

COVID-19 Weekly Epidemiological Update

Edition 110 published 21 September 2022

In this edition:

- [Global overview](#)
- [Special Focus: Update on SARS-CoV-2 variants of interest and variants of concern](#)
- [WHO regional overviews](#)

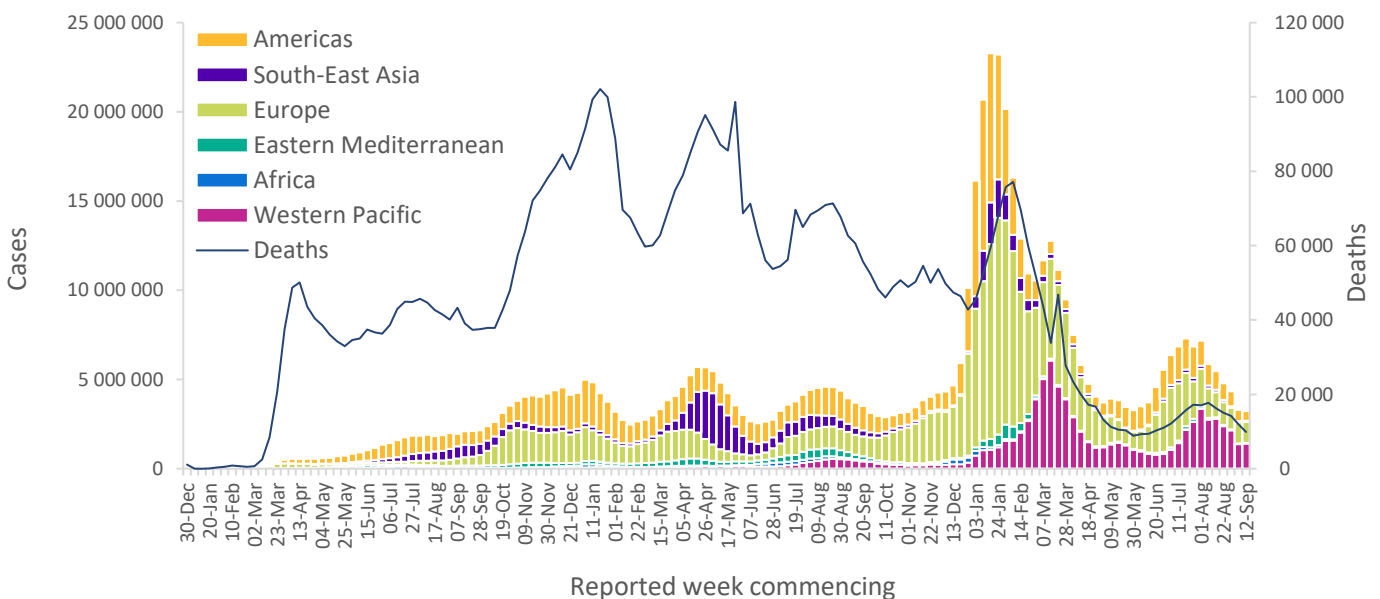
Global overview

Data as of 18 September 2022

Globally, the number of new weekly cases remained stable during the week of 12 to 18 September 2022 as compared to the previous week, with over 3.2 million new cases reported (Figure 1, Table 1). The number of new weekly deaths decreased by 17% as compared to the previous week, with over 9800 fatalities reported. As of 18 September 2022, over 609 million confirmed cases and over 6.5 million deaths have been reported globally.

At the regional level, the number of newly reported weekly cases decreased or remained stable across all six WHO regions: the African Region (-35%), the Eastern Mediterranean Region (-14%), the Region of the Americas (-12%), the South-East Asia Region (-8%), the European Region (-1%) and the Western Pacific Region (+3%). The number of new weekly deaths decreased across all six regions: the Eastern Mediterranean Region (-46%), the African Region (-27%), the Western Pacific Region (-27%), the European Region (-22%), the South-East Asia Region (-6%) and the Region of the Americas (-5%).

Figure 1. COVID-19 cases reported weekly by WHO Region, and global deaths, as of 18 September 2022**



**See [Annex 1: Data, table, and figure notes](#)

At the country level, the highest numbers of new weekly cases were reported from Japan (605 919 new cases; +13%), the United States of America (395 117 new cases; -11%), the Republic of Korea (389 579 new cases; -11%), the Russian Federation (372 485 new cases; +10%) and China (297 693 new cases; 13%). The highest numbers of new weekly deaths were reported from the United States of America (2601 new deaths; +5%), Japan (1162 new deaths; -31%), the Russian Federation (697 new deaths; +9%), Spain (595 new deaths; +83%) and Brazil (487 new deaths; -12%).

Current trends in reported COVID-19 cases and deaths 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. 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 18 September 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 | 1 420 762 (44%) | 3% | 87 985 821 (14%) | 2 415 (24%) | -27% | 267 600 (4%) |
| Europe | 1 164 233 (36%) | -1% | 251 088 626 (41%) | 2 767 (28%) | -22% | 2 087 946 (32%) |
| Americas | 552 342 (17%) | -12% | 177 464 288 (29%) | 4 037 (41%) | -5% | 2 830 423 (44%) |
| South-East Asia | 66 777 (2%) | -8% | 60 192 703 (10%) | 427 (4%) | -6% | 796 871 (12%) |
| Eastern Mediterranean | 23 658 (1%) | -14% | 23 046 219 (4%) | 172 (2%) | -46% | 348 149 (5%) |
| Africa | 6 853 (<1%) | -35% | 9 317 547 (2%) | 44 (<1%) | -27% | 174 453 (3%) |
| Global | 3 234 625 (100%) | -2% | 609 095 968 (100%) | 9 862 (100%) | -17% | 6 505 455 (100%) |

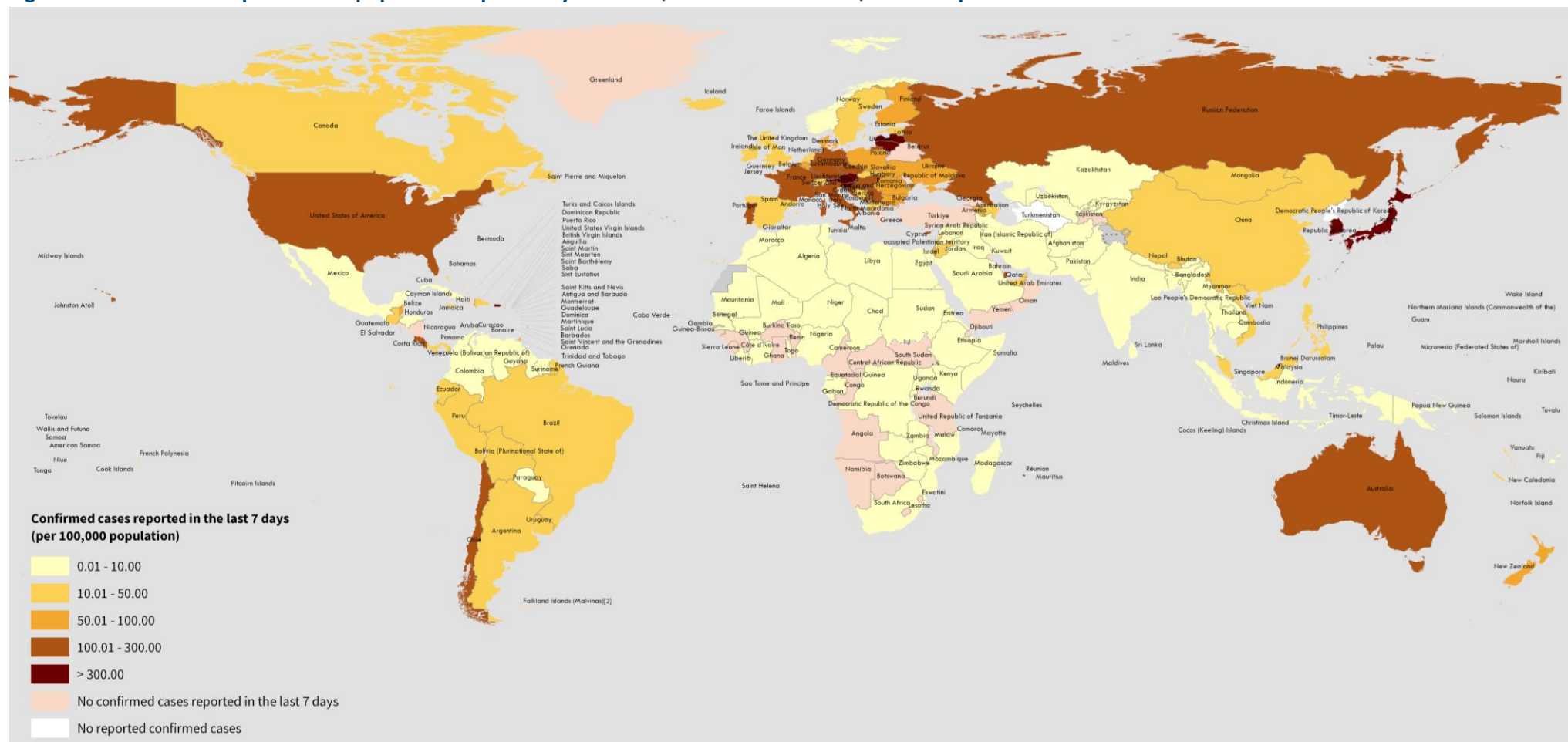
*Percent change in the number of newly confirmed cases/deaths in the past seven days, compared to seven days prior. Data from previous weeks are updated continuously with adjustments received from countries.

**See [Annex 1: Data, table, and figure notes](#)

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](#)
- [WHO COVID-19 detailed surveillance data dashboard](#)

Figure 2. COVID-19 cases per 100 000 population reported by countries, territories and areas, 12 - 18 September 2022*



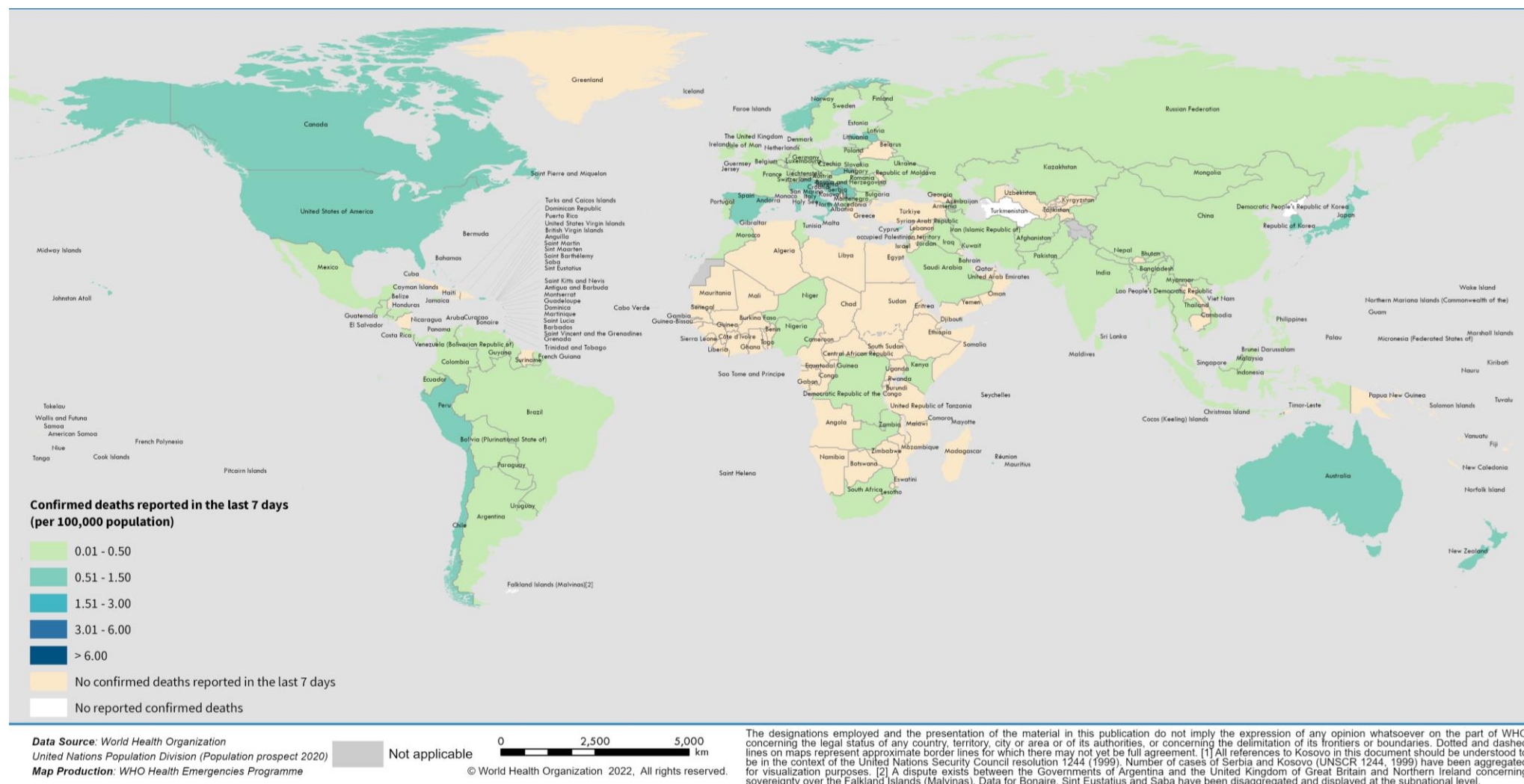
Data Source: World Health Organization
 United Nations Population Division (Population prospect 2020)
 Map Production: WHO Health Emergencies Programme

Not applicable 0 2,500 5,000 km
 © World Health Organization 2022. All rights reserved.

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. COVID-19 deaths per 100 000 population reported by countries, territories and areas, 12 - 18 September 2022**



**See [Annex 1: Data, table, and figure notes](#)

Special Focus: Update on SARS-CoV-2 variants of interest and variants of concern

Geographic spread and prevalence of VOCs

Globally, from 19 August to 19 September 2022, 120 617 SARS-CoV-2 sequences were shared through GISAID. Among these, 119 458 sequences were of the Omicron variant of concern (VOC), accounting for 99.0% of sequences reported globally in the past 30 days. As the number of submitted sequences continues to decline, interpretation of trends should be made with due caution.

The current variant circulation is characterized by Omicron descendent lineages and by a large genetic diversification. More than 230 descendent lineages of Omicron, and more than 30 recombinants have emerged. These variants are being monitored and assessed by WHO based on criteria of genetic constellations of mutations, and/or indications of a rise in prevalence in a geographic location, as well as any evidence of phenotypic changes.ⁱ All of these lineages have different additional mutations, yet the majority do not warrant concern, either based on current knowledge of relevant genetic sites, or based on very low sequence circulation over several weeks. As of epidemiological week 35 (29 August to 4 September 2022), the pooled descendent lineages of BA.5 (BA.5.X) show the highest relative global prevalence of 76.6%, followed by BA.4.X with 7.5% prevalence. During the same period, BA.3.X, BA.2.X (excluding BA.2.75) and BA.1.X have declined in global prevalence to less than 1%.

Six lineages are currently classified as Omicron subvariants under monitoring. BA.2.75 is being monitored due to nine additional mutations in the spike as compared to its parent lineage BA.2; four of these mutations are within the receptor binding domain (RBD), and at least one of these RBD mutations has been associated with immune escape in previous variants.¹ Global prevalence of BA.2.75 is low (1.26% as of week 35), but has been rising over the last weeks. As of epidemiological week 35, a total of 48 countries have been reporting its detection; the majority of the reported sequences are from India. One of its descendent lineages, BA.2.75.2, has three additional spike mutations.

BA.5.1 + V445* (*indicating pooled amino acid substitutions), BA.5.2 + K444*, BA.5.2.1 + R346*, BA.5.2.1 + K444*, and BE.1.1 (BA.5.3.1.1.1) are emerging subvariants under monitoring, with mutations in RBD positions with predicted phenotypic effects (such as antibody escape, changes to ACE2 binding affinity, etc) and increased spread to new locations.ⁱⁱ The prevalence of these Omicron subvariants under monitoring is still low but rising over the last four weeks (see Table 2).

For more information on the assessment of SARS-CoV-2 variants and the WHO classification refer to Annex 2.

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](#)
- [VIEW-hub: repository for the most relevant and recent vaccine data](#)

ⁱ WHO tracking SARS-CoV-2 Variants

ⁱⁱ <https://gisaid.org/publish/>

Figure 4. Panel A and B: The number and percentage of SARS-CoV-2 sequences, as of 19 September 2022

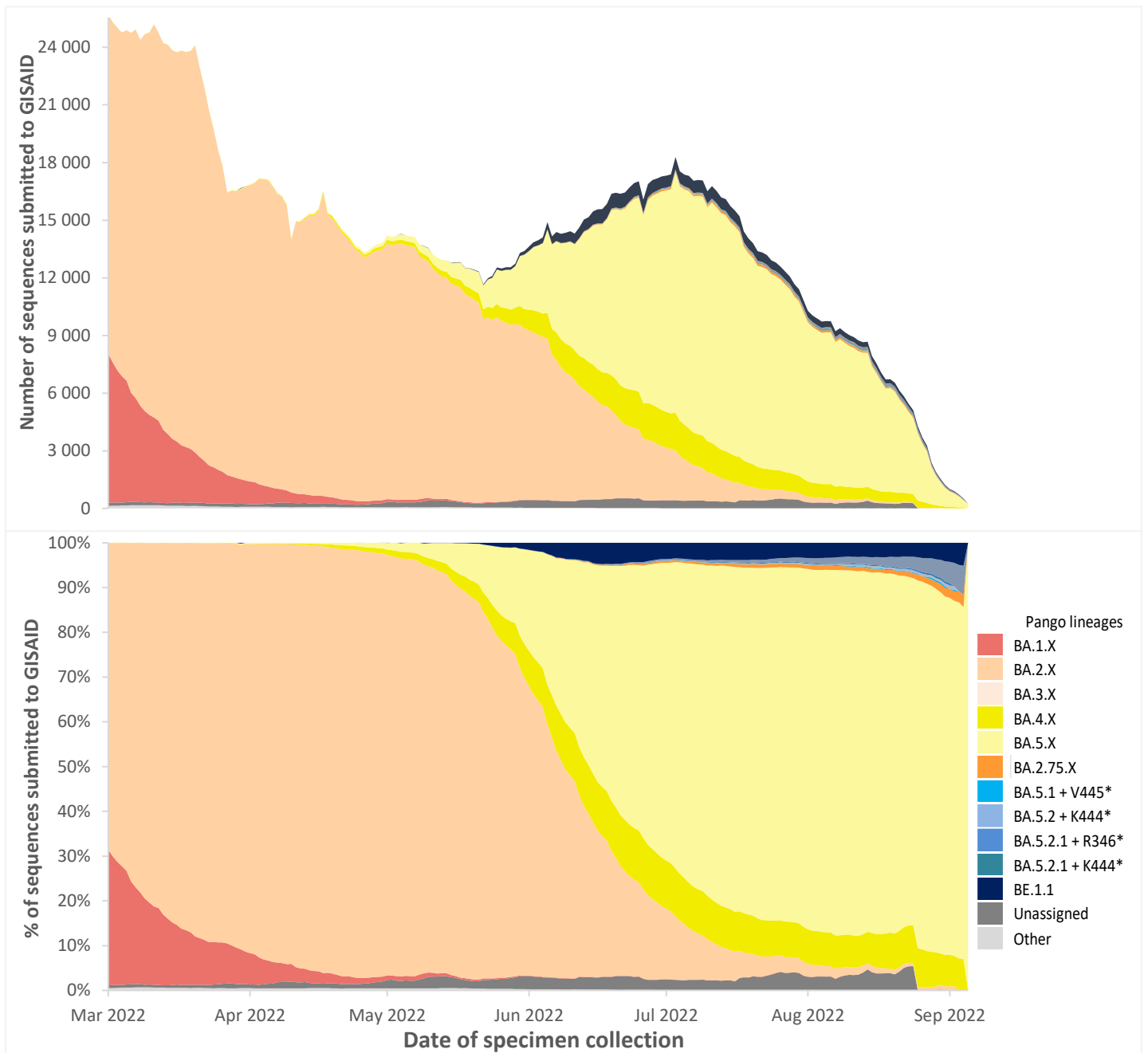


Figure 4 Panel A shows the number, and **Panel B** the percentage, of all circulating variants since March 2022. Omicron sister-lineages and additional Omicron VOC descendent lineages under further monitoring are shown. *BA.1.X*, *BA.2.X*, *BA.3.X*, *BA.4.X* and *BA.5.X* include all BA.1, BA.2, BA.3, 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 other than those listed in the legend. -Source: SARS-CoV-2 sequence data and metadata from GISAID, as of 19 September 2022.

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

| Lineage, (n) ^a | Countries | Sequences ^b | Last 4 weeks by collection date (%) ^c | | | |
|----------------------------|-----------|------------------------|--|----------------------|----------------------|----------------------|
| | | | 2022-32 ^c | 2022-33 ^c | 2022-34 ^c | 2022-35 ^c |
| BA.1.X, (58) | 183 | 2 182 417 | 53 (0.08%) | 17 (0.03%) | 17 (0.04%) | 8 (0.03%) |
| BA.2.X, (123) | 160 | 1 990 074 | 1 555 (2.28%) | 932 (1.54%) | 462 (1.01%) | 158 (0.65%) |
| BA.3.X, (2) | 28 | 764 | 0 | 0 | 0 | 0 |
| BA.4.X, (13) | 116 | 124 630 | 5 131 (7.53%) | 4 259 (7.03%) | 3 726 (8.14%) | 1 841 (7.53%) |
| BA.5.X, (41) | 135 | 774 808 | 55 207 (80.97%) | 49 156 (81.16%) | 36 687 (80.18%) | 18 719 (76.55%) |
| BA.2.75.X | 48 | 5 895 | 622 (0.91%) | 518 (0.86%) | 397 (0.87%) | 308 (1.26%) |
| BA.5.1 + V445* | 36 | 577 | 77 (0.11%) | 102 (0.17%) | 65 (0.14%) | 38 (0.16%) |
| BA.5.2 + K444* | 53 | 1 398 | 176 (0.26%) | 236 (0.39%) | 182 (0.4%) | 125 (0.51%) |
| BA.5.2.1 + R346* | 56 | 7 173 | 851 (1.25%) | 952 (1.57%) | 1 002 (2.19%) | 754 (3.08%) |
| BA.5.2.1 + K444* | 51 | 1 303 | 132 (0.19%) | 98 (0.16%) | 108 (0.24%) | 73 (0.3%) |
| BE.1.1.X (BA.5.3.1.1.1) | 78 | 43 147 | 2 285 (3.35%) | 1 891 (3.12%) | 1 464 (3.2%) | 789 (3.23%) |
| Unassigned | 204 | 6 589 983 | 16 (0.02%) | 6 (0.01%) | 9 (0.02%) | 5 (0.02%) |
| Other ^d | 88 | 87 945 | 2 077 (3.05%) | 2 399 (3.96%) | 1 637 (3.58%) | 1 636 (6.69%) |

^a Lineage, X means descendent lineages are pooled together, n indicates the number of currently designated additional descendent lineages

* Indicating pooled amino acid (AA) substitutions

^b Data source: sequences and metadata from GISAID, retrieved on 19 September 2022

^c Number of sequences and relative proportions in %

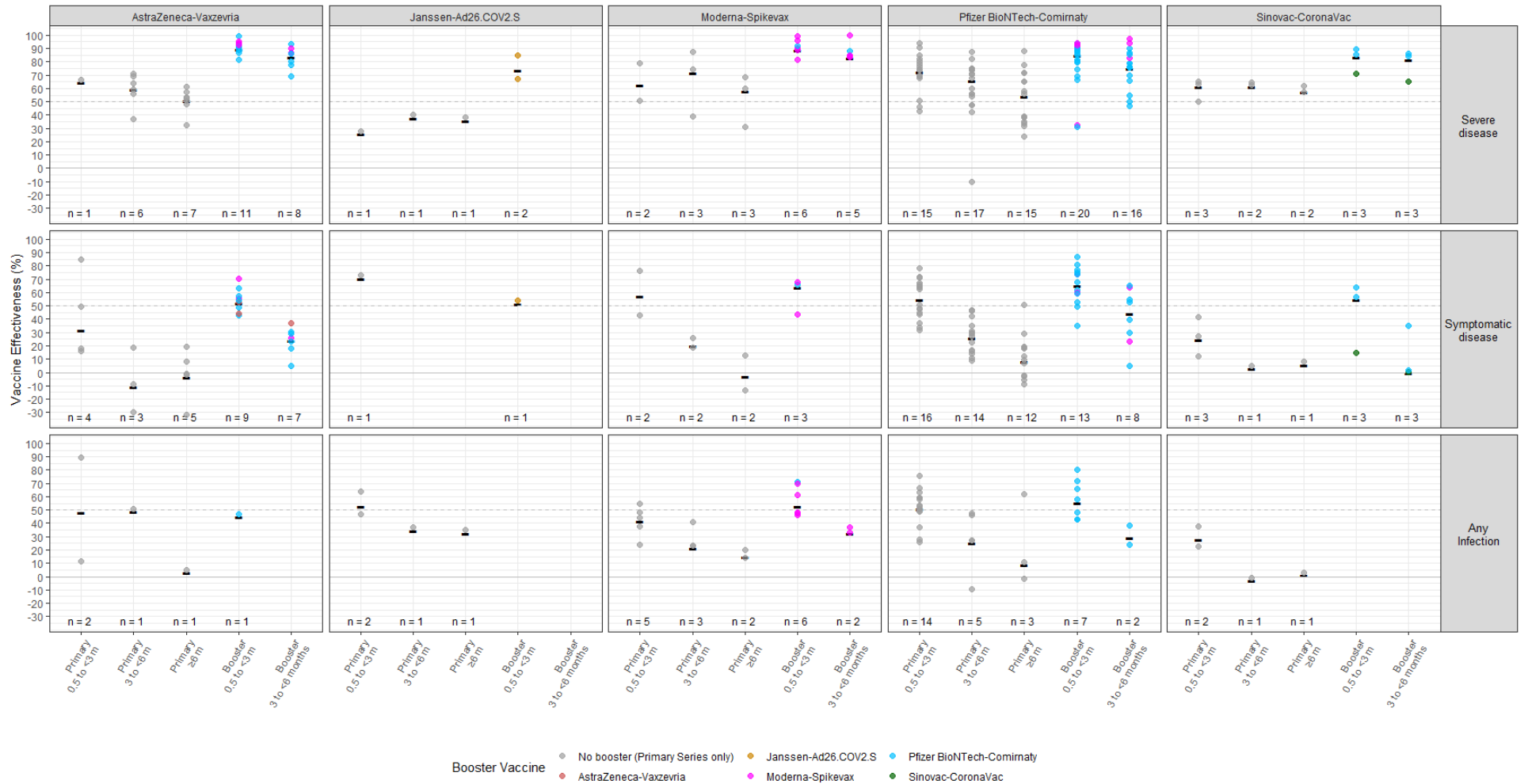
^d indicating *Omicron* lineages other than those of BA.X lineages and those of recombinants

Table 3. Summary of phenotypic characteristics of the Omicron VOCⁱⁱⁱ

| Public health domain of impact | Omicron (B.1.1.529) | Omicron sub lineages | | | |
|-------------------------------------|--|---|--|---|---|
| | Omicron (B.1.1.529) | BA.1 | BA.2 | BA.4 | BA.5 |
| Transmissibility | Growth advantage and increased transmissibility compared to Delta ² | 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 ³⁻⁸ . However, more recent studies report lower ⁹ or similar severity ¹⁰ . | There is evidence of higher disease severity compared to BA.4 and BA.5 ¹¹ | There is evidence, both in favor of higher severity ¹¹ compared to BA.4 and BA.5 , as well as in support of similar disease severity compared to BA.4 and BA.5 ¹² | One preliminary study suggests lower severity compared to BA.1 and BA.2 ¹¹ | There is one preliminary study suggesting increased severity compared to BA.1 and BA.2 ¹³ , while another study found lower disease severity compared to BA.1 and BA.2 ¹¹ . More evidence is needed. |
| Risk of reinfection | Reduced risk of Omicron reinfection among individuals previously infected with a different SARS-CoV-2 variant compared to naive individuals ^{14,15} | Earlier studies reported reduced risk of reinfection with BA.1 after infection with BA.2 ¹⁴ . However, a recent study reported increased risk of reinfection following prior infection with any Omicron sub-lineage, as compared to non-Omicron VOCs ¹⁶ . | Reduced risk of reinfection following infection with BA.1 ¹⁴ However, a recent study reported increased risk of reinfection following prior infection with any Omicron sub-lineage, as compared to non-Omicron VOCs ¹⁶ . | Varying evidence regarding risk of reinfection. One study reported protection against infection following previous BA.2 infection ¹⁷ while a recent study reported increased risk of reinfection following prior infection with any Omicron sub-lineage, as compared to non-Omicron VOCs ¹⁶ . | Varying evidence regarding risk of reinfection. One study reported protection against infection following previous BA.2 infection ¹⁷ while a recent study reported increased risk of reinfection following prior infection with any Omicron sub-lineage, as compared to non-Omicron VOCs ¹⁶ . |
| Impact on antibody responses | Reduction in neutralizing activity reported as compared to other VOCs ¹⁸⁻²⁰ | Lower neutralizing antibody titers compared to the index virus ²⁰ | Lower neutralizing antibody titers compared to the index virus ²⁰ | Lower neutralizing antibody titers compared to BA.1 ^{21,22} | Lower neutralizing antibody titres compared to BA.1 ²¹⁻²³ |
| Impacts on diagnostics | PCR assays that include multiple gene targets maintain their accuracy to detect Omicron ²⁴ ; S gene target failure/positivity (SGTF) may be a proxy for screening. Limited to no impact on sensitivity of Ag-RDTs observed ²⁵⁻²⁸ | 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 ²⁹ . Conserved neutralizing activity for three broadly neutralizing monoclonal antibodies (sotrovimab, S2X259 and S2H97) and reduced effectiveness of other monoclonal antibodies ³⁰⁻³² | Reduced neutralization activity of sotrovimab and casirivimab-imdevimab ³³ | Reduced neutralization activity of sotrovimab and casirivimab-imdevimab ³³ | Reduced neutralization activity of sotrovimab and casirivimab-imdevimab ³³ | Reduced neutralization activity of sotrovimab and casirivimab-imdevimab ³³ |
| Impact on vaccination | Results of vaccine effectiveness (VE) studies should be interpreted with caution because estimates vary with the type of vaccine administered and the number of doses and scheduling (sequential administration of different vaccines). For further information, see the section Interpretation of the results of the VE for the Omicron variant | | | | |

ⁱⁱⁱ 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 is 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%) and Gamaleya-Gam-Covid Vac (64%, 95% CI: -45 to 92.2%). 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). Additional information on vaccine performance against VOCs can also be found in Annex 2.

Since the last [update on 17 August 2022](#), six new studies have been added to the figure. Two studies (not yet peer-reviewed) assessed the VE of mRNA vaccines (Pfizer BioNTech-Comirnaty and Moderna-mRNA-1273) against infection or symptomatic disease due to Omicron over time among children in the United Kingdom and Italy respectively.^{34,35} A third study assessed VE of two and three doses of Pfizer BioNTech-Comirnaty against hospitalization due to Omicron BA.1/BA.2 and due to Omicron BA.4./BA.5 among adults in South Africa.³⁶ A fourth study (not yet peer reviewed) assessed VE of three doses Pfizer BioNTech-Comirnaty against hospitalization due to Omicron among adults in the United Kingdom.³⁷ A fifth study (not yet peer reviewed) evaluated VE of primary series vaccination with Pfizer BioNTech-Comirnaty and Sinovac-CoronaVac against Omicron infection and symptomatic disease among persons five years and older in China (Hong Kong SAR).³⁸ A sixth study (not peer reviewed) provided new evidence on the VE of two doses of Pfizer BioNTech-Comirnaty and the VE of two doses of Gamaleya-Gam-Covid-Vac against hospitalization with severe acute respiratory infection with Omicron in patients 18 years and older in Paraguay.³⁹

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

To date, 43 studies from 18 countries (Argentina, Brazil, Canada, Chile, Czech Republic, Denmark, Finland, China (Hong Kong SAR, Norway, Israel, Italy, 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 (16 studies contributed VE estimates of primary series vaccination only to the plot, five contributed estimates of the first booster vaccination only, and 22 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 index 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, in the majority of studies. 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;⁴⁰ however, studies that assess VE of booster vaccination beyond six months are not yet available.

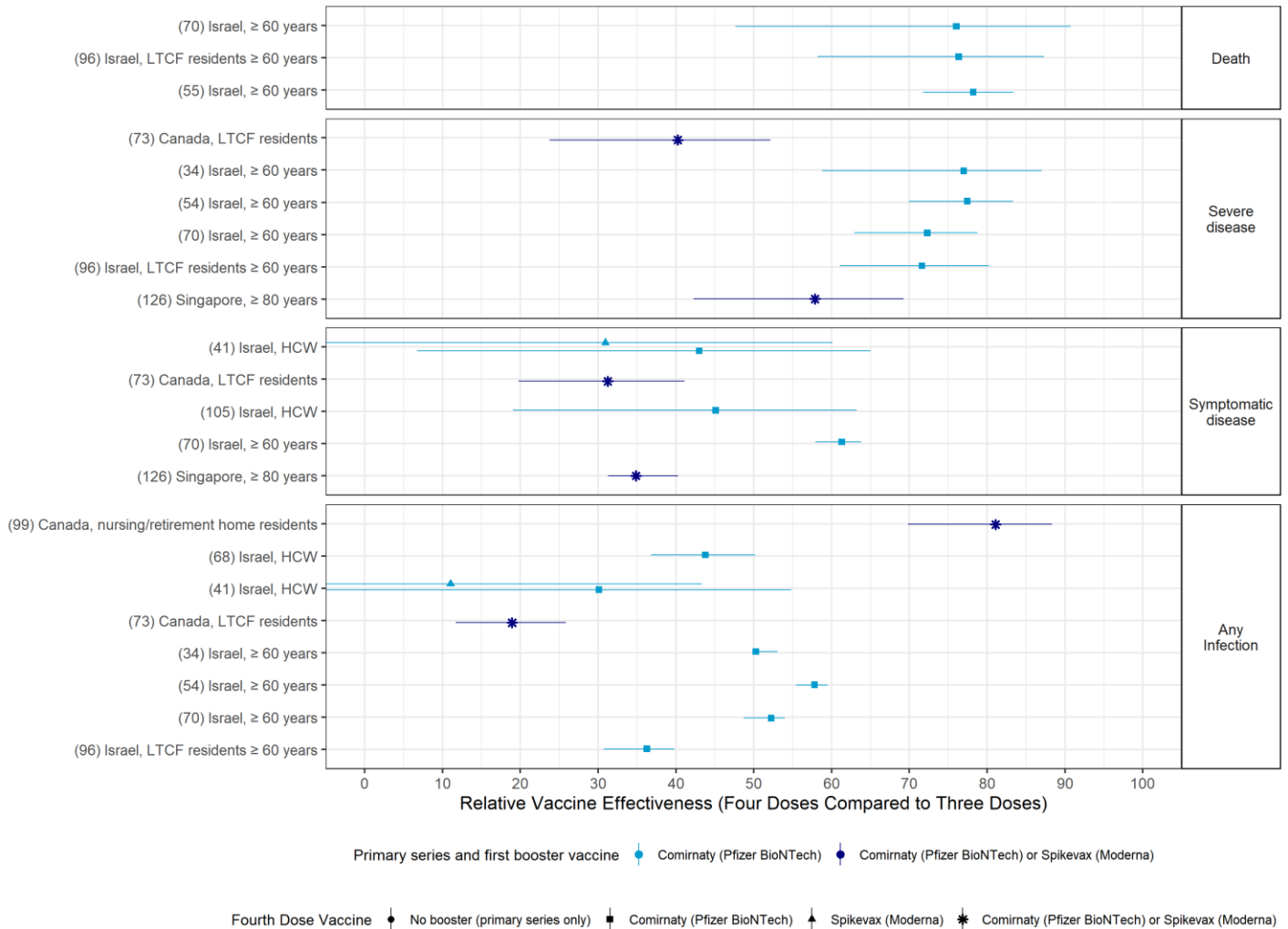
For *severe disease*, VE of the primary series showed little decline over six months. VE was $\geq 70\%$ during the first three months after primary series vaccination for 11 of 17 (65%) VE estimates for the mRNA vaccines (Moderna-Spikevax and Pfizer BioNTech-Comirnaty). Of the three vector vaccines 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.COVID.S. Four estimates were available for inactivated vaccines; none of the three estimates for Sinovac-CoronaVac were $\geq 70\%$ (2 [67%] were $\geq 50\%$). The single estimates for Beijing CNBG-BBIBP-CorV (Sinopharm) and for Gamaleya-Gam-Covid-Vac was $< 70\%$ but $\geq 50\%$ (data not shown in figure). Beyond three months after vaccination with the primary series, VE was $\geq 70\%$ for 14 of 38 (37%) VE estimates for the mRNA vaccines (25 [66%] had VE $\geq 50\%$); one of 13 (8%) AstraZeneca-Vaxzevria VE estimates was $\geq 70\%$ (10 [77%] were $\geq 50\%$); neither of the two estimates for a single dose of the other vector-based vaccine, Janssen-Ad26.COVID.S, was $\geq 50\%$; the four VE estimates for Sinovac-CoronaVac were $\geq 50\%$ but $< 70\%$.

The first booster dose vaccination improved VE against *severe disease* in all studies, and VE was $\geq 70\%$ in 37 (88%) of 42 estimates evaluating VE between 14 days and three months of receipt of a booster dose (39 estimates evaluated an mRNA booster, two evaluated a Janssen-Ad26.COVID.2.S booster, and one evaluated a Sinovac-CoronaVac booster); one Moderna-Spikevax booster dose had VE $< 50\%$ (though confidence intervals were very wide), and one Janssen-Ad26.COVID.2.S booster dose had VE $< 70\%$. At three to six months post mRNA booster, VE was $\geq 70\%$ for 26 of 31 (84%) estimates (the primary series was an mRNA vaccine in 21 of the 29 estimates, AstraZeneca-Vaxzevria in eight and Sinovac-CoronaVac in two). One study found the VE to be $< 70\%$ but $\geq 50\%$ following three to six months from the third dose of Sinovac-CoronaVac.

Of note, a study from South Africa provided the first published evidence of vaccine effectiveness against hospitalization with Omicron BA.4/BA.5 sub-lineages.³⁶ The authors assessed VE Pfizer BioNTech-Comirnaty against hospitalization due to Omicron among adults and found similar magnitude of VE, as well as patterns of decreasing effectiveness over time for Omicron BA.4/BA.5 and Omicron BA.1/BA.2 for both the primary series and first booster dose of Pfizer BioNTech-Comirnaty.

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 four of 18 (22%) VE estimates for the mRNA vaccines were $\geq 70\%$ and only 10 (56%) were $\geq 50\%$; one (25%) of the four VE estimates for AstraZeneca-Vaxzevria was $\geq 70\%$ while the remaining three estimates were $< 50\%$; the single estimate for Janssen-Ad26.COVID.2.S was $\geq 70\%$, and all three estimates for Sinovac (CoronaVac) were $< 50\%$. Beyond three months after vaccination, only one of 40 (3%) VE estimates was $\geq 50\%$ (30 estimates evaluated mRNA vaccines, eight evaluated AstraZeneca-Vaxzevria, and two evaluated Sinovac-CoronaVac). An mRNA booster vaccination after completion of a primary series of an mRNA vaccine, AstraZeneca-Vaxzevria, or Sinovac-CoronaVac improved VE against *symptomatic disease*: seven of 25 (28%) VE estimates between 14 days and three months post booster were $\geq 70\%$, although 20 (80%) were $\geq 50\%$; one (50%) of two VE estimates evaluating three doses of AstraZeneca-Vaxzevria was $\geq 50\%$ but $< 70\%$. First booster dose protection declined rapidly over time: only four of 16 (25%) estimates available at three to six months following receipt of an mRNA booster dose had VE $\geq 50\%$ and none were $\geq 70\%$. Neither the single VE estimate for three doses of AstraZeneca-Vaxzevria nor the single estimate for three doses of Sinovac-CoronaVac that were 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*.

Figure 6. 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, and study population. Reference numbers identify the study and link to the [summary table](#) of VE effectiveness studies on [view-hub.org](#) (Table 2 in summary table). 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.

Interpretation of the results of absolute VE and relative VE for the Omicron variant for second booster dose vaccination

Two studies have evaluated *absolute VE* of two booster doses (i.e. four total doses) of mRNA vaccines, comparing infection and disease events among persons receiving four doses to an unvaccinated comparison group. One second booster dose study among a high-risk population of long-term care facility residents in Canada reported VE for various combinations of mRNA vaccines of 49-52%, 59-73%, and 83-88% against Omicron infection, symptomatic disease, and hospitalization, respectively, with a maximum potential follow-up time post second booster dose of four months.⁴¹ The second study assessed VE of four doses of any combination of Pfizer BioNTech-Comirnaty and

Moderna-mRNA-1273 in persons 50 years and older in the United States, reporting VE estimates of 66% (95% CI: 60-71%) and 80% (95% CI-71-85%) against emergency department/urgent care visits and hospitalization due to Omicron, respectively, within the first two months of receipt of the second booster dose.⁴²

To date, 11 studies (see Figure 6), conducted among long-term care facility residents, older adults, and healthcare workers, have assessed *relative VE* of four doses of mRNA vaccines, by comparing the risk of Omicron infection, disease, and death among persons receiving four doses to persons having received three doses (i.e., first booster) of mRNA vaccines at least three to four months prior. For all outcomes, a fourth dose achieved marginal gains in VE compared to three doses (Figure 6). Relative VE of four doses of mRNA vaccine was 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. Moreover, relative VE cannot be compared across studies due to differences in the absolute VE (which is often not reported) and epidemiological context of the setting of each study. In addition, the follow-up time after the fourth dose in most studies was short (ranging from one to four months) so that waning of the fourth dose is not evaluable. For more information on interpreting relative VE, see the special focus on relative vaccine effectiveness from the [June 29th Weekly Epidemiological Update](#).

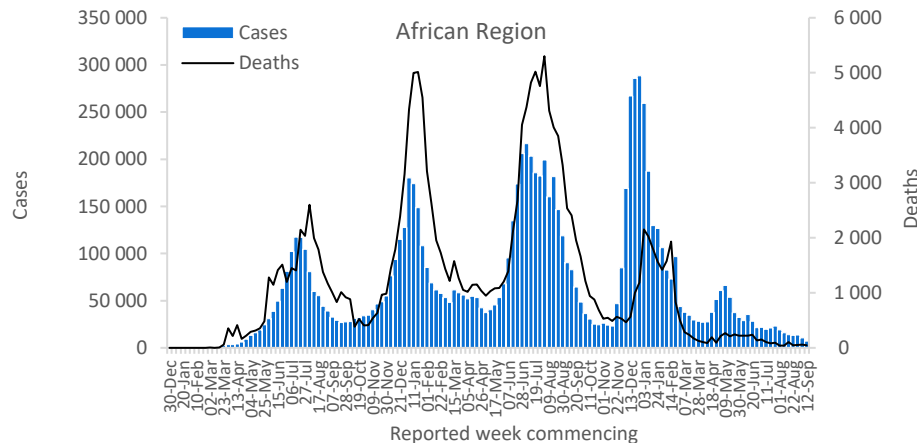
WHO regional overviews:

Epidemiological week 12 - 18 September 2022**

African Region

The African Region reported over 6800 new weekly cases, a 35% decrease as compared to the previous week. Four (8%) countries reported increases in the number of new cases of 20% or greater, with some of the greatest proportional increases seen in the Seychelles (183 vs 94 new cases; +95%), Burundi (358 vs 229 new cases; +56%) and Togo (128 vs 100 new cases; +28%). The highest numbers of new cases were reported from Réunion (2572 new cases; 287.3 new cases per 100 000 population; -45%), South Africa (1603 new cases; 2.7 new cases per 100 000; -11%) and Nigeria (483 new cases; <1 new case per 100 000; -17%).

The number of new weekly deaths in the Region increased by 27% as compared to the previous week, with 44 deaths reported. The highest numbers of new deaths were reported from the Democratic Republic of the Congo (18 new deaths; <1 new death per 100 000 population; similar to the previous week), South Africa (17 new deaths; <1 new death per 100 000; -19%) and Réunion (five new deaths; <1 new death per 100 000; similar to the previous week).

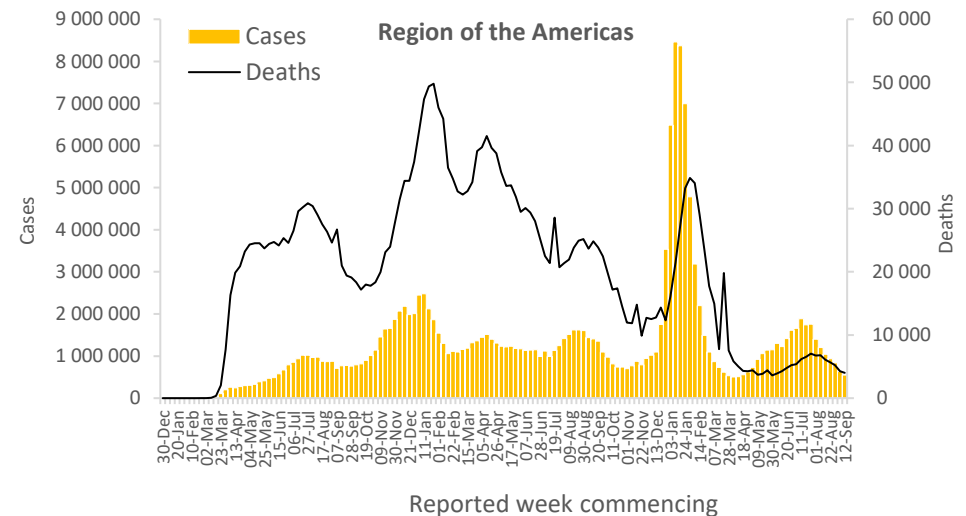


Updates from the [African Region](#)

Region of the Americas

The Region of the Americas reported over 552 000 new cases, a 12% decrease as compared to the previous week. Eight of 56 (14%) countries for which data are available reported increases in the number of new cases of 20% or greater, with some of the greatest proportional increases observed in Honduras (825 vs 232 new cases; +256%), Belize (252 vs 102 new cases; +147%) and Ecuador (2012 vs 1417 new cases; +42%). The highest numbers of new cases were reported from the United States of America (395 117 new cases; 119.4 new cases per 100 000; -11%), Brazil (62 346 new cases; 29.3 new cases per 100 000; similar to the previous week) and Chile (23 853 new cases; 124.8 new cases per 100 000; -26%).

The number of new weekly deaths reported in the Region decreased by 5% as compared to the previous week, with over 4000 new deaths reported. The highest numbers of new deaths were reported from the United States of America (2601 new deaths; <1 new death per 100 000; +5%), Brazil (487 new deaths; <1 new death per 100 000; -12%) and Canada (245 new deaths; <1 new death per 100 000; similar to the previous week).

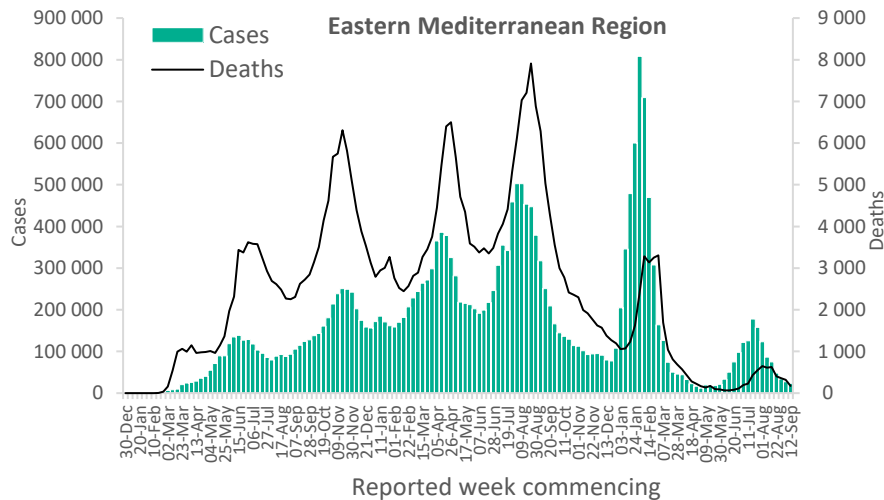


Updates from the [Region of the Americas](#)

Eastern Mediterranean Region

The Eastern Mediterranean Region reported over 23 000 new cases, a 14% decrease as compared to the previous week. Two (9%) countries reported increases in new cases of 20% or greater, with the highest proportional increase observed in Bahrain (2048 vs 1448 new cases; +41%). The highest numbers of new cases were reported from Qatar (5388 new cases; 187.0 new cases per 100 000; +27%), the Islamic Republic of Iran (4105 new cases; 4.9 new cases per 100 000; -47%) and Jordan (3389 new cases; 33.2 new cases per 100 000; similar to the previous week).

The number of new weekly deaths decreased in the Region by 46% as compared to the previous week, with over 100 new deaths reported. The highest numbers of new deaths were reported from the Islamic Republic of Iran (119 new deaths; <1 new death per 100 000; -54%), Saudi Arabia (15 new deaths; <1 new death per 100 000; +15%) and Lebanon (12 new deaths; <1 new death per 100 000; +33%).

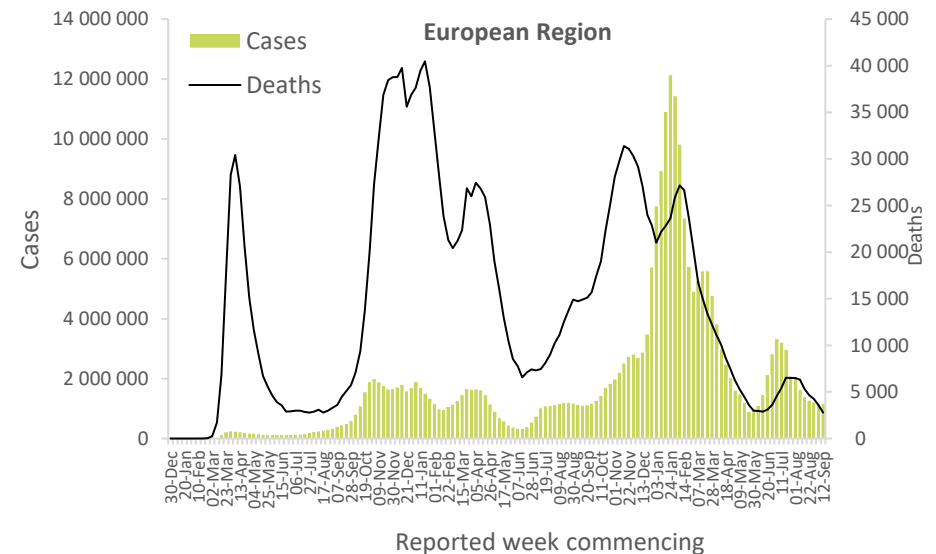


Updates from the [Eastern Mediterranean Region](#)

European Region

In the European Region, the number of new weekly cases remained stable this week as compared to the previous week, with over 1.1 million new cases reported. Nine (15%) countries reported increases in new cases of 20% or greater, with the highest proportional increases observed in Monaco (62 vs 33 new cases; +88%) and Lithuania (8809 vs 5754 new cases; +53%). The highest numbers of new cases were reported from the Russian Federation (372 485 new cases; 255.2 new cases per 100 000; +10%), Germany (206 617 new cases; 248.4 new cases per 100 000; similar to the previous week) and France (183 271 new cases; 281.8 new cases per 100 000; +62%).

Over 2700 new weekly deaths were reported in the Region, a 22% decrease as compared to the previous week. The highest numbers of new deaths were reported from the Russian Federation (697 new deaths; <1 new death per 100 000; +9%), Spain (595 new deaths; 1.3 new deaths per 100 000; +83%) and Italy (371 new deaths; <1 new death per 100 000; similar to the previous week).

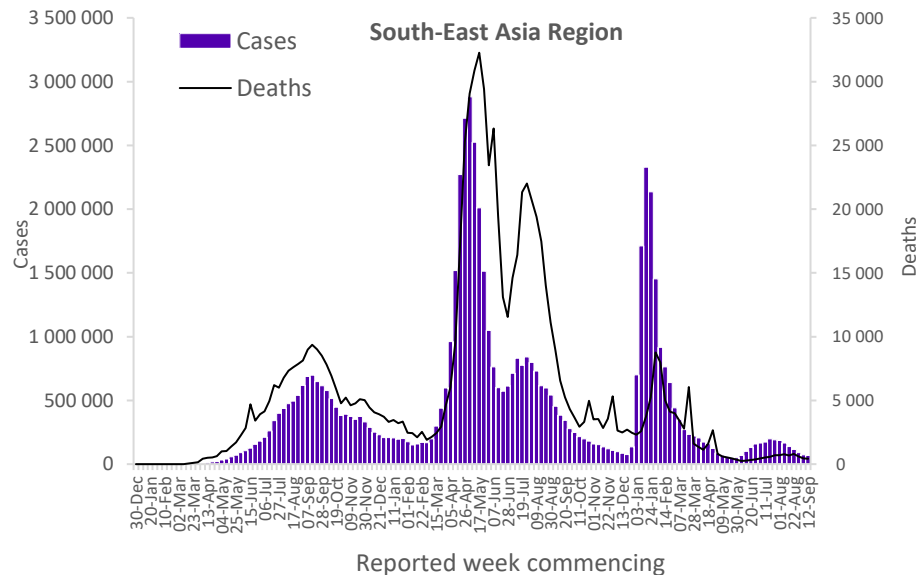


Updates from the [European Region](#)

South-East Asia Region

The South-East Asia Region reported over 66 000 new cases, an 8% decrease as compared to the previous week. Three of the 10 countries (30%) in the Region for which data are available showed an increase in the number of new cases of 20% or greater: Bhutan (311 vs 186 new cases; +67%), Myanmar (2046 vs 1293 new cases; +58%), and Bangladesh (2727 vs 2126; +28%). The highest numbers of new cases were reported from India (38 829 new cases; 2.8 new cases per 100 000; similar to the previous week), Indonesia (16 314 new cases; 6.0 new cases per 100 000; -18%) and Thailand (5841 new cases; 8.4 new cases per 100 000; -35%).

The Region reported over 400 deaths, a 6% decrease as compared to the previous week. The highest numbers of new deaths were reported from India (187 new deaths; <1 new death per 100 000; +18%), Indonesia (122 new deaths; <1 new death per 100 000; similar to the previous week) and Thailand (90 new deaths; <1 new death per 100 000; -35%).

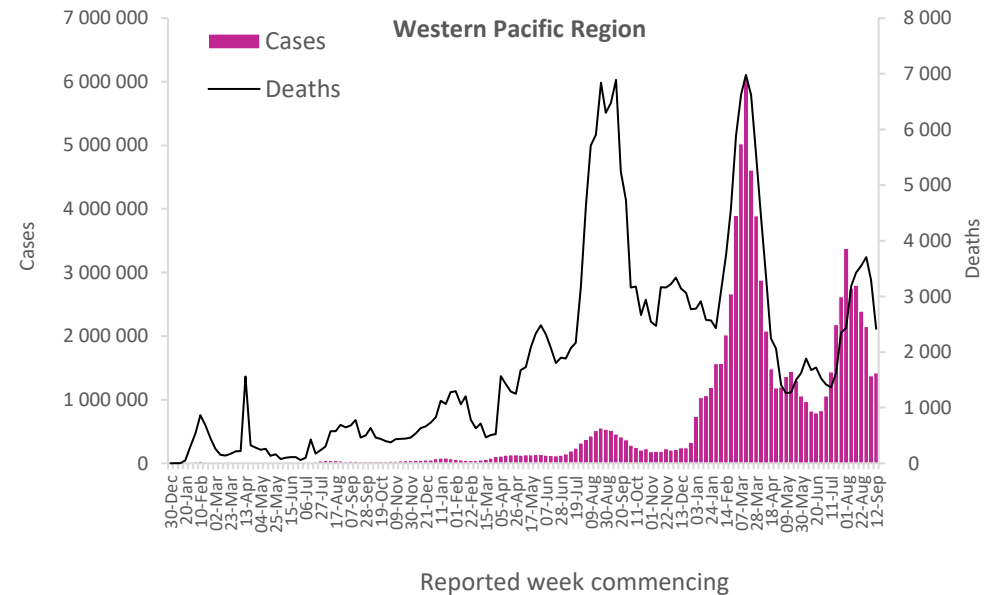


Updates from the [South-East Asia Region](#)

Western Pacific Region

The Western Pacific Region reported a similar case count as the previous week, with over 1.4 million new cases. Four (12%) countries reported increases in new cases of 20% or greater, with the largest proportional increases observed in Marshall Islands (141 vs nine new cases; +1467%), New Caledonia (97 vs 23 new cases; +322%) and Vanuatu (51 vs 36 new cases; +42%). The highest numbers of new cases were reported from Japan (605 919 new cases; 479.1 new cases per 100 000; +13%), the Republic of Korea (389 579 new cases; 759.9 new cases per 100 000; -11%) and China (297 693 new cases; 20.2 new cases per 100 000; +13%).

The Region reported a 27% decrease in new weekly deaths as compared to the previous week, with over 2400 deaths reported. The highest numbers of new deaths were reported from Japan (1162 new deaths; 1 new death per 100 000; -31%), the Republic of Korea (377 new deaths; 1 new death per 100 000; +5%) and China (360 new deaths; <1 new death per 100 000; +20%).



Updates from the [Western Pacific Region](#)

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 is 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.

Annex 3. Summary of results of neutralization studies assessing primary series and booster vaccine performance against Omicron variant of concern (data updated 19 September 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 ₁₃ | HNR ₂ | HNR ₁ | ---- | ---- | HNR ₁ |
| | Beijing CNBG-BBIBP-CorV | HNR ₉ | HNR ₃ | HNR ₂ | ---- | HNR ₁ | HNR ₂ |
| | Bharat-Covaxin | ↓↓ ₁ | ---- | ---- | ---- | ---- | ---- |
| | Cansino-Convidecia | ---- | ---- | ---- | ---- | ---- | ---- |
| | Janssen-Ad26-COV2.S | HNR ₉ | HNR ₁ | HNR ₁ | ---- | ---- | HNR ₁ |
| | Moderna-Spikevax | ↓↓↓ ₁₁ | ↓↓↓to↓↓↓ ₂ | HNR ₁ | ---- | ---- | HNR ₁ |
| | Novavax-Nuvaxovid/SII - Covavax | HNR ₂ | HNR ₁ | HNR ₁ | ---- | ---- | HNR ₁ |
| | Pfizer BioNTech-Comirnaty | HNR ₅₃ | HNR ₈ | HNR ₁ | HNR ₁ | HNR ₁ | HNR ₃ |
| Sinovac-CoronaVac | HNR ₉ | ↓↓↓ ₁ | ---- | ---- | ---- | ↓↓↓ ₁ | |
| 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 | ---- | ---- | ↓↓↓ ₁ | ↓↓↓ ₁ |
| | AstraZeneca-Vaxzevria/SII-Covishield + Moderna-Spikevax | ↓ ₁ | ---- | ---- | ---- | ---- | ---- |
| | AstraZeneca-Vaxzevria/SII-Covishield + Pfizer BioNTech-Comirnaty | ↓↓↓to↓↓↓ ₂ | ↓↓↓ ₁ | ---- | ---- | ↓↓↓ ₁ | ---- |
| | Beijing CNBG-BBIBP-CorV + Beijing CNBG-BBIBP-CorV | ↓↓↓to↓↓↓ ₄ | HNR ₂ | HNR ₁ | ---- | ↓↓↓ ₁ | HNR ₁ |
| | Janssen-Ad26-COV2.S + Janssen-Ad26-COV2.S | HNR ₂ | ---- | ---- | ---- | ---- | ---- |
| | Janssen-Ad26-COV2.S + Moderna-Spikevax | ↓↓↓ ₁ | ---- | ---- | ---- | ---- | ---- |
| | Janssen-Ad26-COV2.S + Pfizer BioNTech-Comirnaty | ↓ ₁ to ↓↓ ₂ | ---- | ---- | ---- | ---- | ---- |
| | Moderna-Spikevax + Moderna-Spikevax | ↓to↓↓ ₉ | ↓↓↓ ₁ | ↓↓↓ ₁ | ---- | ↓↓↓ ₁ | ↓↓↓ ₂ |
| | Moderna-Spikevax + Pfizer BioNTech-Comirnaty | ↓↓↓ ₁ | ---- | ---- | ---- | ---- | ---- |
| | Novavax-Nuvaxovid/SII – Covavax + Novavax-Nuvaxovid/SII - Covavax | ↓↓↓ ₁ | ---- | ---- | ---- | ---- | ---- |
| | Pfizer BioNTech-Comirnaty + Pfizer BioNTech-Comirnaty | ↓to↓↓ ₄₄ | ↓to↓↓ ₁₅ | ↓to↓↓ ₃ | ↓↓ ₁ | ↓to↓↓ ₄ | ↓to↓↓ ₇ |
| | Pfizer BioNTech-Comirnaty + Janssen-Ad26-COV2.S | ↓ ₂ | ---- | ---- | ---- | ---- | ---- |
| | Pfizer BioNTech-Comirnaty + Moderna-Spikevax | ↓to↓ ₂ | ---- | ---- | ↓↓↓ ₁ | ---- | ↓↓↓ ₁ |
| | Sinovac-CoronaVac + Cansino-Convidecia | ↓↓↓ ₁ | ---- | ---- | ---- | ---- | ---- |
| Sinovac-CoronaVac + Sinovac-CoronaVac | ↓to↓↓ ₇ | ↓↓↓ to ↓↓ ₃ | ↓↓ ₁ | ---- | ↓↓↓ ₁ | ↓↓ to ↓↓ ₃ | |
| Sinovac-CoronaVac + Pfizer BioNTech-Comirnaty | ↓↓ ₂ | ↓↓↓ ₁ | ---- | ---- | ---- | ---- | |
| Booster Vaccines without WHO EUL | Anhui ZL-Recombinant + Anhui ZL-Recombinant | ↓to↓ ₂ | ↓↓↓ ₁ | ↓↓↓ ₁ | ---- | ↓↓↓ ₁ | ↓↓↓ ₁ |
| | Beijing CNBG-BBIBP-CorV + Anhui ZL - Recombinant | ↓↓to↓↓ ₄ | HNR ₂ | HNR ₁ | ---- | ↓↓↓ ₁ | HNR ₁ |
| | Gamaleya-Sputnik V + Gamaleya Sputnik Light | ↓↓ ₁ | ---- | ---- | ---- | ---- | ---- |
| | Sinovac-CoronaVac + Anhui ZL - Recombinant | ↓to↓ ₂ | ↓to↓ ₂ | ↓to↓↓ ₂ | ---- | ↓to↓↓ ₂ | ↓to↓ ₁ |
| | Sinovac-CoronaVac + Cansino-Ad5-nCoV-IH | ↓↓↓ 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 | ↓ ₁ | ---- | ---- | ---- | ---- | ---- |
| | Moderna-Spikevax + Moderna-Spikevax + Moderna-Spikevax Bivalent Original/Omicron BA.1 | ↓ ₁ | ---- | ---- | ---- | ---- | ↓↓↓ ₁ |
| | Pfizer BioNTech-Comirnaty + Pfizer BioNTech-Comirnaty + Pfizer BioNTech-Comirnaty | ↓↓↓ ₁ | ---- | ---- | ---- | ---- | ---- |
| | Pfizer BioNTech-Comirnaty + Pfizer BioNTech-Comirnaty + Moderna-Spikevax | ↓↓↓ 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 Table 3

- 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 is persons having completed the primary series) are excluded as the interpretation of relative vaccine effectiveness is not comparable with absolute vaccine effectiveness.

References

1. Greaney AJ, Starr TN, Bloom JD. An antibody-escape estimator for mutations to the SARS-CoV-2 receptor-binding domain. *Virus Evolution*. 2022;8(1):veac021. doi:10.1093/ve/veac021
2. 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.
3. Ulloa AC, Buchan SA, Daneman N, Brown KA. Estimates of SARS-CoV-2 Omicron Variant Severity in Ontario, Canada. *JAMA*. 2022;327(13):1286. doi:10.1001/jama.2022.2274
4. Ferguson N, Ghani AC, Hinsley W, Volz E. Report 50: Hospitalisation risk for Omicron cases in England. WHO Collaborating Centre for Infectious Disease Modelling. <https://www.imperial.ac.uk/media/imperial-college/medicine/mrc-gida/2021-12-22-COVID19-Report-50.pdf>
5. Lewnard JA, Hong VX, Patel MM, Kahn R, Lipsitch M, Tartof SY. *Clinical Outcomes Associated with Omicron (B.1.1.529) Variant and BA.1/BA.1.1 or BA.2 Subvariant Infection in Southern California*. *Epidemiology*; 2022. doi:10.1101/2022.01.11.22269045
6. Nyberg T, Twohig 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
7. Wolter N, Jassat W, Walaza S, et al. *Early Assessment of the Clinical Severity of the SARS-CoV-2 Omicron Variant in South Africa*. *Infectious Diseases (except HIV/AIDS)*; 2021. doi:10.1101/2021.12.21.21268116
8. Grint DJ, Wing K, Gibbs HP, et al. *Accident and Emergency (AE) Attendance in England Following Infection with SARS-CoV-2 Omicron or Delta*. *Infectious Diseases (except HIV/AIDS)*; 2022. doi:10.1101/2022.05.03.22274602
9. Nyberg T, Ferguson NM, Nash SG, et al. Comparative analysis of the risks of hospitalisation and death associated with SARS-CoV-2 omicron (B.1.1.529) and delta (B.1.617.2) variants in England: a cohort study. *The Lancet*. 2022;399(10332):1303-1312. doi:10.1016/S0140-6736(22)00462-7
10. Ward IL, Bermingham C, Ayoubkhani D, et al. Risk of covid-19 related deaths for SARS-CoV-2 omicron (B.1.1.529) compared with delta (B.1.617.2): retrospective cohort study. *BMJ*. 2022;378:e070695. doi:10.1136/bmj-2022-070695
11. Jassat W, Abdool Karim SS, Ozougwu L, et al. *TRENDS IN CASES, HOSPITALISATION AND MORTALITY RELATED TO THE OMICRON BA.4/BA.5 SUB-VARIANTS IN SOUTH AFRICA*. *Epidemiology*; 2022. doi:10.1101/2022.08.24.22279197
12. Lewnard JA, Hong V, Tartof SY. *Association of SARS-CoV-2 BA.4/BA.5 Omicron Lineages with Immune Escape and Clinical Outcome*. *Epidemiology*; 2022. doi:10.1101/2022.07.31.22278258
13. Tamura T, Yamasoba D, Oda Y, et al. *Comparative Pathogenicity of SARS-CoV-2 Omicron Subvariants Including BA.1, BA.2, and BA.5*. *Microbiology*; 2022. doi:10.1101/2022.08.05.502758
14. Chang CC, Vlad G, Vasilescu ER, et al. *Previous SARS-CoV-2 Infection or a Third Dose of Vaccine Elicited Cross-Variant Neutralizing Antibodies in Vaccinated Solid Organ Transplant Recipients*. *Infectious Diseases (except HIV/AIDS)*; 2022. doi:10.1101/2022.04.13.22273829

15. Hansen CH, Friis NU, Bager P, et al. Risk of Reinfection, Vaccine Protection, and Severity of Infection with the BA.5 Omicron Subvariant: A Danish Nation-Wide Population-Based Study. *SSRN Journal*. Published online 2022. doi:10.2139/ssrn.4165630
16. Burkholz S, Rubsamen M, Blankenberg L, Carback RT, Mochly-Rosen D, Harris PE. *Increasing Cases of SARS-CoV-2 Omicron Reinfection Reveals Ineffective Post-COVID-19 Immunity in Denmark and Conveys the Need for Continued Next-Generation Sequencing*. *Public and Global Health*; 2022. doi:10.1101/2022.09.13.22279912
17. Carazo S, Skowronski DM, Brisson M, et al. *Protection against Omicron Re-Infection Conferred by Prior Heterologous SARS-CoV-2 Infection, with and without mRNA Vaccination*. *Infectious Diseases (except HIV/AIDS)*; 2022. doi:10.1101/2022.04.29.22274455
18. Altarawneh HN, Chemaitelly H, Ayoub HH, et al. *Protection of SARS-CoV-2 Natural Infection against Reinfection with the Omicron BA.4 or BA.5 Subvariants*. *Epidemiology*; 2022. doi:10.1101/2022.07.11.22277448
19. Bowen JE, Sprouse KR, Walls AC, et al. *Omicron BA.1 and BA.2 Neutralizing Activity Elicited by a Comprehensive Panel of Human Vaccines*. *Immunology*; 2022. doi:10.1101/2022.03.15.484542
20. Iketani S, Liu L, Guo Y, et al. Antibody evasion properties of SARS-CoV-2 Omicron sublineages. *Nature*. 2022;604(7906):553-556. doi:10.1038/s41586-022-04594-4
21. Yu J, Collier A ris Y, Rowe M, et al. *Comparable Neutralization of the SARS-CoV-2 Omicron BA.1 and BA.2 Variants*. *Infectious Diseases (except HIV/AIDS)*; 2022. doi:10.1101/2022.02.06.22270533
22. Hachmann NP, Miller J, Collier A ris Y, et al. *Neutralization Escape by the SARS-CoV-2 Omicron Variants BA.2.12.1 and BA.4/BA.5*. *Infectious Diseases (except HIV/AIDS)*; 2022. doi:10.1101/2022.05.16.22275151
23. Cao Y, Yisimayi A, Jian F, et al. *BA.2.12.1, BA.4 and BA.5 Escape Antibodies Elicited by Omicron Infection*. *Immunology*; 2022. doi:10.1101/2022.04.30.489997
24. Metzger CM, Lienhard R, Seth-Smith HM. PCR performance in the SARS-CoV-2 Omicron variant of concern? *Swiss Med Wkly*. 2021;151(49-50). doi:10.4414/smw.2021.w30120
25. Drain PK, Bemer M, Morton JF, et al. *Accuracy of Rapid Antigen Testing across SARS-CoV-2 Variants*. *Infectious Diseases (except HIV/AIDS)*; 2022. doi:10.1101/2022.03.21.22272279
26. Soni A, Herbert C, Filippaios A, et al. *Comparison of Rapid Antigen Tests' Performance between Delta (B.1.61.7; AY.X) and Omicron (B.1.1.529; BA1) Variants of SARS-CoV-2: Secondary Analysis from a Serial Home Self-Testing Study*. *Infectious Diseases (except HIV/AIDS)*; 2022. doi:10.1101/2022.02.27.22271090
27. Bayart JL, Degosserie J, Favresse J, et al. Analytical Sensitivity of Six SARS-CoV-2 Rapid Antigen Tests for Omicron versus Delta Variant. *Viruses*. 2022;14(4):654. doi:10.3390/v14040654
28. Bekliz M, Perez-Rodriguez F, Puhach O, et al. *Sensitivity of SARS-CoV-2 Antigen-Detecting Rapid Tests for Omicron Variant*. *Infectious Diseases (except HIV/AIDS)*; 2021. doi:10.1101/2021.12.18.21268018
29. Takashita E, Kinoshita N, Yamayoshi S, et al. Efficacy of Antiviral Agents against the SARS-CoV-2 Omicron Subvariant BA.2. *N Engl J Med*. Published online March 9, 2022;NEJMc2201933. doi:10.1056/NEJMc2201933
30. Planas D, Saunders N, Maes P, et al. *Considerable Escape of SARS-CoV-2 Variant Omicron to Antibody Neutralization*. *Immunology*; 2021. doi:10.1101/2021.12.14.472630

31. VanBlargan LA, Errico JM, Halfmann PJ, et al. *An Infectious SARS-CoV-2 B.1.1.529 Omicron Virus Escapes Neutralization by Several Therapeutic Monoclonal Antibodies*. *Microbiology*; 2021. doi:10.1101/2021.12.15.472828
32. Cameroni E, Saliba C, Bowen JE. Broadly neutralizing antibodies overcome SARS-CoV-2 Omicron antigenic shift. Published December 14, 2021. Accessed December 23, 2021. <https://www.biorxiv.org/content/10.1101/2021.12.12.472269v1>
33. WHO. *Therapeutics and COVID-19: Living Guideline, 16 September 2022*. WHO Accessed September 21, 2022. <https://www.who.int/publications/i/item/WHO-2019-nCoV-therapeutics-2022.5>
34. Powell AA, Kirsebom F, Stowe J, et al. Protection against symptomatic disease with the delta and omicron BA.1/BA.2 variants of SARS-CoV-2 after infection and vaccination in adolescents: national observational test-negative case control study, August 2021 to March 2022, England. Published online August 22, 2022:2022.08.19.22278987. doi:10.1101/2022.08.19.22278987
35. Cocchio S, Zabeo F, Tremolada G, et al. COVID-19 Vaccine Effectiveness against Omicron Variant among Underage Subjects: The Veneto Region's Experience. *Vaccines*. 2022;10(8):1362. doi:10.3390/vaccines10081362
36. Collie S, Nayager J, Bamford L, Bekker LG, Zylstra M, Gray G. Effectiveness and Durability of the BNT162b2 Vaccine against Omicron Sublineages in South Africa. *New England Journal of Medicine*. 2022;0(0):null. doi:10.1056/NEJMc2210093
37. Chatzilena A, Hyams C, Challen R, et al. Effectiveness of BNT162b2 COVID-19 Vaccination in Prevention of Hospitalisations and Severe Disease in Adults with Delta (B.1.617.2) and Omicron (B.1.1.529) Variant SARS-CoV-2 Infection: A Prospective Test Negative Case-Control Study. Published online September 12, 2022. doi:10.2139/ssrn.4216690
38. Tsang NNY, So HC, Cowling BJ, Leung G, Ip DKM. Effectiveness of BNT162b2 and CoronaVac COVID-19 Vaccination Against Asymptomatic and Symptomatic Infection of SARS-CoV-2 Omicron BA.2 in Hong Kong. Published online August 25, 2022. doi:10.2139/ssrn.4200539
39. Penayo E, Dominguez CM, Paredes CB, Irala S, Von Horoch M, Michel F. *Evaluación de La Efectividad de Las Vacunas Contra La COVID-19, Paraguay.*; 2022. <https://www.paho.org/es/node/86378>
40. Higdon MM, Baidya A, Walter KK, et al. Duration of effectiveness of vaccination against COVID-19 caused by the omicron variant. *The Lancet Infectious Diseases*. 2022;0(0). doi:10.1016/S1473-3099(22)00409-1
41. Grewal R, Kitchen SA, Nguyen L, et al. Effectiveness of a fourth dose of covid-19 mRNA vaccine against the omicron variant among long term care residents in Ontario, Canada: test negative design study. *BMJ*. 2022;378:e071502. doi:10.1136/bmj-2022-071502
42. Link-Gelles R. Effectiveness of 2, 3, and 4 COVID-19 mRNA Vaccine Doses Among Immunocompetent Adults During Periods when SARS-CoV-2 Omicron BA.1 and BA.2/BA.2.12.1 Sublineages Predominated — VISION Network, 10 States, December 2021–June 2022. *MMWR Morb Mortal Wkly Rep*. 2022;71. doi:10.15585/mmwr.mm7129e1