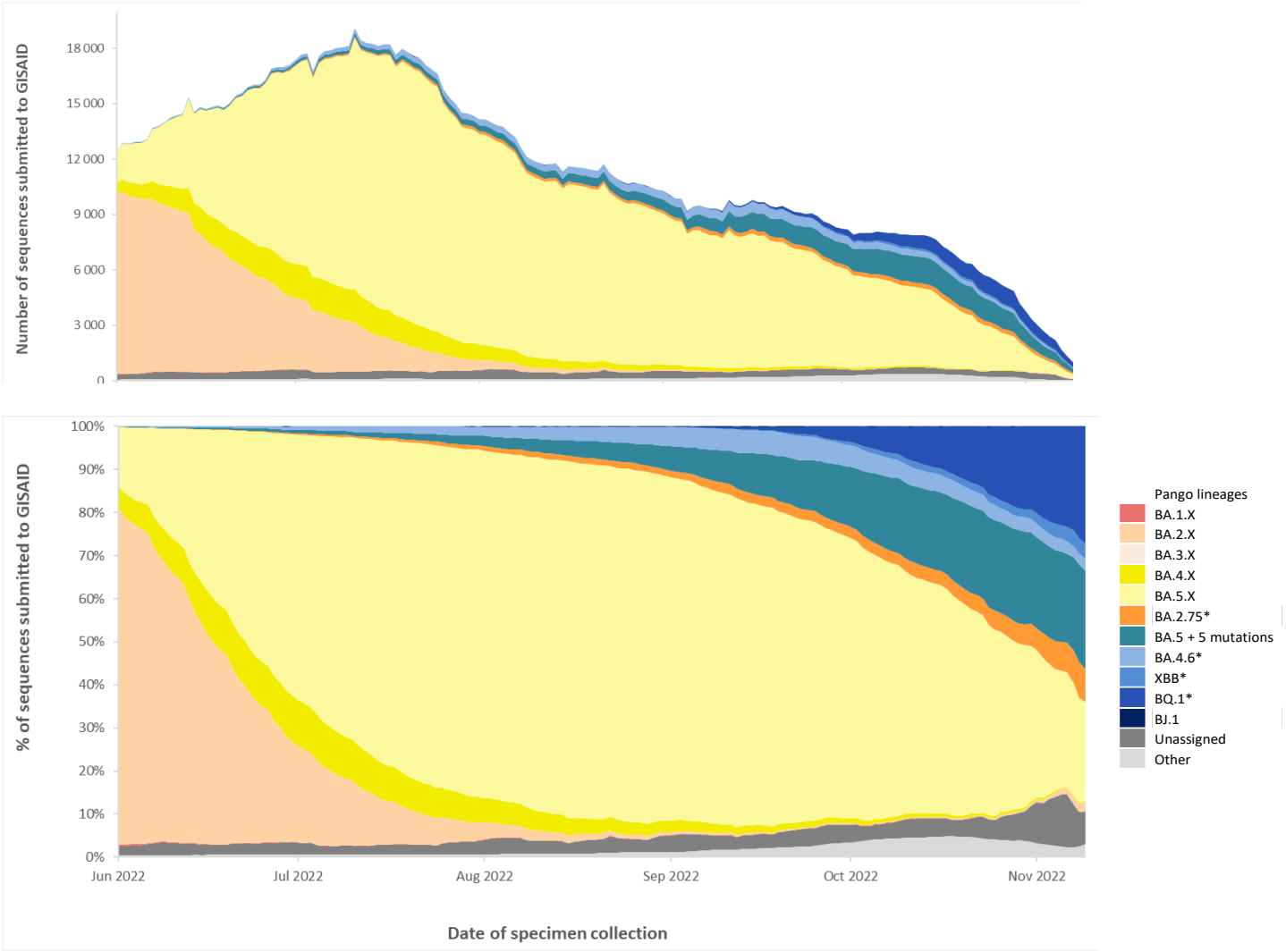



**Figure 4 Panel A** shows the number, and **Panel B** the percentage, of all circulating variants since June 2022. Omicron sister-lineages and additional Omicron VOC descendent lineages under further monitoring are shown. *BA.1.X, BA.2.X, BA.3.X, BA.4.X* and *BA.5.X* include all BA.1, BA.2, BA.3, BA.4 and BA.5 pooled descendent lineages, except the Omicron subvariants under monitoring shown individually. The *Unassigned* category includes lineages pending for a PANGO lineage name, whereas the *Other* category includes lineages that are assigned but not listed in the legend. Source: SARS- CoV-2 sequence data and metadata from GISAID, as of 21 November 2022.

## Table 2. Relative proportions of SARS-CoV-2 sequences over the last four weeks by specimen collection date

| Lineage | Countries | Sequences[a] | 2022-41 | 2022-42 | 2022-43 | 2022-44 |
|---|---|---|---|---|---|---|
| BA.2.3.20* | 38 | 713 | 0.15 | 0.24 | 0.34 | 0.59 |
| BA.2.75* | 75 | 24 021 | 3.27 | 3.86 | 4.78 | 6.78 |
| BA.2* | 169 | 2 028 462 | 0.28 | 0.34 | 0.51 | 1.37 |
| BA.4.6* | 92 | 45 443 | 4.05 | 3.63 | 3.26 | 2.79 |
| BA.4* | 128 | 116 339 | 0.80 | 0.59 | 0.49 | 0.31 |
| BA.5 + 5 mutations | 110 | 92 769 | 18.22 | 20.46 | 21.56 | 20.59 |
| BA.5.X | 146 | 1 208 259 | 53.05 | 45.67 | 37.49 | 26.47 |
| BJ.1 | 12 | 134 | 0.00 | | 0.01 | |
| BQ.1* | 73 | 30 652 | 9.81 | 14.09 | 19.07 | 23.25 |
| XBB* | 47 | 4 524 | 1.41 | 1.79 | 1.93 | 3.33 |
| Other | 205 | 6 641 579 | 4.77 | 4.33 | 3.82 | 2.34 |
| Unassigned | 85 | 112 741 | 4.16 | 4.98 | 6.69 | 12.15 |

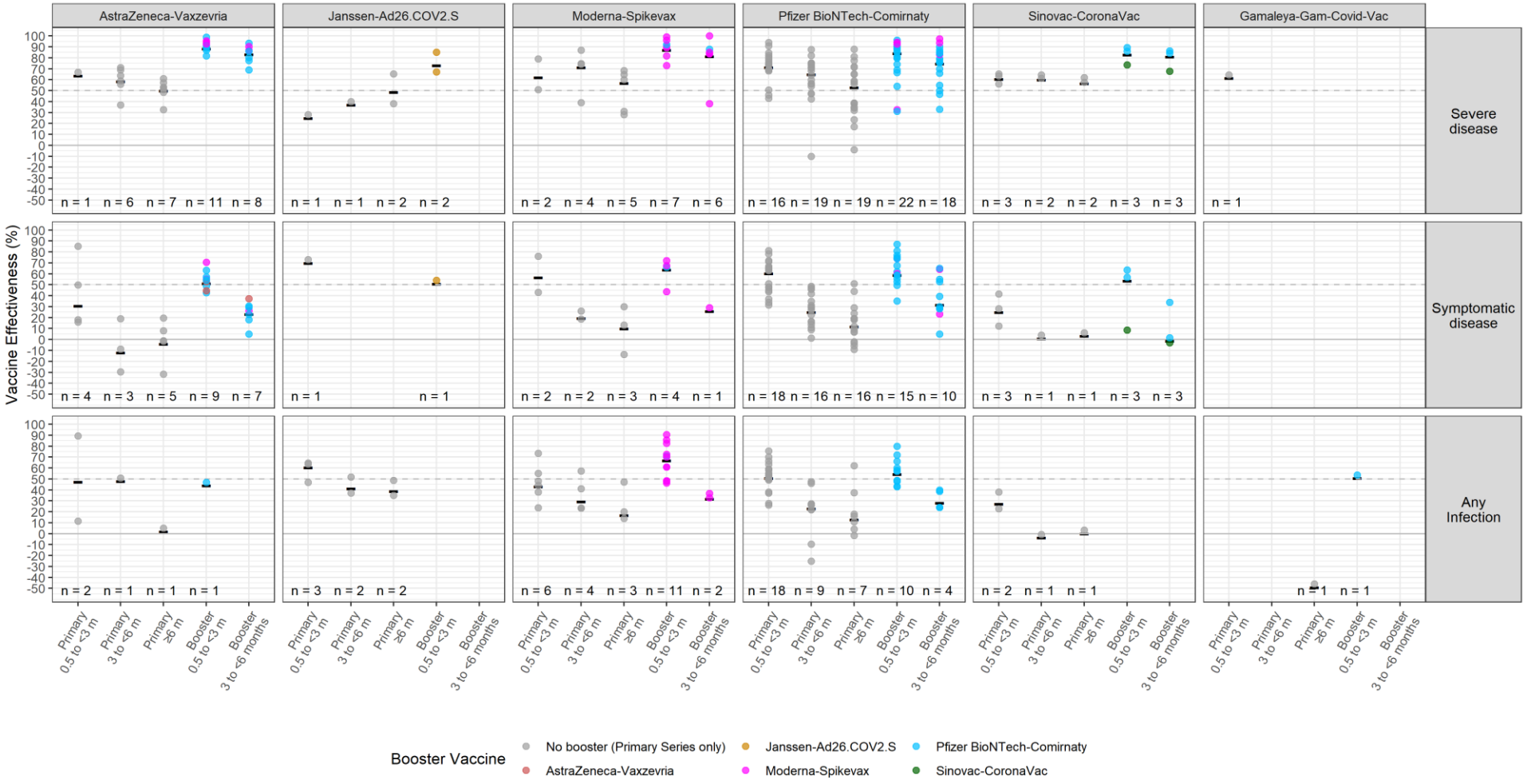
Table 2 shows the number of countries reporting the highlighted lineages, the total number of sequences reported and the prevalence of the lineages for the last four weeks. *BA.1.X, BA.2.X, BA.3.X, BA.4.X* and *BA.5.X* include all BA.1, BA.2, BA.3, BA.4 and BA.5 pooled descendent lineages. The *Unassigned* category includes lineages pending for a PANGO lineage name, whereas the *Other* category includes lineages other than those listed in the legend. Data source: sequences and metadata from GISAID, retrieved on 21 November 2022.

## Table 3. Summary of phenotypic characteristics of the Omicron VOC***

| Public health domain of impact | Omicron (B.1.1.529) | Omicron sublineages | | | |
|---|---|---|---|---|---|
| | **Omicron (B.1.1.529)** | **BA.1** | **BA.2** | **BA.4** | **BA.5** |
| **Transmissibility** | Growth advantage and increased transmissibility compared to Delta [5] | Lower growth rate compared to BA.2, BA.4 and BA.5[2] | Lower growth rate compared to BA.4 and BA.5 [2] | Lower growth advantage compared to BA.5 [2] | Growth advantage compared to BA.1, BA.2 and BA.4 [2] |
| **Disease severity** | Overall evidence suggests lower severity compared to Delta despite contrasting evidence. Earlier studies reported lower severity [6–11]. However, more recent studies report lower[12] or similar severity[13]. | There is evidence of similar severity compared to BA.2[14] . However, there is contrasting evidence in favor of no difference [15] or higher disease severity compared to BA.4 and BA.5[16] | Disease severity has been reported to be similar compared to BA.1 [14]. There is evidence, both in favor of higher severity[16] compared to BA.4 and BA.5, as well as in support of similar disease severity compared to BA.4 and BA.5[17] | One preliminary study suggests lower severity compared to BA.1 and BA.2 [16] while another study reported similar disease severity compared to BA.1 [15]. | There is one preliminary study suggesting increased severity compared to BA.1 and BA.2[18], while another study found lower disease severity compared to BA.1 and BA.2[16]. Another recent study found no difference in severity compared to BA.1 [15]. |
| **Risk of reinfection** | Reduced risk of Omicron reinfection among individuals previously infected with a different SARS-CoV-2 variant compared to naïve individuals[19,20] | Earlier studies reported reduced risk of reinfection with BA.1 after infection with BA.2[19] . However, a recent study reported increased risk of reinfection following prior infection with any Omicron sub-lineage, as compared to non-Omicron VOCs[21]. | There is a reduced risk of reinfection following infection with BA.1 reported earlier [19] and more recently [22]. However, a recent study reported increased risk of reinfection following prior infection with any Omicron sub-lineage, as compared to non-Omicron VOCs[21]. | There is varying evidence regarding the risk of reinfection. Some studies reported protection against infection following previous BA.1 or BA.2 infection[23,24]. A recent study reported increased risk of reinfection following prior infection with any Omicron sub-lineage, as compared to non-Omicron VOCs[21], while another reported reduced risk of reinfection following prior infection with any Omicron sub-lineage, as compared to non-Omicron VOCs[25]. | There is varying evidence regarding the risk of reinfection. Some studies reported protection against infection following previous BA.1 or BA.2 infection[23,24]. A recent study reported increased risk of reinfection following prior infection with any Omicron sub-lineage, as compared to non-Omicron VOCs[21], while another reported reduced risk of reinfection following prior infection with any Omicron sub-lineage, as compared to non-Omicron VOCs [25]. |
| **Impact on antibody responses** | Reduction in neutralizing activity reported as compared to other VOCs[26–28] | Lower neutralizing antibody titers compared to the index virus[28] | Lower neutralizing antibody titers compared to the index virus[28] | Lower neutralizing antibody titres compared to BA.1 [29,30] | Lower neutralizing antibody titres compared to BA.1 [29–31] |
| **Impacts on diagnostics** | PCR assays that include multiple gene targets maintain their accuracy to detect Omicron[32]; S gene target failure/positivity (SGTF) may be a proxy for screening. Limited to no impact on sensitivity of Ag-RDTs observed[33–36] | S gene target failure | The majority will be S gene target positive | S gene target failure | S gene target failure |
| **Impact on treatments** | No difference in the effectiveness of antiviral agents (polymerase and protease inhibitors) against the Omicron variant[37]. Conserved neutralizing activity for three broadly neutralizing monoclonal antibodies (sotrovimab, S2X259 and S2H97) and reduced effectiveness of other monoclonal antibodies[38–40] | Reduced neutralization activity of sotrovimab and casirivimab-imdevimab[41] | Reduced neutralization activity of sotrovimab and casirivimab-imdevimab[41] | Reduced neutralization activity of sotrovimab and casirivimab-imdevimab[41] | Reduced neutralization activity of sotrovimab and casirivimab-imdevimab[41] |

*** Studies contributing to the table are identified from an ongoing review of both the preprint and published literature on SARS-CoV-2 variants.

## Figure 5. Vaccine effectiveness (VE) of primary series and first booster vaccination against the Omicron variant of concern




Dots represent point estimates of VE from each study; dark black horizontal lines represent median VE across all studies in stratum. All data are from a systematic review of COVID-19 VE studies; methods and summary tables of VE studies can be found on view-hub.org. Vertical panels represent VE for full primary series (grey dots) and VE for homologous or heterologous booster vaccination (other colored dots) following completion of primary series vaccination with vaccine of primary series noted in column header. All booster VE estimates are for first booster dose. Severe disease includes hospitalization; symptomatic disease includes disease of any severity level; any infection can include symptomatic and asymptomatic infection. Not shown in plot: VE against severe disease at 0.5-<3 month post primary series of Beijing CNBG-BBIBP-CorV (59%, 95% CI: 4 to 80%). Additional details on the methods for inclusion of the estimates in the plots provided in text.

Figure 5 shows the absolute vaccine effectiveness (VE) over time against the Omicron variant, grouped by the primary series vaccine; booster doses may have been a different vaccine (i.e., both homologous and heterologous booster vaccination VEs are shown). All vaccines included in Figure 5 are vaccines based on the ancestral SARS-CoV-2 strain; no VE data are yet available for variant-based vaccines. Additional information on vaccine performance against VOCs can also be found in Annex 4.

Since the last update on 26 October 2022, two new studies have been added to the figure. One study assessed VE of a primary series of Pfizer BioNTech-Comirnaty and Gamaleya-Gam-Covid-Vac, as well as VE of a booster dose of Pfizer BioNTech-Comirnaty following both primary series regimens, against infection due to Omicron among employees of a national airline company in Lebanon [42]. The second study assessed VE of both primary series and booster dose vaccination with Pfizer BioNTech-Comirnaty against outpatient visits, urgent care visits, emergency department visits, and hospitalization due to Omicron BA.4/BA.5 among adults in the United States [43].

***Interpretation of the results of absolute VE for the Omicron variant for primary series and first booster dose vaccination***

To date, 53 studies from 19 countries (Argentina, Brazil, Canada, Chile, Czech Republic, Denmark, Finland, China (Hong Kong SAR), Israel, Italy, Lebanon, Norway, Paraguay, Qatar, Singapore, South Africa, the United Kingdom, the United States of America and Zambia) have collectively assessed the protection of seven vaccines against the Omicron variant, with evidence for the six vaccines with more than one VE estimate shown in Figure 5 (19 studies contributed VE estimates of primary series vaccination only, seven contributed estimates of the first booster vaccination only, and 27 contributed to both). Findings from these studies show reduced VE of COVID-19 primary series vaccines against the Omicron variant for all outcomes (*severe disease*, *symptomatic disease*, and *infection*) compared to those that have been observed for the original SARS-CoV-2 strain and the other four VOCs (plots of VE against other VOCs can be found on the VIEW-hub.org Resources Page). Importantly though, VE estimates against the Omicron variant remain higher for *severe disease* than the other outcomes for Omicron. The first booster vaccination substantially improves VE for all outcomes and for all combinations of schedules with estimates available for both primary series and booster vaccination. VE declines more in the first six months after the first booster vaccination for symptomatic disease and infection than it does for severe disease;[44] however, few studies assess VE of booster vaccination beyond six months.

For *severe disease*, VE of the primary series showed little decline over six months. During the first three months after primary series vaccination, VE was ≥70% for 12 of 18 (67%) VE estimates for the mRNA vaccines (Moderna-Spikevax and Pfizer BioNTech-Comirnaty). Of the three vector vaccines studies available, all had VE <70%: two reported VE <70% for AstraZeneca-Vaxzevria and Gamaleya-Gam-Covid-Vac, and the other reported VE <50% for Janssen-Ad26.COV2.S. Four estimates were available for inactivated vaccines: all three estimates for Sinovac-CoronaVac and the single estimate for Beijing CNBG-BBIBP-CorV (Sinopharm) were <70%, but ≥50% (the single estimate for Beijing CNBG-BBIBP-CorV (Sinopharm) is not shown in the figure). Beyond three months after vaccination with the primary series, VE was ≥70% for 17 of 47 (36%) VE estimates for the mRNA vaccines (31 [66%] had VE ≥50%); one of 13 (8%) AstraZeneca-Vaxzevria VE estimates was ≥70% (10 [77%] were ≥50%); none of the three estimates for a single dose of the other vector-based vaccine, Janssen-Ad26.COV2.S, was ≥70% (one was ≥50%); the four VE estimates for Sinovac-CoronaVac were ≥50% but <70%.

The first booster dose vaccination improved VE against *severe disease* in all studies, and VE was ≥70% in 39 (87%) of 45 estimates evaluating VE between 14 days and three months of receipt of a booster dose (42 estimates evaluated an mRNA booster, two evaluated a Janssen-Ad26.COV2.S booster, and one evaluated a Sinovac-CoronaVac booster); one Pfizer BioNTech-Comirnaty booster dose VE and one Moderna-Spikevax booster dose VE were <50% (though confidence intervals were wide, particularly for Moderna-Spikevax). After three months post mRNA booster, VE was

≥70% for 28 of 36 (78%) estimates (the primary series was a mRNA vaccine in 26 of the 36 estimates, AstraZeneca-Vaxzevria in eight and Sinovac-CoronaVac in two). Only one study of a third dose of Sinovac-CoronaVac found the VE to be <70% but ≥50% three to six months after the third dose.

VE against *symptomatic disease* and *infection* within the first three months of primary series vaccination was lower than against *severe disease*, and VE decreased more rapidly over time. For *symptomatic disease*, only five of 20 (25%) VE estimates for the mRNA vaccines were ≥70%, and 12 (60%) were ≥50%; one (25%) of the four VE estimates for AstraZeneca-Vaxzevria was ≥70%, while the remaining three estimates were <50%; the single estimate for Janssen-Ad26.COV2.S was ≥70%; and all three estimates for Sinovac (CoronaVac) were <50%. Beyond three months after vaccination (35 estimates evaluated mRNA vaccines, eight evaluated AstraZeneca-Vaxzevria, and two evaluated Sinovac-CoronaVac), only one of 45 (2%) VE estimates was ≥50%. mRNA booster vaccination after completion of a primary series of an mRNA vaccine, AstraZeneca-Vaxzevria, or Sinovac-CoronaVac improved VE against *symptomatic disease*: eight of 28 (29%) VE estimates between 14 days and three months post booster were ≥70%, although 23 (82%) were ≥50%; one (50%) of two VE estimates evaluating three doses of AstraZeneca-Vaxzevria was ≥50% but <70% while the second was <50%; the single estimate for two doses of Janssen-Ad26.CoV2.S was ≥50% but <70%, and the single estimate for three doses of Sinovac-CoronaVac was <50%. First booster dose protection against *symptomatic disease* declined rapidly over time: only four of 20 (20%) estimates available three or more months following receipt of an mRNA booster dose had VE ≥50%, and none were ≥70%. Neither the single VE estimate for three doses of AstraZeneca-Vaxzevria nor the single estimate for three doses of Sinovac-CoronaVac assessed three to six months post booster vaccination was above 50%. VE against *infection* showed a similar pattern of steep waning as that against *symptomatic disease*.

Of note, since the last update, one study of 24,356 healthcare encounters among adults in the United States provided new evidence of vaccine effectiveness against Omicron sublineages. The study found that primary series vaccination with Pfizer BioNTech-Comirnaty provided little protection against outpatient, urgent care, or emergency department visits and hospital admission due to BA.4/BA.5. A booster dose of Pfizer BioNTech-Comirnaty resulted in VE of >70% against hospitalization, which waned to <50%by six months; and in VE of >50% against milder outcomes, which waned to <50% by three months.[45]

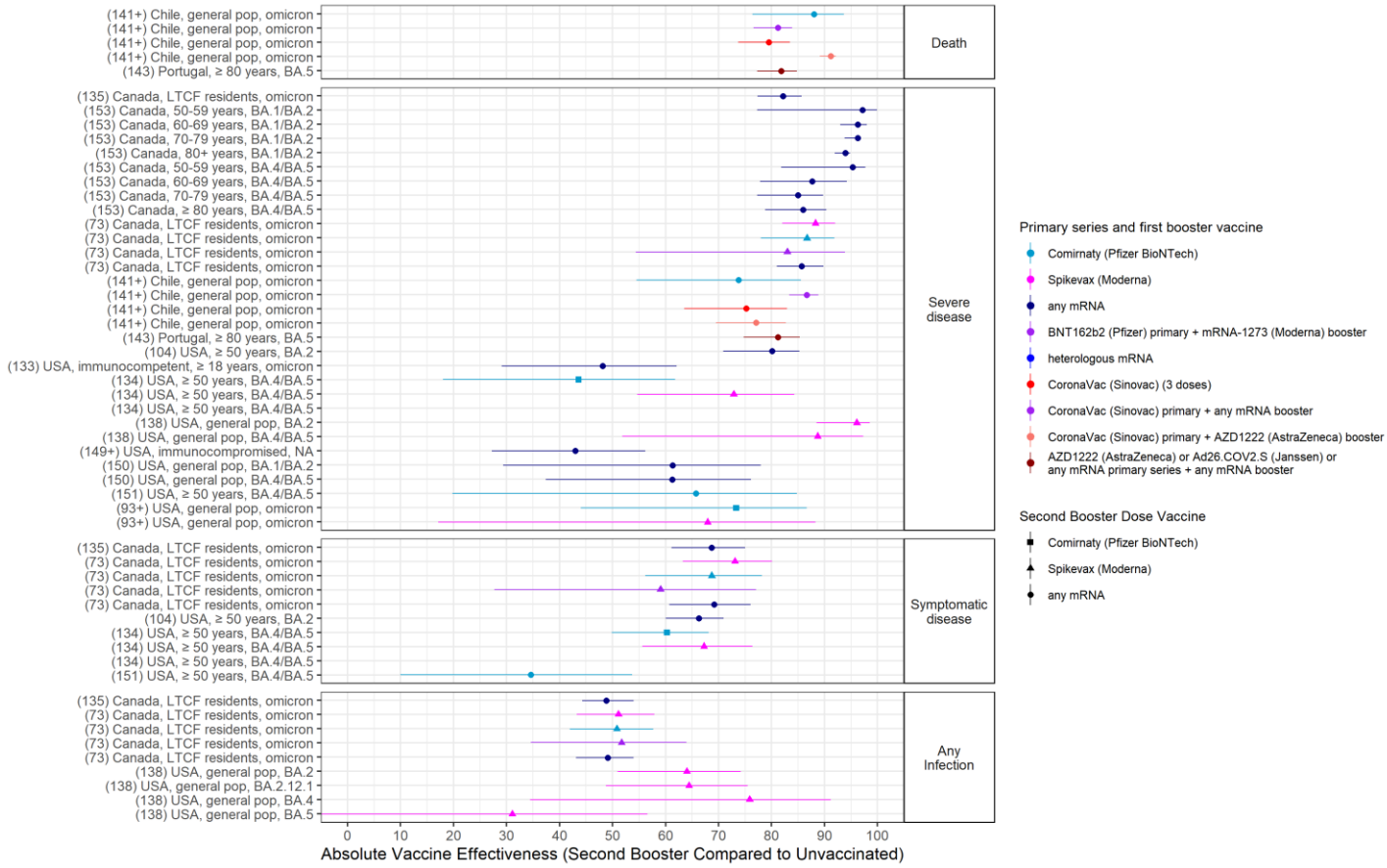
***Results of absolute VE and relative VE for the Omicron variant for second booster dose vaccination***

Thirteen studies have evaluated *absolute VE* of a second booster dose of mRNA vaccines, comparing infection and disease events among persons receiving four doses to an unvaccinated comparison group. VE of a second booster dose with a mRNA vaccine against *death*, *severe disease*, *symptomatic disease*, and *infection* due to Omicron was ≥70% among 100% (5/5), 74% (23/31), 10% (1/10), and 11% (1/9) of estimates, respectively (Figure 6). Most of the estimates included had follow-up time of less than four months after the second booster dose. Limited evidence is available on the duration of protection of a second booster dose; however, five studies found similar declines over time as has been seen with the first booster dose.[45–49]

To date 17 studies (see Figure 7), conducted among long-term care facility residents, older adults, healthcare workers, and adults 18 years and older, have assessed *relative VE* of a second booster dose of mRNA vaccines, by comparing the risk of Omicron *infection*, *symptomatic disease*, *severe disease* and *death* among persons receiving their second booster dose to persons having received only a first booster dose of mRNA vaccines at various time points ranging from relatively recently up to nine months ago. Relative VE of a second booster dose of mRNA vaccine is higher for *severe disease* and *death* than for *symptomatic disease* and *infection*.

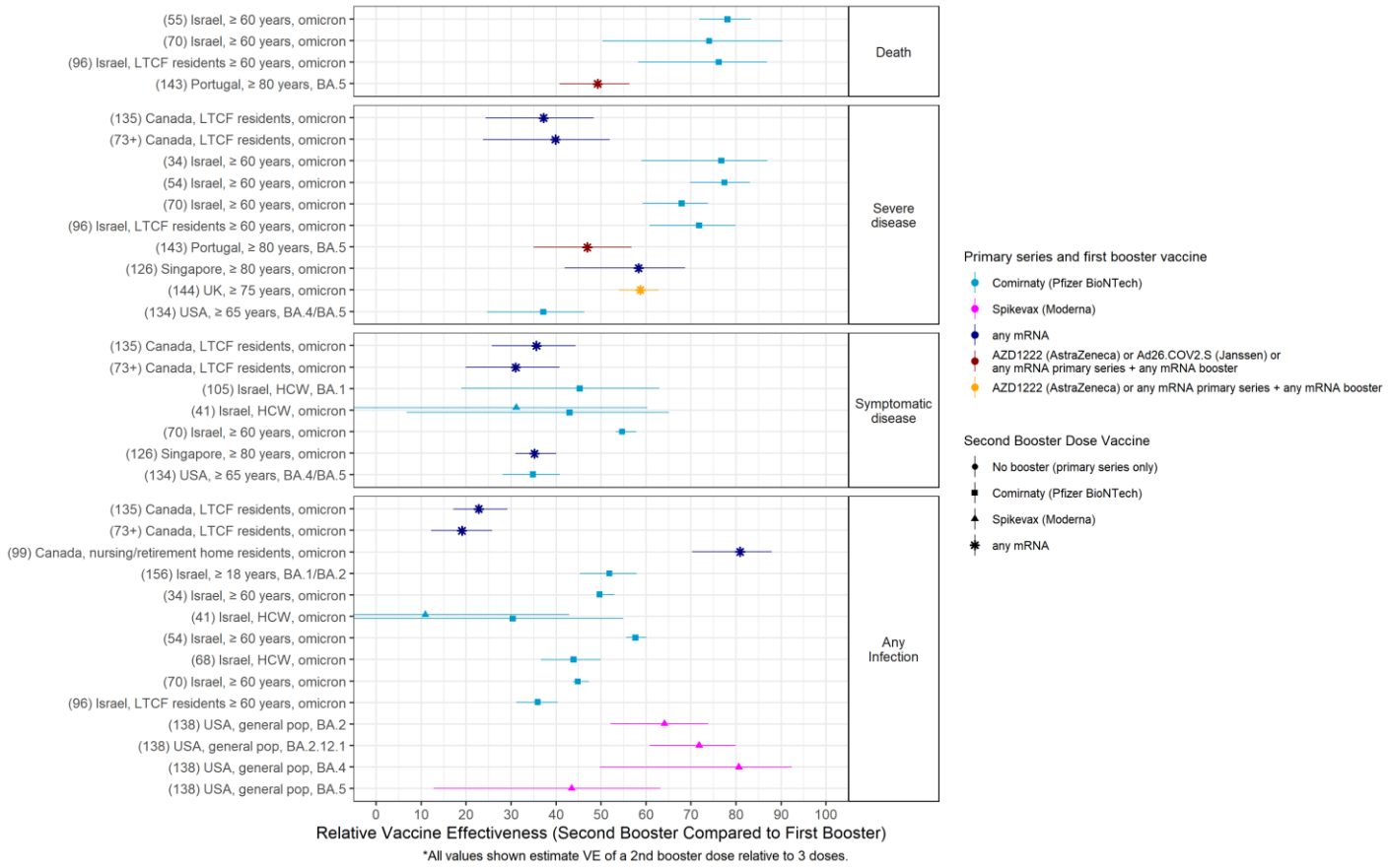
It is important to note that interpretation of relative VE is not straightforward; it cannot be translated into absolute VE or cases prevented after a second booster dose. High relative VE can translate into marginal gains in absolute VE. Moreover, relative VE cannot be compared across studies due to differences in the absolute VE (which is often not reported) and the epidemiological context of the setting of each study. For more information on interpreting relative VE, see the special focus on relative vaccine effectiveness from the 29 June 2022 Weekly Epidemiological Update.

**Figure 6. Absolute vaccine effectiveness of second booster vaccination against Omicron (*compared to receiving no doses*)**




Abbreviations: LTCF=long-term care facility, pop=population. Dots represent point estimates of vaccine effectiveness; horizontal lines represent the 95% confidence intervals. Labels along left side of plot indicate reference numbers, country, study population, and Omicron sub-lineage (if specified). Reference numbers identify the study and link to the summary table of VE effectiveness studies on view-hub.org (Table 2 in summary table). (+) indicates maximum potential follow-up period extends beyond four months post receipt of second booster dose. *Severe disease* includes any hospitalization and hospitalization with severe illness; *symptomatic disease* includes disease of any severity level; any *infection* can include symptomatic and asymptomatic infection.

## Figure 7. Relative vaccine effectiveness of second booster vaccination against Omicron (relative to first booster vaccination)




Abbreviations: LTCF=long-term care facility; HCW=healthcare workers. Dots represent point estimates of vaccine effectiveness; horizontal lines represent the 95% confidence intervals. Labels along left side of plot indicate reference numbers, country, study population, and Omicron sub-lineage (if specified). Reference numbers identify the study and link to the summary table Reference numbers identify the study and link to the summary table of VE effectiveness studies on view-hub.org (Table 2 in summary table). (+) indicates maximum potential follow-up period extends beyond four months post receipt of second booster dose. Severe disease includes any hospitalization and hospitalization with severe illness; symptomatic disease includes disease of any severity level; any infection can include symptomatic and asymptomatic infection.

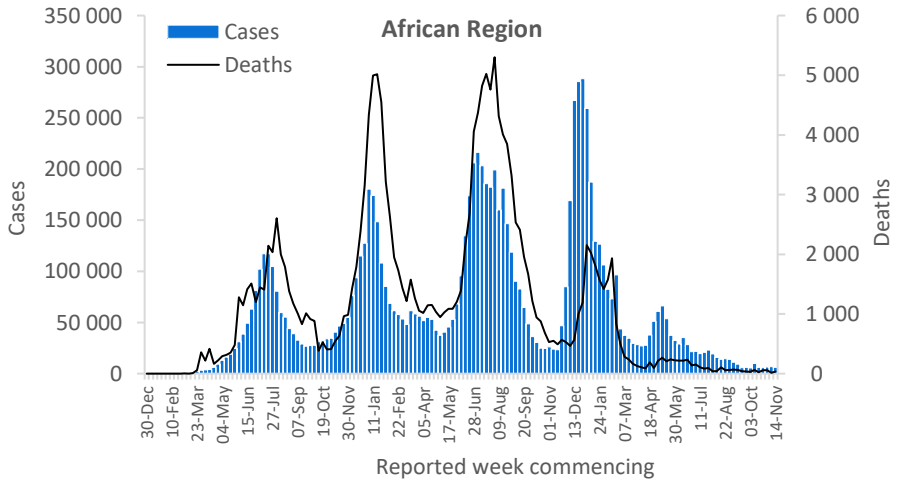
# WHO regional overviews:

**Epidemiological week 14-20 November 2022**

## African Region

The African Region reported 6074 new cases, a 9% decrease as compared to the previous week. Four (8%) of the 49 countries for which data are available reported increases in new cases of 20% or greater, with the highest proportional increases observed in Mayotte (197 vs 76 new cases; +159%), Algeria (71 vs 34 new cases; +109%) and Chad (six vs four new cases; +50%). The highest numbers of new cases were reported from South Africa (4039 new cases; 6.8 new cases per 100 000; +17%), Kenya (604 new cases; 1.1 new cases per 100 000; -14%) and Réunion (575 new cases; 64.2 new cases per 100 000; +13%).

The number of new weekly deaths in the region increased by 124% as compared to the previous week, with 38 new deaths reported. The highest numbers of new deaths were reported from South Africa (24 new deaths; <1 new death per 100 000; +200%), Kenya (six new deaths; <1 new death per 100 000; no deaths reported the previous week), and the Democratic Republic of the Congo (three new deaths; <1 new death per 100 000; +50%).

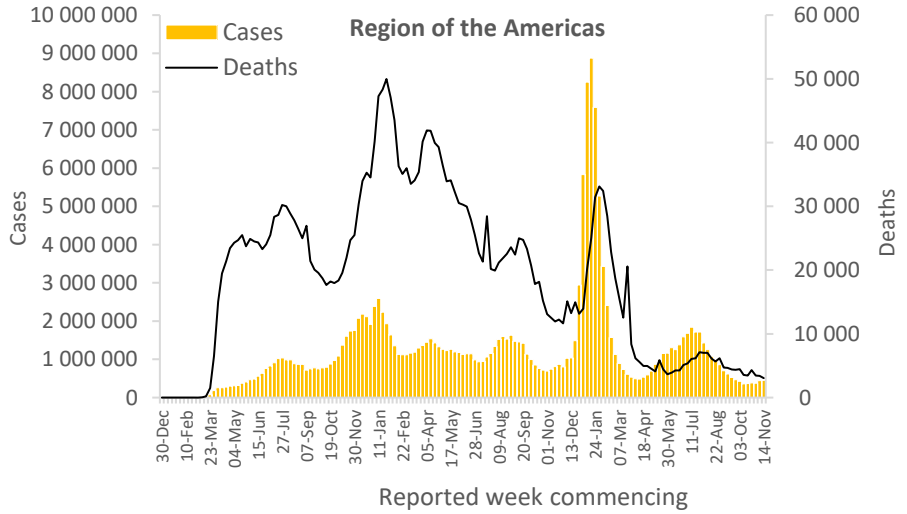



Updates from the African Region

## Region of the Americas

The Region of the Americas reported over 454 000 new cases, a 3% increase as compared to the previous week. Twelve (21%) of the 56 countries for which data are available reported increases in new cases of 20% or greater, with the highest proportional increases observed in Guyana (61 vs 19 new cases; +221%), French Guiana (308 vs 112 new cases; +175%) and the Dominican Republic (490 vs 222 new cases; +121%). The highest numbers of new cases were reported from the United States of America (274 067 new cases; 82.8 new cases per 100 000; -3%), Brazil (91 297 new cases; 43.0 new cases per 100 000; +54%) and Chile (39 013 new cases; 204.1 new cases per 100 000; -16%).

The number of new weekly deaths in the region decreased by 11% as compared to the previous week, with 3060 new deaths reported. The highest numbers of new deaths were reported from the United States of America (2202 new deaths; <1 new death per 100 000; -5%), Canada (268 new deaths; <1 new death per 100 000; -16%), and Brazil (251 new deaths; <1 new death per 100 000; -23%).

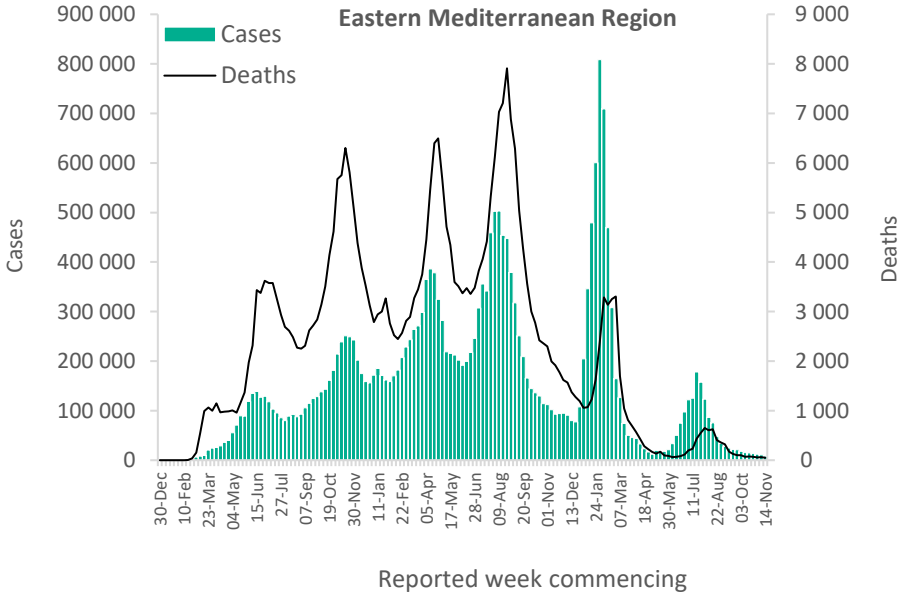



Updates from the Region of the Americas

## Eastern Mediterranean Region

The Eastern Mediterranean Region reported over 8500 new cases, a 22% decrease as compared to the previous week. One (5%) of the 22 countries for which data are available reported increases in new cases of 20% or greater: Egypt (eight vs six new cases; +33%). The highest numbers of new cases were reported from Qatar (2186 new cases; 75.9 new cases per 100 000; -10%), the United Arab Emirates (1519 new cases; 15.4 new cases per 100 000; -12%) and Bahrain (1479 new cases; 86.9 new cases per 100 000; -16%).

The number of new weekly deaths in the region decreased by 20% as compared to the previous week, with 49 new deaths reported. The highest numbers of new deaths were reported from the Islamic Republic of Iran (15 new deaths; <1 new death per 100 000; -17%), Saudi Arabia (14 new deaths; <1 new death per 100 000; -7%), and Lebanon (seven new deaths; <1 new death per 100 000; no deaths reported the previous week).

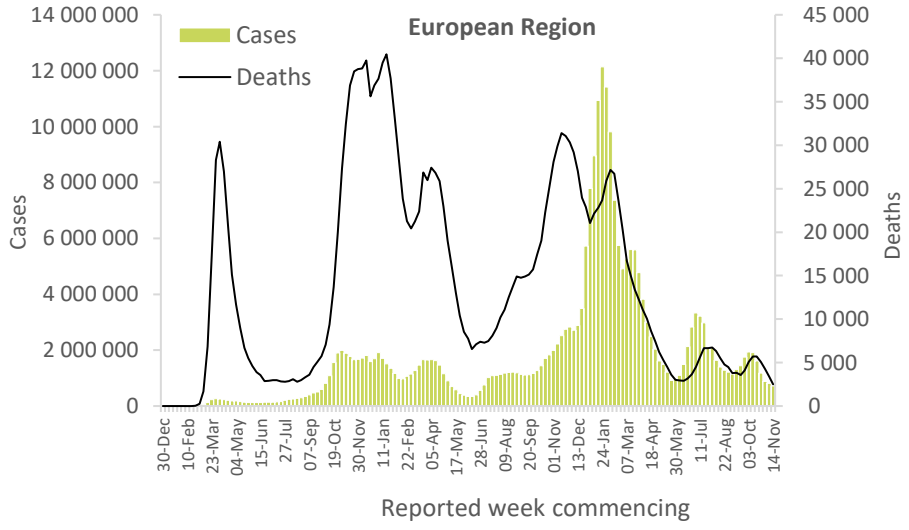



Updates from the Eastern Mediterranean Region

## European Region

The European Region reported over 724 000 new cases, an 11% decrease as compared to the previous week. Nine (15%) of the 61 countries for which data are available reported increases in new cases of 20% or greater, with the highest proportional increases observed in Uzbekistan (428 vs 181 new cases; +136%), Andorra (160 vs 76 new cases; +111%) and Kyrgyzstan (19 vs 12 new cases; +58%). The highest numbers of new cases were reported from France (186 446 new cases; 286.7 new cases per 100 000; +23%), Germany (153 843 new cases; 185.0 new cases per 100 000; -24%) and Italy (153 345 new cases; 257.1 new cases per 100 000; -15%).

The number of new weekly deaths in the region decreased by 26% as compared to the previous week, with 2513 new deaths reported. The highest numbers of new deaths were reported from France (441 new deaths; <1 new death per 100 000; +9%), the Russian Federation (430 new deaths; <1 new death per 100 000; -1%) and Italy (379 new deaths; <1 new death per 100 000; -22%).

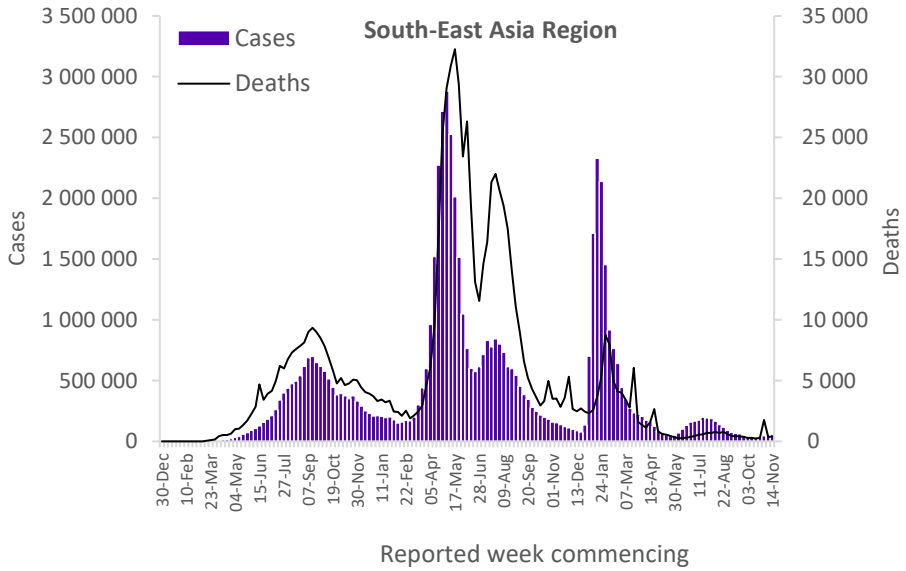



Updates from the European Region

## South-East Asia Region

The South-East Asia Region reported over 54 000 new cases, an 8% increase as compared to the previous week. Two (20%) of the 10 countries for which data are available reported increases in new cases of 20% or greater, with the highest proportional increase observed in Timor-Leste (13 vs nine new cases; +44%). The highest numbers of new cases were reported from Indonesia (46 863 new cases; 17.1 new cases per 100 000; +17%), Thailand (3957 new cases; 5.7 new cases per 100 000; +25%) and India (2638 new cases; <1 new case per100 000; -55%).

The number of new weekly deaths in the region increased by 13% as compared to the previous week, with 399 new deaths reported. The highest numbers of new deaths were reported from Indonesia (275 new deaths; <1 new death per 100 000; no deaths reported the previous week), Thailand (69 new deaths; <1 new death per 100 000; +64%) and India (43 new deaths; <1 new death per 100 000; +39%).

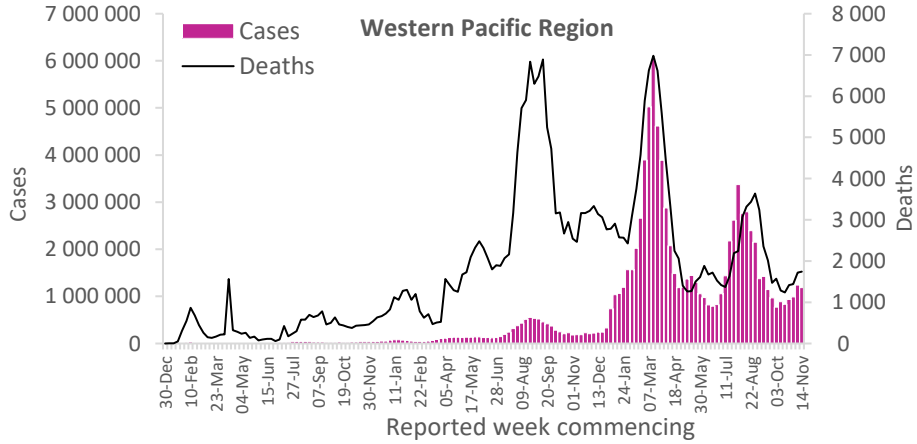



Updates from the South-East Asia Region

## Western Pacific Region

The Western Pacific Region reported over one million new cases, a 4% decrease as compared to the previous week. This decrease has occurred within the context of an overall six-week upward trend in the number of cases. Five (15%) of the 34 countries for which data are available reported increases in new cases of 20% or greater, with the highest proportional increases observed in the Pacific Islands locations of the Marshall Islands (115 vs four new cases; +2775%), Niue (13 vs two new cases; +550%), and Guam (128 vs 61 new cases; +110%). The highest numbers of new cases were reported from Japan (593 075 new cases; 468.9 new cases per 100 000; +18%), the Republic of Korea (364 536 new cases; 711.0 new cases per 100 000; +2%) and China (158 813 new cases; 10.8 new cases per 100 000; -8%).

The number of new weekly deaths in the region increased by 1% as compared to the previous week, with 1743 new deaths reported. The highest numbers of new deaths were reported from Japan (702 new deaths; <1 new death per 100 000; +27%), China (476 new deaths; <1 new death per 100 000; +16%), and the Republic of Korea (366 new deaths; <1 new death per 100 000; +26%).




Updates from the Western Pacific Region

## Hospitalizations and ICU admissions

At the global level, during epidemiological week 45 (7 to 13 November 2022), a total of 28 011 new hospitalizations and 948 new intensive care unit (ICU) admissions were reported, a 1% increase and 7% decrease, respectively, as compared to the previous week. The presented hospitalization data are preliminary and might change as new data become available. Furthermore, hospitalization data are subject to reporting delays. These data are also likely to include both hospitalizations with incidental cases of SARS-CoV-2 infection and those due to COVID-19 disease.

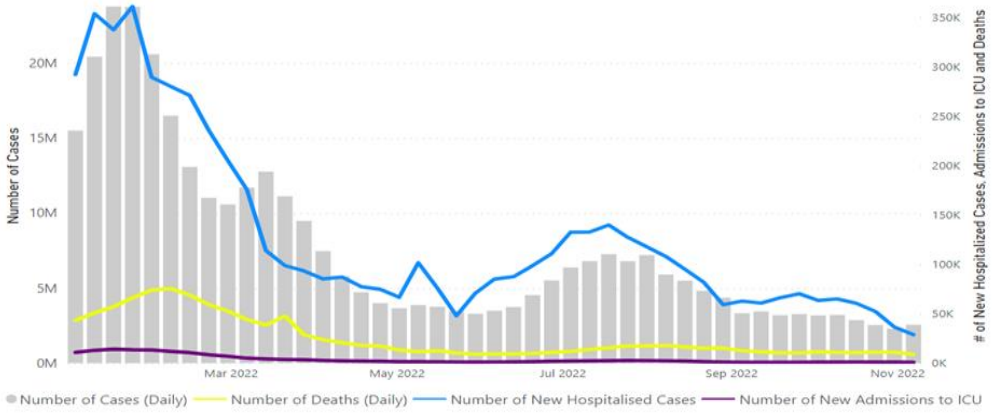
Globally, in week 45, 33 (17%) countries reported data to WHO on new hospitalizations. The region with the highest proportion of countries reporting data on new hospitalizations was the European Region (28%; 17 countries), followed by the Eastern Mediterranean Region (18%; four countries), the Region of the Americas (9%; five countries), the Western Pacific Region (9%; three countries), the South-East Asia Region (9%; one country) and the African Region (6%; three countries).

Across the six WHO regions, in week 45, a total of 19 (8%) countries reported data to WHO on new ICU admissions. The region with the highest proportion of countries reporting data on new ICU admissions was the European Region (15%; nine countries), followed by the Eastern Mediterranean Region (14%; three countries), the Western Pacific region (11%; four countries), the Region of the Americas (4%; two countries) and the African Region (2%, one country). So far, no country in the South-East Asia Region has reported data on new ICU admissions.

Among the 21 countries that reported more than 50 new hospitalizations, seven countries showed an increasing trend compared to the previous week: China (9639 vs 4164 new hospitalizations; +131%), Uzbekistan (69 vs 37 new hospitalizations; +86%), Ukraine (3031 vs 1990 new hospitalizations; +52%), South Africa (50 vs 35 new hospitalizations; +34%), Qatar (95 vs 71 new hospitalizations; +34%), Malaysia (4145 vs 3632 new hospitalizations; +14%) and Mexico (143 vs 132 new hospitalizations; +8%).

Among the 10 countries that reported more than 10 new ICU admissions, three countries showed an increasing trend compared to the previous week: Malaysia (81 vs 65 new ICU admissions; +25%), Australia (61 vs 50 new ICU admissions; +22%), and Bulgaria (436 vs 411 new ICU admissions; +6%).

**Figure 8. COVID-19 cases, deaths, hospital, and ICU admissions reported weekly to WHO, as of 13 November 2022.**




Source: WHO Detailed Surveillance Dashboard

## Annex 1. Data, table, and figure notes

Data presented are based on official laboratory-confirmed COVID-19 cases 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 incidences, and variable delays to reflecting these data at the 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.

A record of historic data adjustment made is available upon request by emailing epi-data-support@who.int. Please specify the countries of interest, time period, 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. 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.

'Countries' may refer to countries, territories, areas or other jurisdictions of similar status. 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 except, 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, the number of cases of Serbia and Kosovo (UNSCR 1244, 1999) have been aggregated for visualization purposes.
[2] A dispute exists between the Governments of Argentina and the United Kingdom of Great Britain and Northern Ireland concerning sovereignty over the Falkland Islands (Malvinas).

Updates on the COVID-19 outbreak in the Democratic People's Republic of Korea are not included in this report as the number of laboratory-confirmed COVID-19 cases is not reported.

## Annex 2. SARS-CoV-2 variants assessment and classification

WHO, in collaboration with national authorities, institutions and researchers, routinely assesses if variants of SARS-CoV-2 alter transmission or disease characteristics, or impact the effectiveness of vaccines, therapeutics, diagnostics or public health and social measures (PHSM) applied to control disease spread. Potential variants of concern (VOCs), variants of interest (VOIs) or variants under monitoring (VUMs) are regularly assessed based on the risk posed to global public health.

The classifications of variants will be revised as needed to reflect the continuous evolution of circulating variants and their changing epidemiology. Criteria for variant classification, and the lists of currently circulating and previously circulating VOCs, VOIs and VUMs, are available on the WHO Tracking SARS-CoV-2 variants website. National authorities may choose to designate other variants and are strongly encouraged to investigate and report newly emerging variants and their impact.

WHO continues to monitor SARS-CoV-2 variants, including descendent lineages of VOCs, to track changes in prevalence and viral characteristics. The current trends describing the circulation of Omicron descendent lineages should be interpreted with due consideration of the limitations of the COVID-19 surveillance systems. These include differences in sequencing capacity and sampling strategies between countries, changes in sampling strategies over time, reductions in tests conducted and sequences shared by countries, and delays in uploading sequence data to GISAID.

## Annex 3. Summary of results of neutralization studies assessing primary series and booster vaccine performance against Omicron variant of concern (data updated as of 20 November 2022)

| | | Omicron Sub-Lineage | | | | | |
|---|---|---|---|---|---|---|---|
| | | **BA.1** | **BA.2** | **BA.2.12.1** | **BA.2.75** | **BA.3** | **BA.4/BA.5** |
| **Primary Series Vaccination** | | | | | | | |
| WHO Emergency Use Listing (EUL) Qualified Vaccines | AstraZeneca-Vaxzevria/SII-Covishield | $HNR_{15}$ | $HNR_{2}$ | $HNR_{1}$ | ---- | ---- | $HNR_{1}$ |
| | Beijing CNBG-BBIBP-CorV | $HNR_{9}$ | $HNR_{3}$ | $HNR_{2}$ | ---- | $HNR_{1}$ | $HNR_{2}$ |
| | Bharat-Covaxin | $\downarrow\downarrow_{1}$ | ---- | ---- | ---- | ---- | ---- |
| | Cansino-Convidecia | ---- | ---- | ---- | ---- | ---- | ---- |
| | Janssen-Ad26.COV2.S | $HNR_{10}$ | $HNR_{1}$ | $HNR_{1}$ | ---- | ---- | $HNR_{1}$ |
| | Moderna-Spikevax | $\downarrow\downarrow\downarrow_{11}$ | $\downarrow\downarrow$to$\downarrow\downarrow\downarrow_{2}$ | $HNR_{1}$ | ---- | ---- | $HNR_{1}$ |
| | Novavax-Nuvaxovid/SII - Covavax | $HNR_{2}$ | $HNR_{1}$ | $HNR_{1}$ | ---- | ---- | $HNR_{1}$ |
| | Pfizer BioNTech-Comirnaty | $HNR_{57}$ | $HNR_{10}$ | $HNR_{3}$ | $HNR_{1}$ | $HNR_{1}$ | $HNR_{5}$ |
| | Sinovac-CoronaVac | $HNR_{11}$ | $HNR_{2}$ | $HNR_{1}$ | ---- | ---- | $HNR_{2}$ |
| Vaccines without WHO EUL | Anhui ZL-Recombinant | ---- | ---- | ---- | ---- | ---- | ---- |
| | Gamaleya-Sputnik V | $HNR_{3}$ | $HNR_{1}$ | $HNR_{1}$ | ---- | ---- | $HNR_{1}$ |
| | Chumakov-Covi-Vac | $HNR_{2}$ | ---- | ---- | ---- | ---- | ---- |
| **First Booster Vaccination (Primary Series Vaccine + Booster Vaccine)** | | | | | | | |
| WHO Emergency Use Listing (EUL) Qualified Booster Vaccines | AstraZeneca-Vaxzevria/SII-Covishield + AstraZeneca-Vaxzevria/SII Covishield | $HNR_{2}$ | $HNR_{2}$ | ---- | ---- | $\downarrow\downarrow_{1}$ | $\downarrow\downarrow\downarrow_{1}$ |
| | AstraZeneca-Vaxzevria/SII-Covishield + Moderna-Spikevax | $\downarrow_{1}$ | ---- | ---- | ---- | ---- | ---- |
| | AstraZeneca-Vaxzevria/SII-Covishield + Pfizer BioNTech-Comirnaty | $\downarrow\downarrow$to$\downarrow\downarrow\downarrow_{2}$ | $\downarrow\downarrow_{1}$ | ---- | ---- | $\downarrow\downarrow_{1}$ | ---- |
| | Beijing CNBG-BBIBP-CorV + Beijing CNBG-BBIBP-CorV | $\downarrow\downarrow$to$\downarrow\downarrow\downarrow_{6}$ | $\downarrow_{4}$ | $HNR_{2}$ | $\downarrow_{1}$ | $\downarrow\downarrow_{2}$ | $\downarrow_{5}$ |
| | Cansino-Convidecia + Cansino-Convidecia | $\downarrow_{1}$ | ---- | ---- | ---- | ---- | ---- |
| | Janssen-Ad26.COV2.S + Janssen-Ad26.COV2.S | $HNR_{3}$ | ---- | ---- | ---- | ---- | ---- |
| | Janssen-Ad26.COV2.S + Moderna-Spikevax | $\downarrow\downarrow\downarrow_{1}$ | ---- | ---- | ---- | ---- | ---- |
| | Janssen-Ad26.COV2.S + Pfizer BioNTech-Comirnaty | $\downarrow$ to $\downarrow\downarrow\downarrow_{2}$ | ---- | ---- | ---- | ---- | ---- |
| | Moderna-Spikevax + Moderna-Spikevax | $\downarrow$to$\downarrow\downarrow\downarrow_{11}$ | $\downarrow\downarrow$ to$\downarrow\downarrow\downarrow_{4}$ | $\downarrow\downarrow_{1}$ | $\downarrow_{2}$ | $\downarrow\downarrow_{1}$ | $\downarrow\downarrow\downarrow_{4}$ |
| | Moderna-Spikevax + Pfizer BioNTech-Comirnaty | $\downarrow\downarrow\downarrow_{1}$ | ---- | ---- | ---- | ---- | ---- |
| | Novavax-Nuvaxovid/SII – Covavax + Novavax-Nuvaxovid/SII - Covavax | $\downarrow\downarrow_{1}$ | ---- | ---- | ---- | ---- | ---- |
| | Pfizer BioNTech-Comirnaty + Pfizer BioNTech-Comirnaty | $\downarrow$to$\downarrow\downarrow\downarrow_{52}$ | $\downarrow$to$\downarrow\downarrow_{24}$ | $\downarrow$to$\downarrow\downarrow_{9}$ | $\downarrow\downarrow_{3}$ | $\downarrow$to$\downarrow\downarrow_{5}$ | $\downarrow\downarrow$to$\downarrow\downarrow\downarrow_{15}$ |
| | Pfizer BioNTech-Comirnaty + Janssen-Ad26.COV2.S | $\downarrow_{2}$ | ---- | ---- | ---- | ---- | ---- |
| | Pfizer BioNTech-Comirnaty + Moderna-Spikevax | $\downarrow$to$\downarrow\downarrow_{3}$ | $\downarrow\downarrow_{1}$ | ---- | $\downarrow\downarrow\downarrow_{1}$ | ---- | $\downarrow\downarrow\downarrow_{1}$ |
| | Sinovac-CoronaVac + Sinovac-CoronaVac | $HNR_{11}$ | $\downarrow\downarrow$ to$\downarrow\downarrow\downarrow_{6}$ | $HNR_{3}$ | $\downarrow\downarrow_{1}$ | $\downarrow\downarrow_{1}$ | $HNR_{5}$ |
| | Sinovac-CoronaVac + AstraZeneca-Vaxzevria | $\downarrow\downarrow_{1}$ | ---- | ---- | ---- | ---- | ---- |
| | Sinovac-CoronaVac + Pfizer BioNTech-Comirnaty | $\downarrow\downarrow_{6}$ | $\downarrow$to$\downarrow\downarrow_{4}$ | $\downarrow$to$\downarrow\downarrow_{2}$ | ---- | ---- | $\downarrow$to$\downarrow\downarrow\downarrow_{3}$ |
| Booster Vaccines without WHO EUL | Anhui ZL-Recombinant + Anhui ZL-Recombinant | $\downarrow$to$\downarrow\downarrow_{3}$ | $\downarrow\downarrow_{1}$ | $\downarrow\downarrow_{1}$ | ---- | $\downarrow\downarrow\downarrow_{1}$ | $\downarrow\downarrow\downarrow_{1}$ |
| | Beijing CNBG-BBIBP-CorV + Anhui ZL - Recombinant | $\downarrow\downarrow$to$\downarrow\downarrow\downarrow_{5}$ | $\downarrow\downarrow$to$\downarrow\downarrow\downarrow_{2}$ | $HNR_{2}$ | $\downarrow\downarrow\downarrow_{1}$ | $\downarrow\downarrow\downarrow_{2}$ | $HNR_{2}$ |
| | Cansino-Convidecia + Anhui ZL - Recombinant | $\downarrow_{1}$ | ---- | ---- | ---- | ---- | ---- |
| | Gamaleya-Sputnik V + Gamaleya Sputnik Light | $\downarrow\downarrow_{1}$ | ---- | ---- | ---- | ---- | ---- |
| | Sinovac-CoronaVac + Anhui ZL - Recombinant | $\downarrow$to$\downarrow\downarrow_{2}$ | $\downarrow$to$\downarrow\downarrow_{2}$ | $\downarrow$to$\downarrow\downarrow\downarrow_{2}$ | ---- | $\downarrow$to$\downarrow\downarrow\downarrow_{2}$ | $\downarrow\downarrow_{1}$ |
| | Sinovac-CoronaVac + Cansino-Ad5-nCoV-IH | $\downarrow\downarrow\downarrow_{1}$ | ---- | ---- | ---- | ---- | ---- |
| **Second Booster Vaccination (Primary Series + First Booster Vaccine + Second Booster Vaccine)** | | | | | | | |
| WHO Emergency Use Listing (EUL) Qualified Booster Vaccines | Moderna-Spikevax + Moderna-Spikevax + Moderna-Spikevax | $\downarrow_{1}$ | ---- | ---- | ---- | ---- | ---- |
| | Moderna-Spikevax + Moderna-Spikevax + Moderna-Spikevax Bivalent Original/Omicron BA.1 | $\downarrow_{1}$ | ---- | ---- | ---- | ---- | $\downarrow\downarrow_{1}$ |
| | Pfizer BioNTech-Comirnaty + Pfizer BioNTech-Comirnaty + Pfizer BioNTech-Comirnaty | $\downarrow\downarrow\downarrow_{1}$ | ---- | ---- | ---- | ---- | ---- |
| | Pfizer BioNTech-Comirnaty + Pfizer BioNTech-Comirnaty + Moderna-Spikevax | $\downarrow\downarrow\downarrow_{1}$ | ---- | ---- | ---- | ---- | ---- |

Abbreviations: HNR=high non-response. Arrows generalize the magnitude of reduction in VE or neutralization: "↔" indicates <2-fold reduction in neutralization relative to the ancestral strain; "↓" indicates 2 to <5-fold reduction; "↓↓" indicates 5 to <10-fold reduction; "↓↓↓" indicates ≥10-fold reduction. When more than one neutralization study is available, the interquartile range (25th and 75th percentiles) of fold-reductions across all studies for specific vaccine/sub-lineage was used. HNR indicates a median percent response across all studies of <75%; in these instances, fold-reductions can be biased, and thus are not presented. The number of studies is shown as subscripts.

### Additional notes on Annex 3 table

- Studies contributing to the table are identified from an ongoing review of the preprint and published literature on neutralization of SARS-CoV-2 variants by COVID-19 vaccines.
- The following sets of results are excluded from the table:
    - Samples collected <7 days or ≥6 months after final dose
    - Strain other than ancestral SARS-CoV-1 strain used as the reference
    - Samples collected from immunocompromised persons
    - More than 20% of samples collected from persons previously infected with SARS-CoV-2
- It is important to note that studies vary in population and other methodological considerations which may in part explain some differences when comparing products between different studies. In addition, the reductions summarized in the table do not incorporate uncertainty intervals around the fold reductions which can vary substantially across studies when reported.

## Annex 4. Methods for Figure 5

- VE studies included in the plot were identified from an ongoing systematic review of COVID-19 vaccine effectiveness studies. All studies were cohort or test-negative designs conducted when Omicron was the predominant circulating variant. Methods for the systematic review and inclusion/exclusion criteria are available on view-hub.org.
- Only studies providing VE estimates of individual vaccines are included in the plot; studies assessing combined VE of more than one vaccine are excluded except for studies of heterologous primary and booster schedules where all participants included in a VE estimate received the same brands of vaccines in the same order.
- Only studies providing VE estimates for discrete time intervals since vaccination or estimates with limited follow-up time (such that the median time point falls clearly in one of the intervals for the plot) are included. Studies that only provide VE estimates over a cumulative period of time covering more than one time interval are excluded because they are difficult to interpret due to the marked waning of VE over time with Omicron.
- Only estimates of absolute vaccine effectiveness (i.e., the comparison group is unvaccinated persons) are included in the plot; estimates of relative vaccine effectiveness (e.g., the comparison group for booster doses is persons having completed the primary series) are excluded as the interpretation of relative vaccine effectiveness is not comparable with absolute vaccine effectiveness.

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