COVID-19 Weekly Epidemiological Update

Edition 105 published 17 August 2022

In this edition:

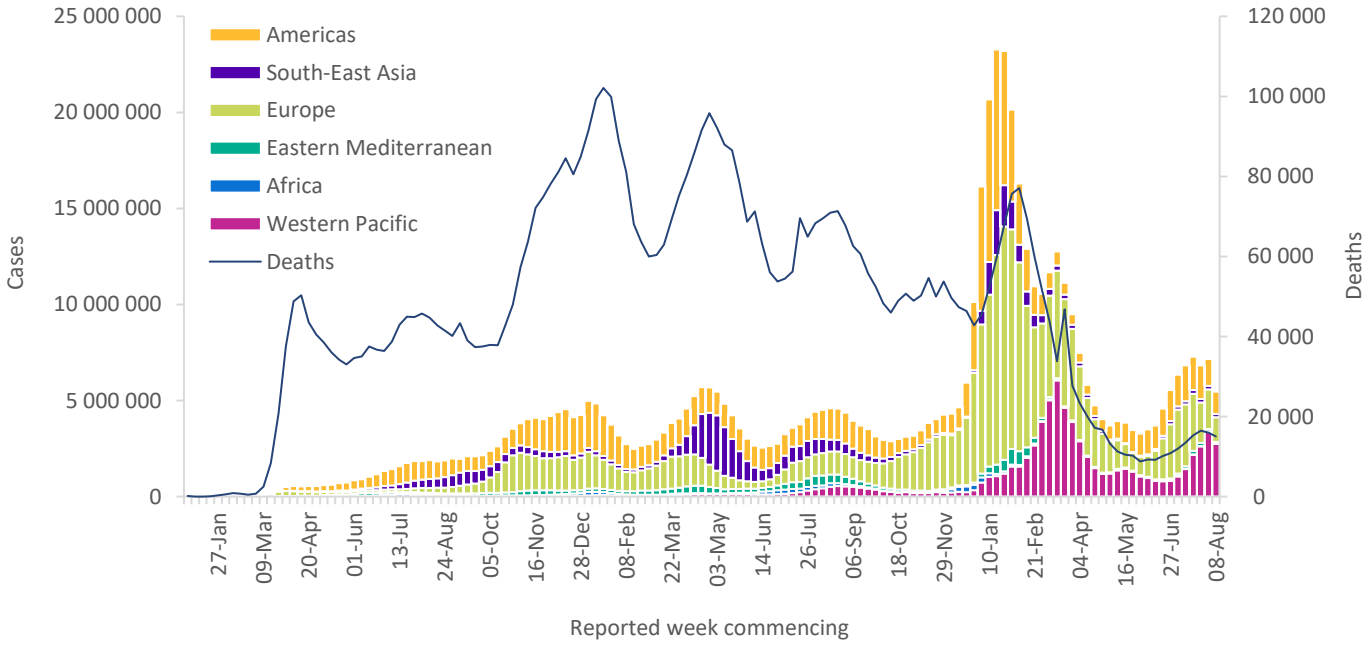
Global overview

Data as of 14 August 2022

Globally, the number of new weekly cases decreased by 24% during the week of 8 to 14 August 2022, as compared to the previous week, with over 5.4 million new cases reported (Figure 1, Table 1). The number of new weekly deaths decreased by 6%, as compared to the previous week, with over 15 000 fatalities reported. As of 14 August 2022, 587 million confirmed cases and 6.4 million deaths have been reported globally.

At the regional level, the number of reported new weekly cases decreased across all six regions: the African Region (-38%), the European Region (-38%), the Eastern Mediterranean Region (-30%), the Western Pacific Region (-18%), the Region of the Americas (-17%), and the South-East Asia Region (-11%). The number of new weekly deaths increased in the Western Pacific (+31%) and the South-East Asia Region (+12%), while it decreased or remained stable in the African Region (-33%), the European Region (-25%), the Eastern Mediterranean Region (-7%), and the Region of the Americas (-4%).

Figure 1. COVID-19 cases reported weekly by WHO Region, and global deaths, as of 14 August 2022**



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

At the country level, the highest numbers of new weekly cases were reported from Japan (1 395 301 new cases; -7%), the Republic of Korea (866 830 new cases; +22%), the United States of America (679 653 new cases; -14%), Germany (271 277 new cases; -25%), and Italy (193 305 new cases; -32%). The highest numbers of new weekly deaths were reported from the United States of America (2 907 new deaths; -4%), Japan (1 647 new deaths; 64%), Brazil (1 495 new deaths; +3%), Italy (920 new deaths; -13%), and Spain (573 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 countries are continuously updated by WHO to incorporate changes in reported COVID-19 cases and deaths made by countries retrospectively.

Table 1. Newly reported and cumulative COVID-19 confirmed cases and deaths, by WHO Region, as of 14 August 2022**

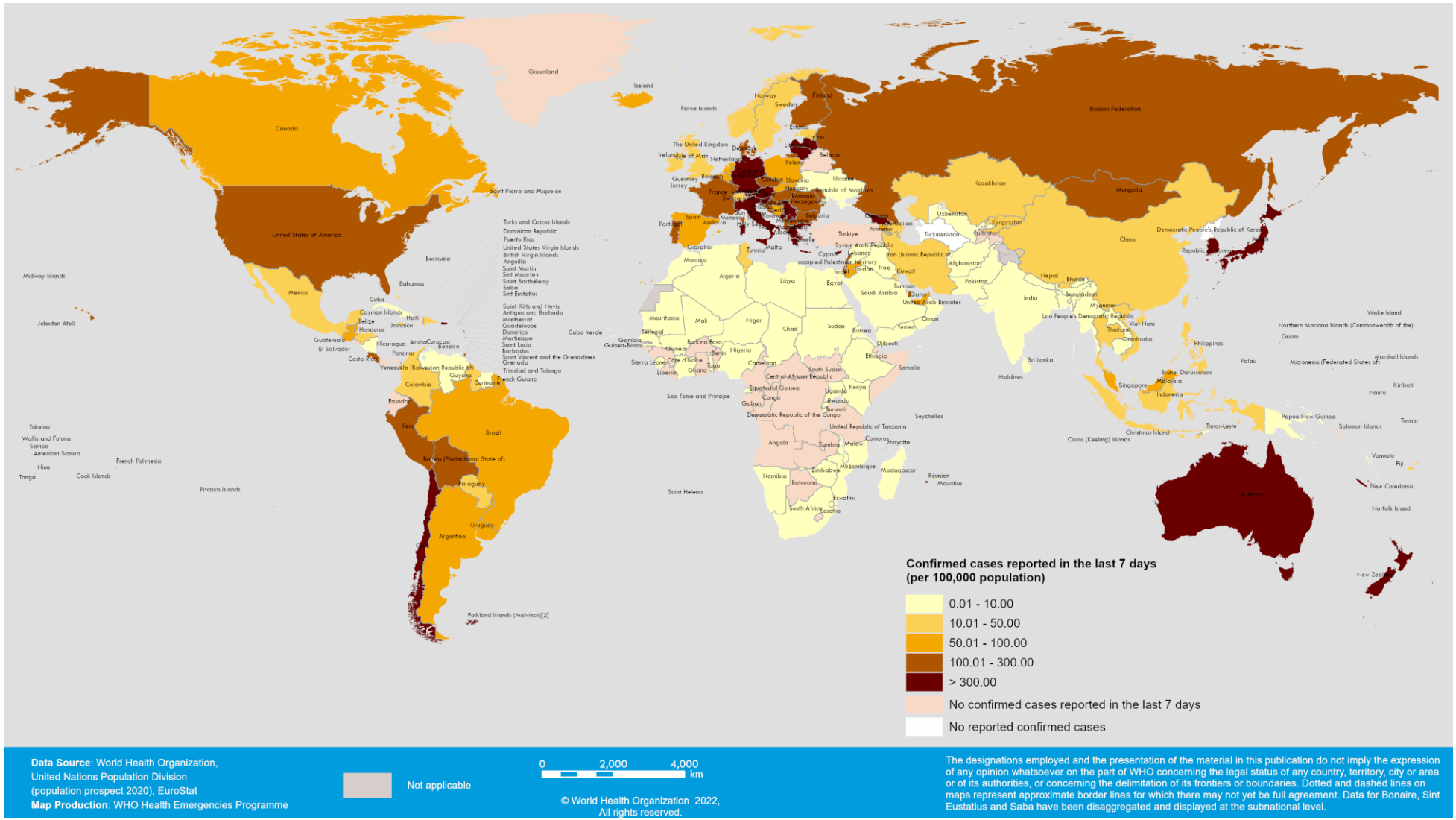
WHO Region	New cases in last 7 days (%)	Change in new cases in last 7 days *	Cumulative cases (%)	New deaths in last 7 days (%)	Change in new deaths in last 7 days *	Cumulative deaths (%)
Western Pacific	2 751 736 (50%)	-18%	77 847 591 (13%)	3 184 (21%)	31%	251 213 (4%)
Europe	1 288 470 (24%)	-38%	244 507 196 (42%)	4 333 (29%)	-25%	2 062 695 (32%)
Americas	1 156 829 (21%)	-17%	173 361 614 (30%)	6 150 (41%)	-4%	2 803 004 (44%)
South-East Asia	166 382 (3%)	-11%	59 709 418 (10%)	774 (5%)	12%	793 911 (12%)
Eastern Mediterranean	86 220 (2%)	-30%	22 837 954 (4%)	607 (4%)	-7%	346 268 (5%)
Africa	11 004 (<1%)	-38%	9 252 860 (2%)	24 (<1%)	-33%	174 123 (3%)
Global	**5 460 641 (100%)**	**-24%**	**587 517 397 (100%)**	**15 072 (100%)**	**-6%**	**6 431 227 (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:

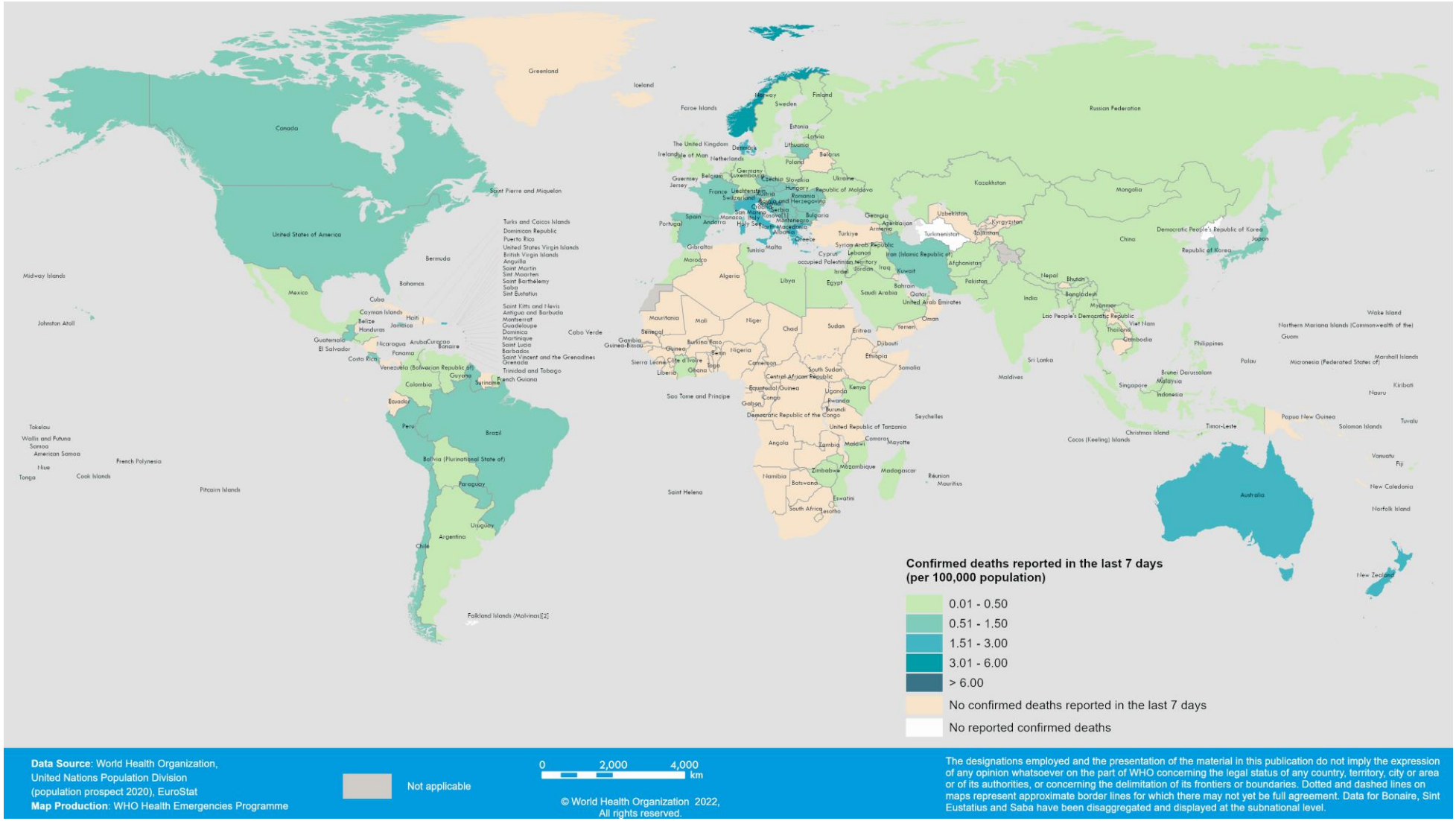
- WHO COVID-19 Dashboard
- WHO COVID-19 Weekly Operational Update and previous editions of the Weekly Epidemiological Update
- WHO COVID-19 detailed surveillance data dashboard

Figure 2. COVID-19 cases per 100 000 population reported by countries, territories and areas, 8 - 14 August 2022*



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

Figure 3. COVID-19 deaths per 100 000 population reported by countries, territories and areas, 8 - 14 August 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 15 July to 15 August 2022, 172 042 SARS-CoV-2 sequences were submitted to GISAID. Among these sequences, the Omicron variant of concern (VOC) remains the dominant variant circulating globally, accounting for 99.3% (170 905) of sequences.

As the number of submitted sequences continues to decline, interpretation of trends should be made with due consideration of the limitations of surveillance systems, including differences in sequencing capacity and sampling strategies between countries, as well as changes in sampling and sequencing strategies in multiple countries.

There is now a large diversity within the Omicron VOC, an expected phenomenon that is the result of the accumulation of mutations as part of the virus replication process and/or immune pressure from the host. More than 200 descendent lineages of Omicron have emerged; these variants are being monitored by WHO, depending on the specific genetic constellations of mutations, indications of a rise in prevalence in a specific location or geographic spread, as well as any evidence of phenotypic changes[i].

The current SARS-CoV-2 variant landscape is characterized by the emergence of an Omicron descendent lineage, the increase in the prevalence followed by the spread to many countries globally and replacement of the former dominant descendent lineage(s). The surge of cases linked to a specific descendent lineage is either due to its higher intrinsic transmissibility or higher immune evasion characteristics. The extent to which the emergence of a variant causes a rise in the number of cases, hospitalizations, and deaths in a country depends on a number of factors, including the levels of population immunity following either SARS-CoV-2 infection, vaccination, or a combination of the two, and the stringency of public health and social measures in place.

Figure 4, Table 2 and Annex 5 indicate the proportion of Omicron descendent variants. Notably, BA.1.X, BA.2.X (incl. BA.2.12.1 and BA.2.75) and BA.3.X have a prevalence of <1%, 3% and <1%, respectively, during week 30 (from 24 to 30 July 2022). The prevalence of BA.4.X is 8%, representing a declining trend as compared to previous weeks. BA.5 and its descendent lineages continue to rise in relative prevalence as compared to other descendent lineages and account for 74% of submitted sequences in week 31 (from 31 July to 6 August 2022).

Genetic diversification of BA.5 has also resulted in multiple descendent lineages, with additional mutations in both the spike and non-spike regions. These are indicated in Table 2 and Annex 5. Thirty-five BA.5 descendent lineages have been assigned a Pango lineage. Among all BA.5 descendent lineages, the relative proportions of BA.5.1, BA.5.2 and BA.5.2.1 are rising, accounting for 29%, 22% and 30% of submitted sequences, respectively during week 31 (from July 31 to 6 August 2022). BA.5.2.1 is the most prevalent variant in all six WHO regions since the week of 7 to 13 August 2022.

Among the Omicron descendent lineages that continue to emerge is BA.2.75, with the earliest sequences reported in May 2022. This variant, currently an Omicron subvariant under monitoring, has 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.[2] As compared to 18 July when only 250 sequences from 15 countries were submitted to GISAID, more than 2700 sequences from 16 countries have been reported as of 15 August 2022. The majority of the reported sequences are from India. The

[i] WHO tracking SARS-CoV-2 Variants

global prevalence of this variant was highest in week 27 (from 3 to 9 July 2022) and has declined in recent weeks, but it is not known if this is a true decline in prevalence or the result of a delay in sequence submissions.

Preliminary laboratory-based studies indicate a relative growth advantage of BA.2.75 as compared to BA.2 and BA.5.[2] Further, there is an indication of higher fusogenicity[ii], more efficient replication in lung cells and more pathogenicity in a hamster model as compared to BA.2. More studies are required to confirm these preliminary findings.

Figure 4. Panel A and B: The number and percentage of SARS-CoV-2 sequences, as of 15 August 2022

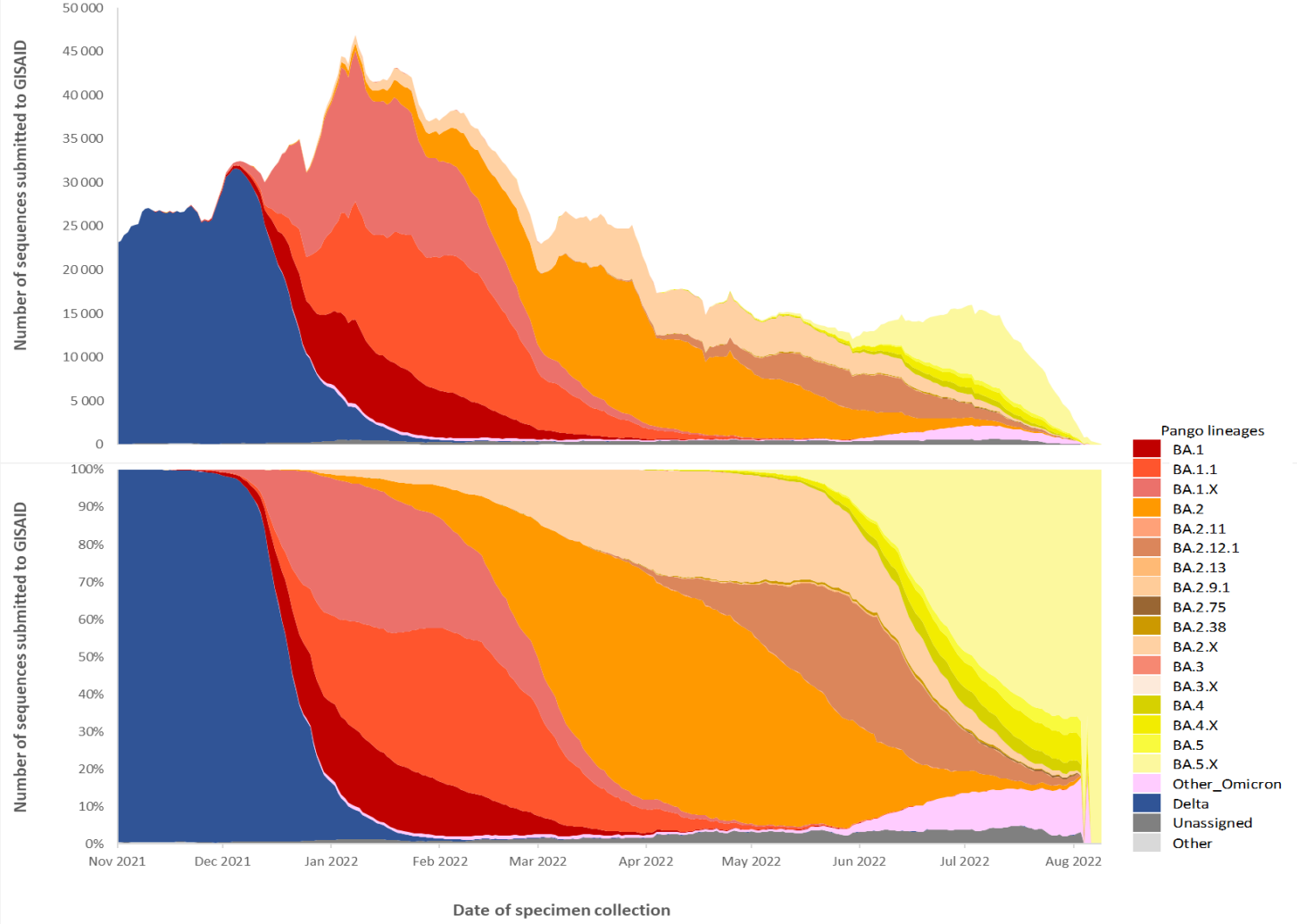


Figure 4 Panel A shows the number and **Panel B** the percentage of all circulating variants since 1 November 2022. Omicron sister-lineages and additional Omicron VOC descendent lineages under further monitoring (VOC-VUM) are shown. *BA.1.X, BA.2.X, BA.3.X, BA.4.X* and *BA.5.X* include all BA.1, BA.2, BA.3, BA.4 and BA.5 pooled descendent lineages, except those already shown in the figure above. The category *Other_Omicron* indicates sequences not part of the above-mentioned Omicron 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. Source: SARS-CoV-2 sequence data and metadata from GISAID, as of 15 August 2022.

[ii] Fusogenicity: a measure of the binding between a pathogen's membrane/receptor to a host membrane/receptor.

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

			Last 4 weeks by collection date (%) [c]			
Lineage (n)[a]	**Countries**	**Sequences[b]**	**2022-28**	**2022-29**	**2022-30**	**2022-31**
BA.1.X, (n=54)	195	2 372 883	26 (<1%)	22 (<1%)	18 (<1%)	0 (0%)
BA.2.X, (n=117)	165	2 039 486	7465 (9%)	3589 (6%)	1082 (4%)	89 (3%)
BA.3.X, (n=1)	44	1334	37 (<1%)	24 (<1%)	5 (<1%)	0 (0%)
BA.4.X, (n=11)	103	91 020	9358 (12%)	6101 (11%)	2760 (10%)	235 (8%)
BA.5.X, (n=35)	121	364 487	52 633 (65%)	39 442 (69%)	18 806 (70%)	2067 (74%)
Other_Omicron[d]	176	145 604	8050 (10%)	6443 (11%)	3474 (13%)	371 (13%)
Recombinants[e], (n=27)	-	Pooled 6517	4 (<1%)	4 (<1%)	2 (<1%)	0 (0%)
Delta[f]	205	4 369 710	5 (<1%)	4 (<1%)	0 (0%)	1 (<1%)
Other	209	2 702 359	3942 (5%)	1899 (3%)	642 (2%)	31 (1%)

[a] Lineage, *X* means descendent lineages are pooled, *n* indicates the number of currently designated additional descendent lineages
[b] Data source: sequences and metadata from GISAID, retrieved on 12 August 2022
[c] Number of sequences and relative proportions in %
[d] indicating *Omicron* lineages other than those of BA.X lineages and those of recombinants
[e] indicating the sum of recombinant lineages
[f] Previously circulating VOC

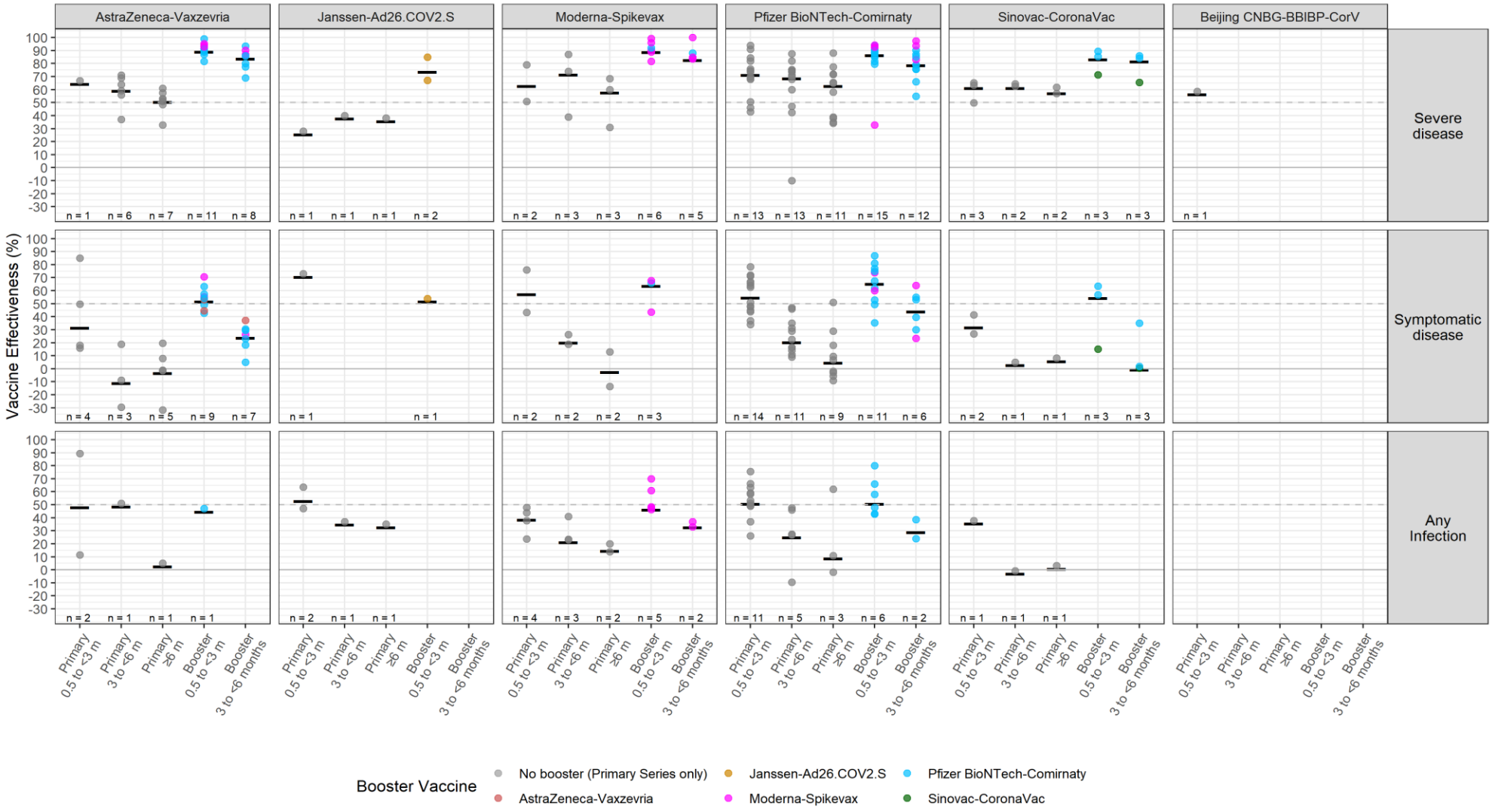
Table 3. Summary of phenotypic characteristics of the Omicron VOC[3]

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 [4]	Lower growth rate compared to BA.2[1], BA.4 and BA.5 [3]	Lower growth rate compared to BA.4 and BA.5 [1,2]	Growth advantage compared to BA.2 [2]	Growth advantage compared to BA.4 [2]
Disease severity	Overall evidence suggests lower severity compared to Delta despite contrasting evidence. Earlier studies reported lower severity.[4–10] However, more recent studies report lower [11]or similar severity.[12,13]	No difference in disease severity compared to BA.2, BA.4 and BA.5[12]	There is evidence, both in favor of lower severity[14] compared to BA.5 and in support of similar disease severity compared to BA.4 and BA.5[12]	Currently available evidence does not suggest a difference in disease severity compared to BA.2 and BA.5 [12]	There is one preliminary study suggesting increased severity[14] compared to BA.2 while other studies suggests similar disease severity compared to BA.2 and BA.4[12]. More evidence is needed to understand the disease severity
Risk of reinfection	Reduced risk of Omicron reinfection among individuals previously infected with a different SARS-CoV-2 variant compared to naïve individuals[15,16]	Reduced risk of reinfection with BA.1 after infection with BA.2[16]	Reduced risk of reinfection following infection with BA.1 [16]	Varying evidence regarding risk of reinfection. One study reported protection against infection following previous BA.2 infection [17] while another reported reduced protection from reinfection.[12]	Varying evidence regarding risk of reinfection. One study reported protection against infection following previous BA.2 infection [17] while another reported reduced protection from reinfection.
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 a reduced effectiveness of other monoclonal antibodies[30–33]	Reduced efficacy of cilgavimab[34] and casirivimab-imdevimab[35]	Reduced neutralizing activity of sotrovimab, bamlanivimab, casirivimab, etesevimab, imdevimab and tixagevimab [36]	Reduced neutralizing activity of sotrovimab, bamlanivimab, casirivimab, etesevimab, imdevimab and tixagevimab. Increased resistance to cilgavimab compared to BA.2[36]	Reduced neutralizing activity of sotrovimab, bamlanivimab, casirivimab, etesevimab, imdevimab and tixagevimab. Increased resistance to cilgavimab compared to BA.2[36]
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				

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

[4] Similar methodology used as Reference [1]

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 panel header. All booster VE estimates are for first booster dose. Severe disease includes hospitalization, and pneumonia; symptomatic disease includes disease of any severity level; any infection can include symptomatic and asymptomatic infection. Additional details on the methods for inclusion of the estimates in the plots provided in text.

Figure 5 summarizes the impact of the Omicron variant on absolute vaccine effectiveness (VE) over time, 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 4.

Since the last update on 20 July 2022, five new studies have been added to the figure. Four studies (two not yet peer-reviewed) assessed the VE of two doses of Pfizer BioNTech-Comirnaty against infection, symptomatic disease, emergency department/urgent care encounters, or hospitalization due to Omicron over time among children in Canada, Qatar, Singapore, and the United States of America.[36–39] Another study evaluated VE of primary series vaccination with Sinovac-CoronaVac, as well as VE of two doses of Sinovac-CoronaVac followed by a booster dose of Pfizer BioNTech-Comirnaty against Omicron symptomatic disease, hospitalization, and death among adults 18 years and older in Brazil.[40]

Interpretation of the results of absolute VE for the Omicron variant

To date, 37 studies from 15 countries (Argentina, Brazil, Canada, Chile, Czech Republic, Denmark, Finland, Norway, Israel, Qatar, Singapore, South Africa, the United Kingdom, the United States of America, and Zambia) have collectively assessed the protection of six vaccines against the Omicron variant. Thirteen studies contributed VE estimates of primary series vaccination only to the plot, four contributed to estimates of the first booster vaccination only, and 20 contributed estimates 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 four previously circulating VOCs. However, importantly, 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 with time after the first booster vaccination for symptomatic disease and infection than it does for severe disease[41]; however, studies that assess VE of booster vaccination beyond six months to evaluate longer duration of protection are not yet available.

For *severe disease*, VE estimates of the primary series showed little decline over six months. VE estimates were ≥70% during the first three months after primary series vaccination for nine of 15 (60%) VE estimates for the mRNA vaccines (Moderna-Spikevax and Pfizer BioNTech-Comirnaty). Of the two vector vaccines for which data were available, both had VE <70%: one reported VE <70% for AstraZeneca-Vaxzevria and the other reported VE <50% for Janssen-Ad26.COV2.S. Four estimates were available for inactivated vaccines: none of the three estimates for Sinovac-CoronaVac were ≥ 70% (two [67%] VE estimates were ≥ 50%); the single estimate for Beijing CNBG-BBIBP-CorV (Sinopharm) was ≥50% but <70%. Beyond three months after vaccination, VE estimates were ≥70% for 14 of 34 (41%) VE estimates for the mRNA vaccines (24 [71%] estimates had VE ≥50%); one of 13 (8%) VE estimates for

AstraZeneca-Vaxzevria was ≥70% (10 [77%] estimates were ≥50%). The two estimates for the vector-based Janssen-Ad26.COV2.S vaccine were <50%; the four VE estimates for Sinovac-CoronaVac were ≥50% but <70%.

The first booster dose vaccination improved VE estimates against *severe disease* in all studies, and VE was ≥70% in 37 of 39 (95%) estimates evaluating VE between 14 days and three months of receipt of a booster dose. Thirty-six estimates evaluated an mRNA booster, two evaluated a Janssen-Ad26.COV2.S booster, and one evaluated a Sinovac-CoronaVac booster. One Moderna-Spikevax booster dose had VE estimate of <50% (though confidence intervals were very wide), and one Janssen-Ad26.COV2.S booster dose had VE <70%. At three to six months post mRNA booster, VE was ≥70% for 26 of 29 (90%) estimates (the primary series was an mRNA vaccine in 19 of the 29 estimates, AstraZeneca-Vaxzevria in eight and Sinovac-CoronaVac in two). One study found the VE to be ≥50% but <70% following three to six months from the third dose of Sinovac-CoronaVac.

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 substantially over time. For *symptomatic disease*, only four of 16 (25%) VE estimates for the mRNA vaccines were ≥70% and only nine (56%) 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 both estimates for Sinovac (CoronaVac) were <50%. Beyond three months after vaccination, only one of 38 (3%) VE estimates was ≥50% (28 estimates evaluated mRNA vaccines, eight evaluated AstraZeneca-Vaxzevria, and two evaluated Sinovac-CoronaVac). A booster vaccination with an mRNA vaccine after completion of a primary series of AstraZeneca-Vaxzevria, an mRNA vaccine, or Sinovac-CoronaVac improved VE against *symptomatic disease*: seven of 25 (28%) VE estimates between 14 days and three months post booster were ≥70%, although 20 (80%) estimates were ≥50%; one (50%) of two VE estimates evaluating three doses of AstraZeneca-Vaxzevria was ≥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 ≥50% and none were ≥70%. Both the single estimate for three doses of AstraZeneca-Vaxzevria and the single estimate for three doses of Sinovac-CoronaVac assessed at three to six months post booster vaccination were <50%. VE estimates against *infection* showed similar patterns of lower protection and steep waning as those against *symptomatic disease.*

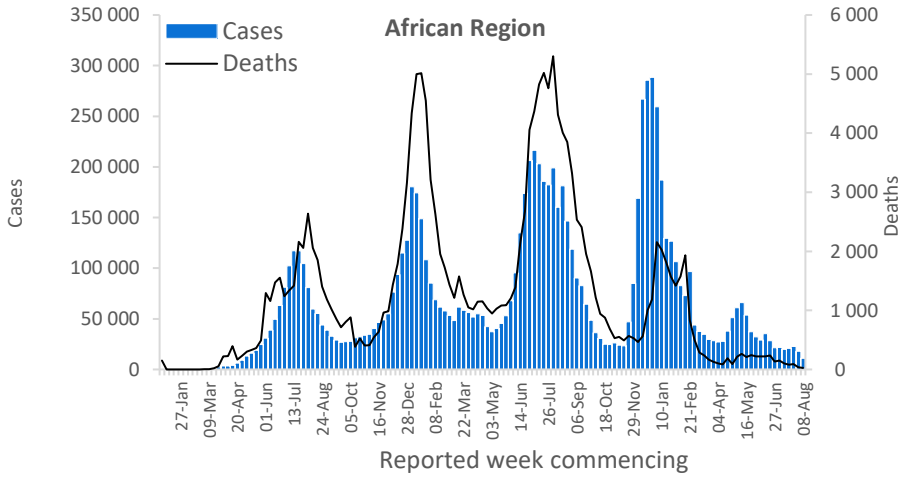
WHO regional overviews:

Epidemiological week 8 - 14 August 2022**

African Region

The African Region reported just over 11 000 new cases, a 38% decrease as compared to the previous week. Five (10%) countries reported an increase in the number of new cases of 20% or greater, with the greatest proportional increases seen in Niger (18 vs six new cases; +200%), Mayotte (642 vs 385 new cases; +67%), and Mozambique (182 vs 132 new cases; +38%). The highest numbers of new cases were reported from Réunion (4590 new cases; 512.7 new cases per 100 000 population; -21%), South Africa (1293 new cases; 2.2 new cases per 100 000; -26%), and Algeria (867 new cases; 2.0 new cases per 100 000; +13%).

The number of new weekly deaths in the Region decreased by 33% as compared to the previous week, with 24 deaths reported. The highest numbers of new deaths were reported from Réunion (eight new deaths; <1 new death per 100 000 population; +14%), Zimbabwe (four new deaths; <1 new death per 100 000; -43%), and Côte d'Ivoire[#] (four new deaths; <1 new death per 100 000 population).

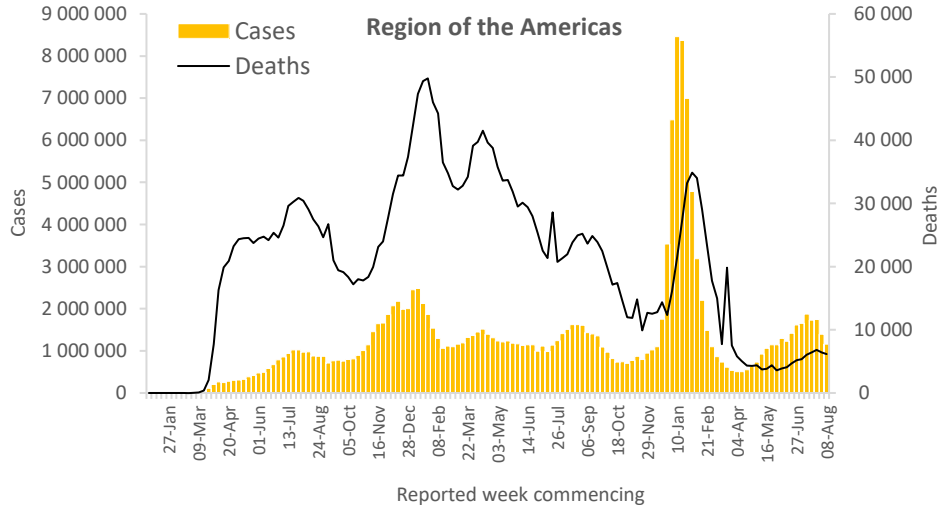


Updates from the African Region

Region of the Americas

The Region of the Americas reported over 1.1 million new cases, a 17% decrease as compared to the previous week. Six of 56 (11%) countries for which data are available reported increases in the number of new cases of 20% or greater, with the greatest proportional increases observed in the Falkland Islands (Malvinas) (20 vs eight new cases; +150%), Antigua and Barbuda (33 vs 14 new cases; +136%), and Grenada (73 vs 36 new cases; +103%). The highest numbers of new cases were reported from the United States of America (679 653 new cases; 205.3 new cases per 100 000; -14%), Brazil (153 661 new cases; 72.3 new cases per 100 000; -25%), and Chile (72 562 new cases; 379.6 new cases per 100 000; +14%).

The number of new weekly deaths reported in the Region remained stable as compared to the previous week, with over 6100 deaths reported. The highest numbers of new deaths were reported from the United States of America (2907 new deaths; <1 new death per 100 000; -4%), Brazil (1495 new deaths; <1 new death per 100 000; +3%), and Peru (344 new deaths; 1 new death per 100 000; -2%).

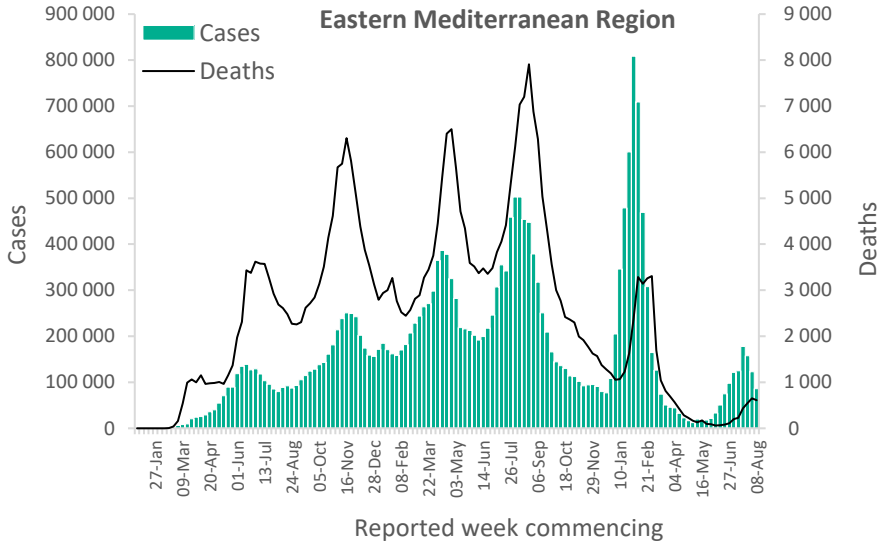


Updates from the Region of the Americas

Eastern Mediterranean Region

The Eastern Mediterranean Region reported a decrease in cases for the third consecutive week, with over 86 000 new cases reported, a 30% decrease as compared to the previous week. Two (9%) countries reported increases in the number of new cases of 20% or greater: Bahrain (3967 vs 3182 new cases; +25%) and Afghanistan (1785 vs 1466 new cases; +22%). The highest numbers of new cases were reported from the Islamic Republic of Iran (33 949 new cases; 40.4 new cases per 100 000; -37%), Lebanon (10 379 new cases; 152.1 new cases per 100 000; -21%), and the occupied Palestinian territory (6382 new cases; 125.1 new cases per 100 000; -29%).

The number of new weekly deaths in the Region decreased by 7% as compared to the previous week, with over 600 new deaths reported. The highest numbers of new deaths were reported from the Islamic Republic of Iran (463 new deaths; <1 new death per 100 000; similar to the previous week), Tunisia (48 new deaths; <1 new death per 100 000; -25%), and Lebanon (26 new deaths; <1 new death per 100 000; +53%).

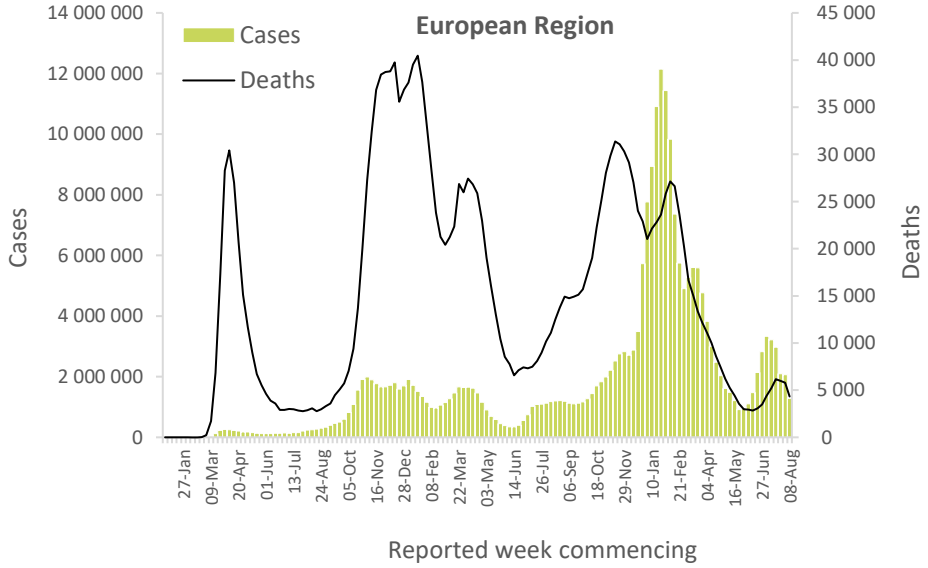


Updates from the Eastern Mediterranean Region

European Region

The European Region reported over 1.2 million new cases, a 38% decrease as compared to the previous week. Four (7%) countries in the Region reported increases in new cases of 20% or greater, with some of the highest proportional increases observed in Gibraltar (96 vs 36 new cases; +167%), and Ukraine (3893 vs 556 new cases; +40%). The highest numbers of new cases were reported from Germany (271 277 new cases; 326.2 new cases per 100 000; -25%), Italy (193 305 new cases; 324.1 new cases per 100 000; -32%), and the Russian Federation (169 259 new cases; 116.0 new cases per 100 000; +53%).

Over 4300 new weekly deaths were reported in the Region, a 25% decrease as compared to the previous week. The highest numbers of new deaths were reported from Italy (920 new deaths; 1.5 new deaths per 100 000; -13% decrease), Spain (573 new deaths; 1.2 new deaths per 100 000; -12%), and France (466 new deaths; <1 new death per 100 000; -11%).

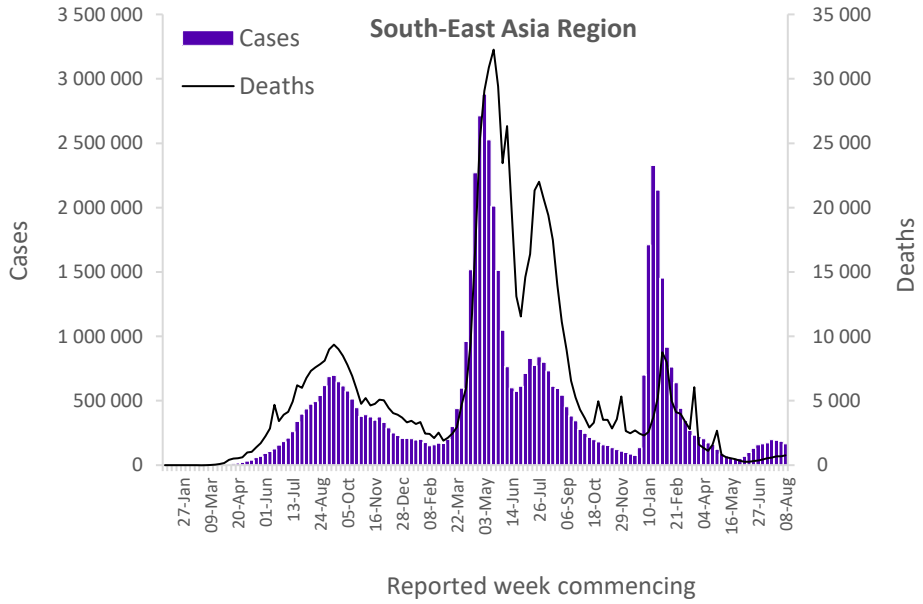


Updates from the European Region

South-East Asia Region

The South-East Asia Region reported over 166 000 new cases, an 11% decrease as compared to the previous week. Three of the 10 countries (30%) for which data are available showed increases in the number of new cases of 20% or greater: Myanmar (191 vs 106 new cases; +80%), Timor Leste (43 vs 35 new cases; +23%) and Sri Lanka (1248 vs 1025 new cases, 22%). The highest numbers of new cases were reported from India (107 732 new cases; 7.8 new cases per 100 000; -14%), Indonesia (37 796 new cases; 13.8 new cases per 100 000; similar to the previous week), and Thailand (14 816 new cases; 21.2 new cases per 100 000; -4%).

The Region reported under 800 deaths, a 12% increase as compared to the previous week. The highest numbers of new deaths were reported from India (348 new deaths; <1 new death per 100 000; +5%), Thailand (232 new deaths; <1 new death per 100 000; +10%), and Indonesia (131 new deaths; <1 new death per 100 000; +28%).

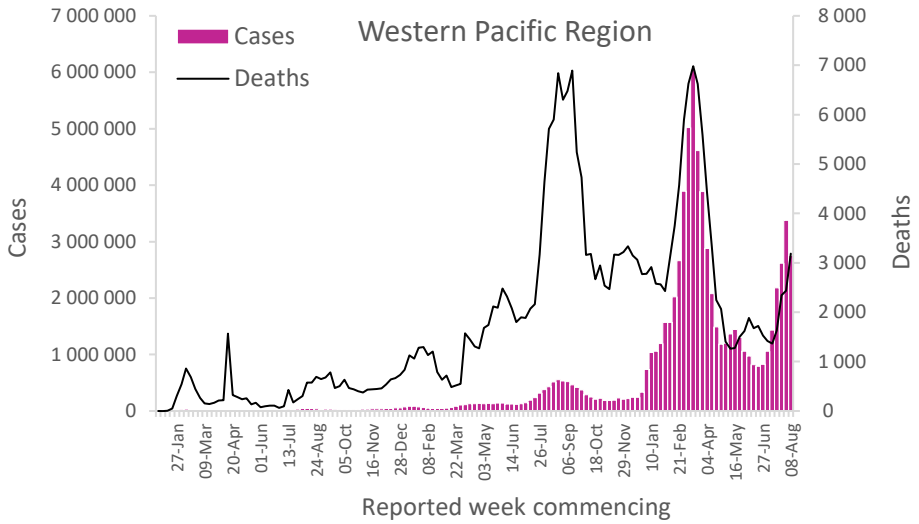


Updates from the South-East Asia Region

Western Pacific Region

After an increasing trend in cases since the end of July 2022, the Western Pacific Region reported an 18% decrease in new cases as compared to previous week, with over 2.7 million new cases reported. Five (15%) countries reported increases in new cases of 20% or greater, with some of the largest proportional increases observed in Commonwealth of the Northern Mariana Islands (215 vs one new case; +21 400%) and Marshall Islands (758 vs four new cases; +18 850% and Nauru (196 vs two new cases, +9700%). The highest numbers of new cases were reported from Japan (1 395 301 new cases; 1103.2 new cases per 100 000; -7%), the Republic of Korea (866 830 new cases; 1690.7 new cases per 100 000; +22%), and Australia (171 173 new cases; 671.3 new cases per 100 000; -35%).

The Region reported over 3100 new weekly deaths, a 31% increase as compared to the previous week. The highest numbers of new deaths were reported from Japan (1647 new deaths; 1.3 new deaths per 100 000; + 64%), Australia (539 new deaths; 2.1 new deaths per 100 000; +2%), and the Republic of Korea (360 new deaths; <1 new death per 100 000; +67%).



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 of an outbreak of COVID-19 reported in the Democratic People's Republic of Korea continue through official media since 12 May 2022; however, at present, no confirmed cases or deaths have been reported to WHO.

For some countries, it was not possible to calculate the weekly percentage change in the number of cases and / or deaths due to either batch reporting or no reporting during the last week.

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.[1]

Annex 3. Summary of Primary Series and First Booster Vaccine Performance against Omicron Variant of Concern (data as of 25 July 2022)

		Omicron Sub-Lineage				
		BA.1	**BA.2**	**BA.2.12.1**	**BA.3**	**BA.4/BA.5**
Primary Series Vaccination						
WHO Emergency Use Listing (EUL) Qualified Vaccines	AstraZeneca-Vaxzevria/SII-Covishield	HNR_{12}	HNR_{2}	HNR_{1}	----	HNR_{1}
	Beijing CNBG-BBIBP-CorV	HNR_{8}	HNR_{3}	HNR_{2}	HNR_{1}	HNR_{2}
	Bharat-Covaxin	$\downarrow\downarrow_{1}$	----	----	----	----
	Cansino-Convidecia	----	----	----	----	----
	Janssen-Ad26-COV2.S	HNR_{9}	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_{49}	HNR_{7}	HNR_{1}	HNR_{1}	HNR_{2}
	Sinovac-CoronaVac	HNR_{8}	$\downarrow\downarrow\downarrow_{1}$	----	----	$\downarrow\downarrow\downarrow_{1}$
Vaccines without WHO EUL	Anhui ZL-Recombinant	----	----	----	----	----
	Gamaleya-Sputnik V	HNR_{3}	HNR_{1}	HNR_{1}	----	HNR_{1}
	Chumakov-Covi-Vac	HNR_{2}	----	----	----	----
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	$\downarrow\downarrow_{1}$	$\downarrow\downarrow_{1}$	----	$\downarrow\downarrow_{1}$	----
	Beijing CNBG-BBIBP-CorV + Beijing CNBG-BBIBP-CorV	$\downarrow\downarrow$to$\downarrow\downarrow\downarrow_{4}$	HNR_{2}	HNR_{1}	$\downarrow\downarrow_{1}$	HNR_{1}
	Janssen-Ad26-COV2.S + Janssen-Ad26-COV2.S	HNR_{2}	----	----	----	----
	Janssen-Ad26-COV2.S + Pfizer BioNTech-Comirnaty	$\downarrow_{1}$ to $\downarrow\downarrow\downarrow_{2}$	----	----	----	----
	Moderna-Spikevax + Moderna-Spikevax	$\downarrow$to$\downarrow\downarrow\downarrow_{8}$	$\downarrow\downarrow_{1}$	$\downarrow\downarrow_{1}$	$\downarrow\downarrow_{1}$	$\downarrow\downarrow\downarrow_{1}$
	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$\downarrow\downarrow\downarrow_{42}$	$\downarrow$to$\downarrow\downarrow\downarrow_{14}$	$\downarrow$to$\downarrow\downarrow\downarrow_{3}$	$\downarrow$to$\downarrow\downarrow_{4}$	$\downarrow\downarrow$to$\downarrow\downarrow\downarrow_{6}$
	Pfizer BioNTech-Comirnaty + Janssen-Ad26-COV2.S	$\downarrow_{2}$	----	----	----	----
	Pfizer BioNTech-Comirnaty + Moderna-Spikevax	$\downarrow$to$\downarrow\downarrow_{2}$	----	----	----	----
	Sinovac-CoronaVac + Sinovac-CoronaVac	$\downarrow$to$\downarrow\downarrow\downarrow_{7}$	$\downarrow\downarrow$ to$\downarrow\downarrow\downarrow_{3}$	$\downarrow\downarrow_{1}$	$\downarrow\downarrow_{1}$	$\downarrow\downarrow$ to$\downarrow\downarrow\downarrow_{2}$
	Sinovac-CoronaVac + Pfizer BioNTech-Comirnaty	$\downarrow\downarrow_{2}$	$\downarrow\downarrow_{1}$	----	----	----
Booster Vaccines without WHO EUL	Anhui ZL-Recombinant + Anhui ZL-Recombinant	$\downarrow$to$\downarrow\downarrow_{2}$	$\downarrow\downarrow_{1}$	$\downarrow\downarrow_{1}$	$\downarrow\downarrow\downarrow_{1}$	$\downarrow\downarrow\downarrow_{1}$
	Beijing CNBG-BBIBP-CorV + Anhui ZL - Recombinant	$\downarrow\downarrow$to$\downarrow\downarrow\downarrow_{4}$	HNR_{2}	HNR_{1}	$\downarrow\downarrow\downarrow_{1}$	HNR_{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$\downarrow\downarrow\downarrow_{2}$	$\downarrow\downarrow_{1}$

Abbreviations: HNR=high non-response. Arrows generalize the magnitude of reduction in VE or neutralization: "↔" indicates <2-fold reduction in neutralization; "↓" 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.
- Studies that use samples collected >7 days and < 6 months after complete vaccination and that use an ancestral strain as the reference are included in the table.
- Studies of immunocompromised persons are excluded.
- 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.

Annex 5. Relative proportions of selected BA.5 descendent lineages in the last four weeks by specimen collection date

			Last 4 weeks by collection date			
Lineage	**Countries**	**Sequences**	**2022-28**	**2022-29**	**2022-30**	**2022-31**
BA.5	83	21849	3 147 (5.98%)	2 256 (5.72%)	1 134 (6.03%)	139 (6.72%)
BA.5.1	99	120192	14 967 (28.44%)	11 364 (28.81%)	5 488 (29.18%)	591 (28.59%)
BA.5.1.1	51	5608	897 (1.70%)	630 (1.60%)	262 (1.39%)	27 (1.31%)
BA.5.1.2	45	2204	337 (0.64%)	274 (0.69%)	160 (0.85%)	13 (0.63%)
BA.5.1.3	52	4025	409 (0.78%)	271 (0.69%)	177 (0.94%)	10 (0.48%)
BA.5.1.4	34	794	82 (0.16%)	68 (0.17%)	15 (0.08%)	3 (0.15%)
BA.5.2	105	57755	9 454 (17.96%)	7 861 (19.93%)	4 069 (21.64%)	459 (22.21%)
BA.5.2.1	104	92110	15 240 (28.96%)	11 396 (28.89%)	5 340 (28.40%)	628 (30.38%)
BA.5.2.2	44	2166	257 (0.49%)	205 (0.52%)	84 (0.45%)	8 (0.39%)
BA.5.2.3	47	2768	486 (0.92%)	345 (0.87%)	166 (0.88%)	29 (1.40%)
BA.5.2.4	20	294	41 (0.08%)	38 (0.10%)	17 (0.09%)	2 (0.10%)
BA.5.3	49	2795	124 (0.24%)	75 (0.19%)	38 (0.20%)	3 (0.15%)
BA.5.3.1	68	4344	429 (0.82%)	346 (0.88%)	218 (1.16%)	17 (0.82%)
BA.5.3.2	31	1765	57 (0.11%)	28 (0.07%)	9 (0.05%)	1 (0.05%)
BA.5.3.3	35	1479	161 (0.31%)	138 (0.35%)	68 (0.36%)	10 (0.48%)
BA.5.3.4	22	618	20 (0.04%)	5 (0.01%)	5 (0.03%)	1 (0.05%)
BA.5.5	69	29355	3 996 (7.59%)	2 456 (6.23%)	902 (4.8%)	65 (3.14%)
BA.5.6	70	14366	2 529 (4.80%)	1 686 (4.27%)	654 (3.48%)	61 (2.95%)
BA.5.X (total)	121	364487	52 633 (100%)	39 442 (100%)	18 806 (100%)	2 067 (100%)

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