COVID-19 Weekly Epidemiological Update

Edition 115 published 26 October 2022

In this edition:

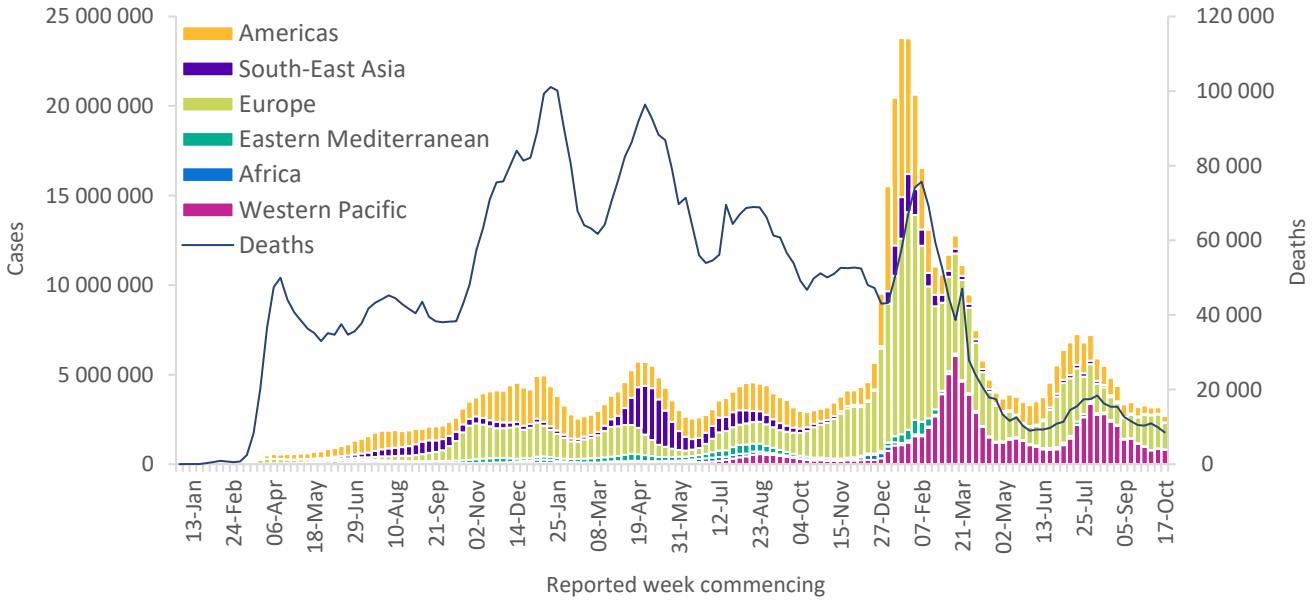
Global overview

Data as of 23 October 2022

Globally, the number of new weekly cases decreased by 15% during the week of 17 to 23 October 2022 as compared to the previous week, with over 2.6 million new cases reported (Figure 1, Table 1). The number of new weekly deaths decreased by 13% as compared to the previous week, with over 8500 fatalities reported. As of 23 October 2022, over 624 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 (-41%), the European Region (-23%), the Eastern Mediterranean Region (-9%), the Western Pacific Region (-5%), the South-East Asia Region (-4%) and the Region of the Americas (+2%). The number of new weekly deaths decreased across four of the six regions: the African Region (-72%), the European Region (-24%), the South-East Asia Region (-13%), and the Western Pacific Region (-8%); while the number remained stable in the Region of the Americas (-1%) and increased in the Eastern Mediterranean Region (+9%).

Figure 1. COVID-19 cases reported weekly by WHO Region, and global deaths, as of 23 October 2022**



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

At the country level, the highest numbers of new weekly cases were reported from Germany (498 787 new cases; -23%), France (307 610 new cases; -22%), China (285 348 new cases; -13%), the United States of America (255 116 new cases; -1%) and Italy (252 777 new cases; -12%). The highest numbers of new weekly deaths were reported from the United States of America (2538 new deaths; similar to the previous week), the Russian Federation (636 new deaths; -9%), Italy (586 new deaths; +23%), France (484 new deaths; +21%) and China (469 new deaths; +9%).

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 23 October 2022**

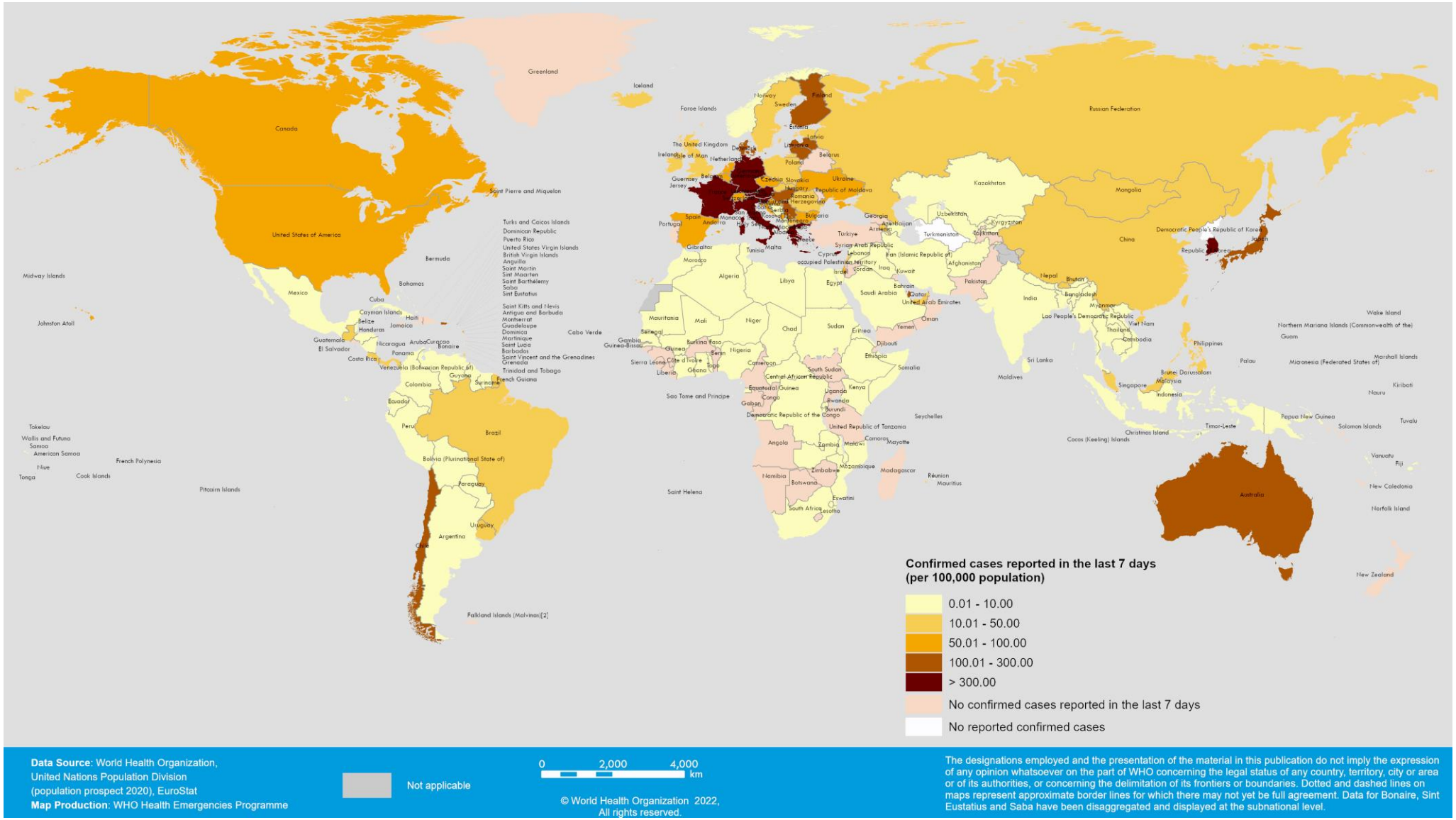
WHO Region	New cases in last 7 days (%)	Change in new cases in last 7 days *	Cumulative cases (%)	New deaths in last 7 days (%)	Change in new deaths in last 7 days *	Cumulative deaths (%)
Europe	1 459 654 (54%)	-23%	259 685 070 (42%)	3 525 (41%)	-24%	2 110 275 (32%)
Western Pacific	812 828 (30%)	-5%	92 535 787 (15%)	1 234 (14%)	-8%	275 361 (4%)
Americas	365 303 (14%)	2%	179 627 426 (29%)	3 468 (41%)	-1%	2 853 216 (43%)
South-East Asia	34 905 (1%)	-4%	60 410 703 (10%)	245 (3%)	-13%	798 460 (12%)
Eastern Mediterranean	13 973 (1%)	-9%	23 137 354 (4%)	73 (1%)	9%	348 619 (5%)
Africa	3 961 (<1%)	-41%	9 351 867 (1%)	17 (<1%)	-72%	174 676 (3%)
Global	**2 690 624 (100%)**	**-15%**	**624 748 971 (100%)**	**8 562 (100%)**	**-13%**	**6 560 620 (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:

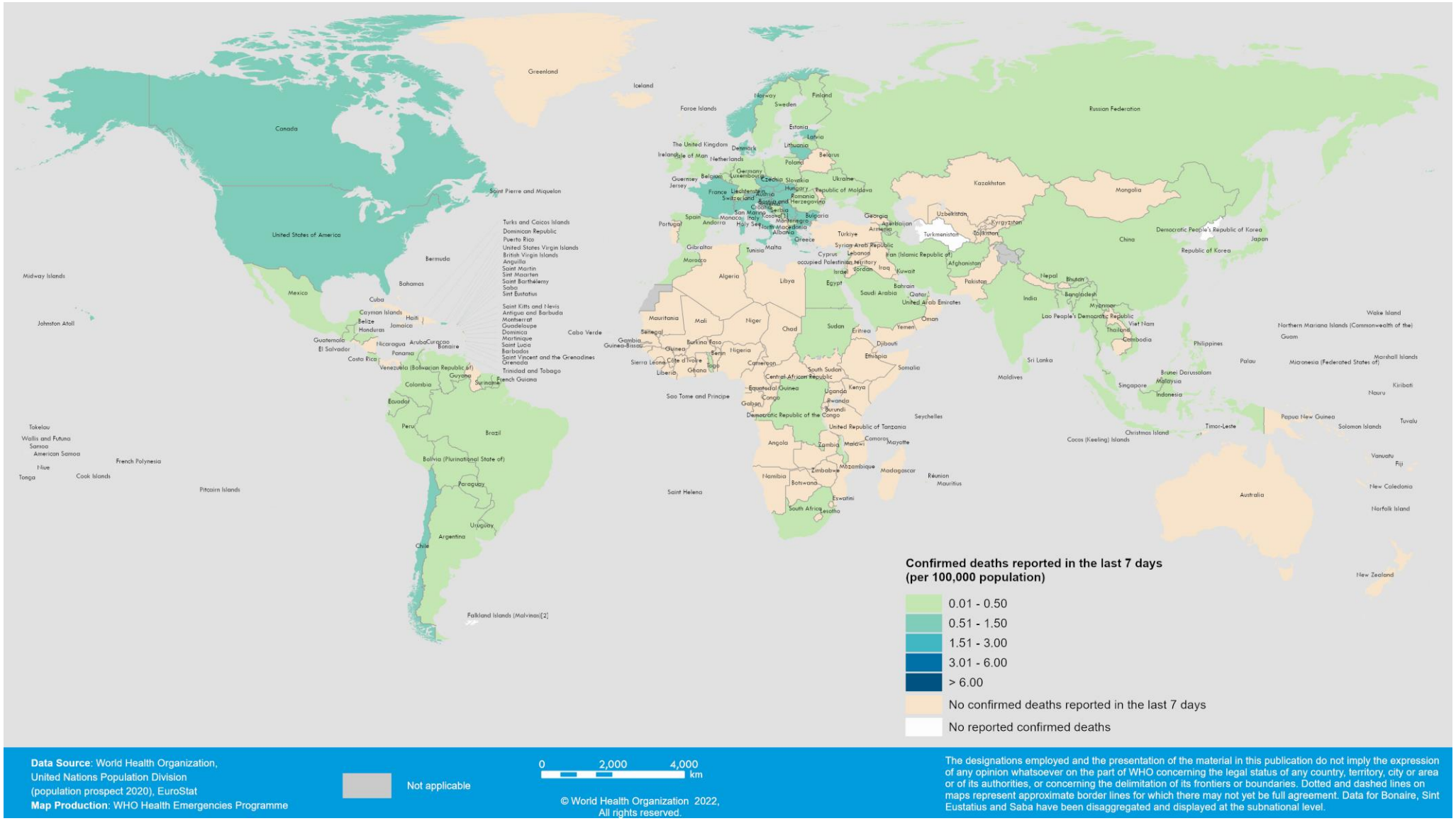
- WHO COVID-19 Dashboard
- WHO COVID-19 Weekly Operational Update and previous editions of the Weekly Epidemiological Update
- WHO COVID-19 detailed surveillance data dashboard
- WHO COVID-19 policy briefs

Figure 2. COVID-19 cases per 100 000 population reported by countries, territories and areas, 17 - 23 October 2022*



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

Figure 3. COVID-19 deaths per 100 000 population reported by countries, territories and areas, 17 - 23 October 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 24 September to 24 October 2022, 107 952 SARS-CoV-2 sequences were shared through GISAID. Among these, 107 678 sequences were the Omicron variant of concern (VOC), which accounted for 99.7% of sequences reported globally in the past 30 days. During epidemiological week 40, (3 to 9 October 2022), 11.7% of all shared sequences have not yet been assigned a specific Pango name but are presumed to be descendent lineages of Omicron (category unassigned). In the same reporting period, 1.4% of sequences are assigned as recombinants, the majority of which are XBB and its descendent subvariant XBB.1. No sequences other than Omicron have been reported in the past 30 days.

The trends describing the circulation of Omicron descendent lineages should be interpreted with due consideration of the limitations of the COVID-19 surveillance systems. These include differences in sequencing capacity and sampling strategies between countries, changes in sampling strategies over time, reductions in tests conducted and sequences shared by countries around the world and delays in sequence submission.

Genetic diversification continues and has given rise to 390 Omicron descendent lineages, as well as 48 identified recombinants. All 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.

BA.5 descendent lineages remain predominant with a prevalence of 77.1% as of epidemiological week 40, followed by BA.4 descendent lineages with a prevalence of 5.4%. BA.2 descendent lineages have risen in prevalence, accounting for 4.3% of sequences within the same reporting period. The prevalence of BA.1.X is <1% and BA.3.X sequences have not been reported at the global level within the last eight weeks. Figure 4 and Table 2 report the global proportions and prevalence of the six variants currently classified as Omicron subvariants under monitoring, a list that is regularly updated. [i]

The relevant Spike protein (S) amino acid positions and substitutions under monitoring are S:R346X, S:K444X, S:V445X, S:N450X and S:N460X. BA.2, BA.4 and BA.5 and their various subvariants have in many cases acquired the same mutations at the same position, indicating convergent evolution. Convergent evolution refers to the independent genetic adaptation of two or more different variants at the same genomic position, i.e., the same nucleotide or amino acid change is observed in multiple variants, with these variants not being direct descendants of each other. Areas of convergent evolution point to a potential role in the adaptation and further evolution of the virus. Convergent evolution can be effective in identifying the drivers of phenotypic adaptation and effect. Furthermore, it shows the ongoing adaptive potential of the virus to further evolve.

As of 25 October 2022, XBB and XBB.1 have been reported by 35 countries with 1453 sequences. BQ.1 and its descendent lineages are reported from 65 countries with 8077 sequences. BQ.1 is a BA.5 subvariant with additional spike mutations K444T and N460K, while BQ.1.1 also has spike mutation R346T.

The WHO Technical Advisory Group on Virus Evolution (TAG-VE) met on 24 October 2022 to share and evaluate evidence on XBB and BQ.1 . The TAG-VE will publish a statement on these lineages.

[i] WHO tracking SARS-CoV-2 Variants

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

Figure 4. Panel A and B: The number and percentage of SARS-CoV-2 sequences, as of 24 October 2022

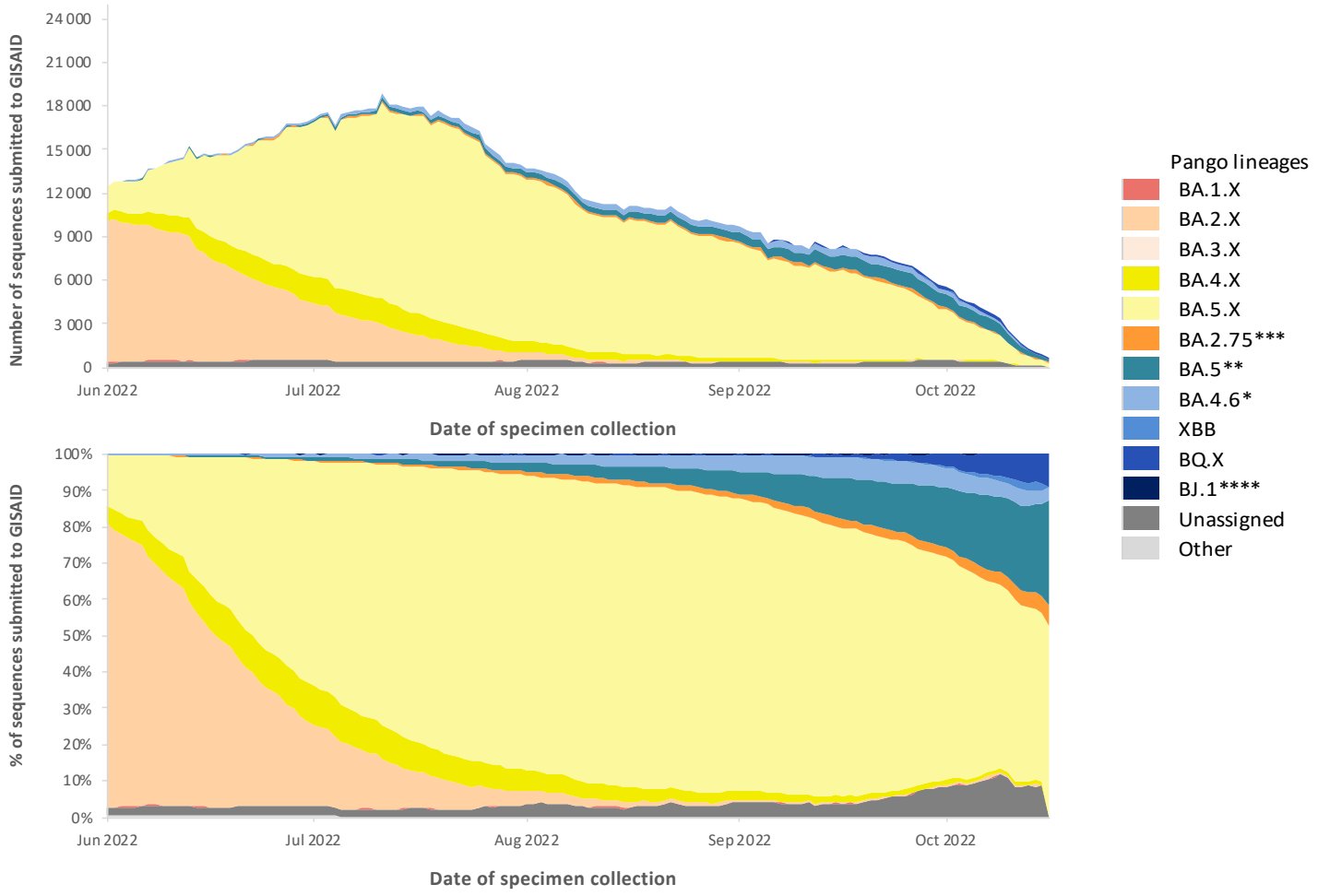


Figure 4 Panel A shows the number, and **Panel B** the percentage, of all circulating variants since June 2022. Omicron sister-lineages and additional Omicron VOC descendent lineages under further monitoring are shown. *BA.1.X, BA.2.X, BA.3.X, BA.4.X* and *BA.5.X* include all BA.1, BA.2, BA.3, BA.4 and BA.5 pooled descendent lineages, except the Omicron subvariants under monitoring shown individually. The *Unassigned* category includes lineages pending for a Pango lineage name, whereas the *Other* category includes lineages that are assigned but not listed in the legend. Source: SARS-CoV-2 sequence data and metadata from GISAID, as of 24 October 2022.

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

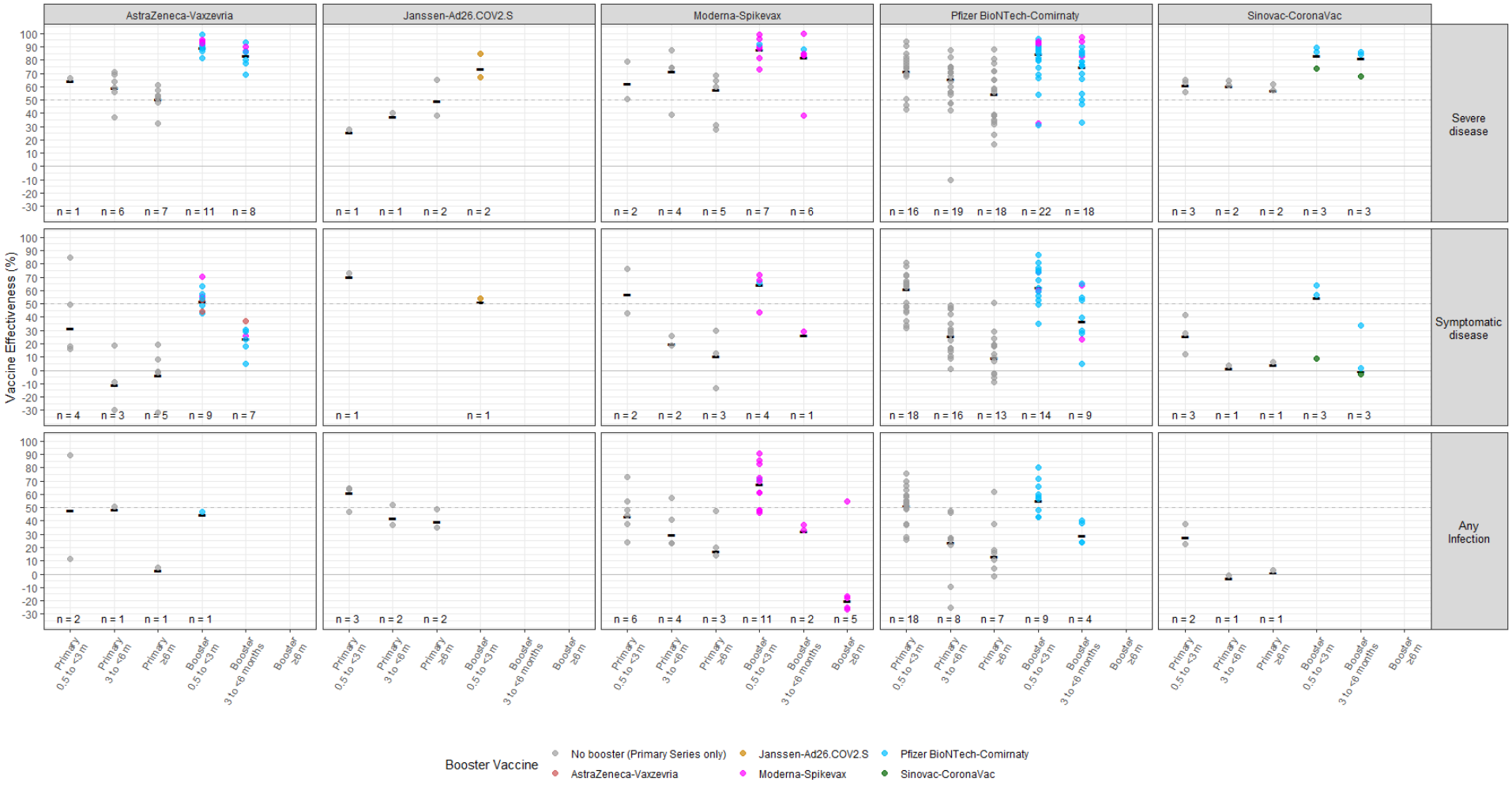
			Last 4 weeks by collection date (%)			
Lineage	**Countries**	**Sequences**	**2022-37**	**2022-38**	**2022-39**	**2022-40**
BA.1.X	184	2 192 470	0.04	0.04	0.02	0.03
BA.2.X	164	2 018 702	2.93	3.12	3.61	4.34
BA.3.X	28	791	0.0	0.0	0.0	0.0
BA.4.X	124	113 056	7.42	7.24	6.68	5.39
BA.5.X	142	1 067 974	85.84	83.47	80.15	77.12
Unassigned	86	102 296	3.49	5.71	8.86	11.68
Other	204	6 595 633	0.17	0.14	0.13	0.15
Omicron subvariants under monitoring						
BA.5 (+ 5 mutations)	103	57 679	11.58	13.75	16.77	20.71
BA.2.75.X	63	15 585	2.27	2.51	2.76	3.22
BA.4.6.X	87	36 469	5.77	5.82	5.48	4.39
BJ.1 (BA.2 subvariant)	11	118	0.01	0.01	0.01	0.01
XBB.X	27	880	0.11	0.27	0.56	1.29
BA.2.3.20.X	27	613	0.21	0.24	0.35	0.36
BQ.1.X (BA.5 subvariant)	51	4 855	0.84	1.64	3.51	5.96

Table 2 shows the number of countries reporting the highlighted lineages, the total number of sequences reported and the prevalence of the lineages for the last four weeks. *BA.1.X, BA.2.X, BA.3.X, BA.4.X* and *BA.5.X* include all BA.1, BA.2, BA.3, BA.4 and BA.5 pooled descendent lineages. The *Unassigned* category includes lineages pending for a Pango lineage name, whereas the *Other* category includes lineages other than those listed in the legend. The Omicron subvariants under monitoring are updated regularly, more detailed information can be found at the WHO variant tracking site. Data source: sequences and metadata from GISAID, retrieved on 24 October 2022.

Table 3. Summary of phenotypic characteristics of the Omicron VOC

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 [1]	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 [2–7]. However, more recent studies report lower[8] or similar severity [9]	There is evidence of similar severity compared to BA.2 [10] . However, there is contrasting evidence in favor of similar [11] or higher disease severity compared to BA.4 and BA.5 [12]	Similar disease severity compared to BA.1 [10]. There is evidence, both in favor of higher severity [12] compared to BA.4 and BA.5, as well as in support of similar disease severity compared to BA.4 and BA.5 [13]	One preliminary study suggests lower severity compared to BA.1 and BA.2 [12] while another study reported similar disease severity compared to BA.1 [11]	A preliminary study suggested increased severity compared to BA.1 and BA.2[14], while another study found lower disease severity compared to BA.1 and BA.2[12]. A recent study found no difference in severity compared to BA.1 [11]
Risk of reinfection	Reduced risk of Omicron reinfection among individuals previously infected with a different SARS-CoV-2 variant compared to immune-naïve individuals [15,16]	Earlier studies reported reduced risk of reinfection with BA.1 after infection with BA.2 [15]. However, a recent study reported increased risk of reinfection following prior infection with any Omicron sublineage, as compared to non-Omicron VOCs [17]	There is a reduced risk of reinfection following infection with BA.1 reported in earlier [15] and more recently studies [18]. However, a recent study reported increased risk of reinfection following prior infection with any Omicron sub-lineage, as compared to non-Omicron VOCs[17]	There is varying evidence regarding the risk of reinfection. One study reported protection against infection following previous BA.2 infection [19]. A recent study reported increased risk of reinfection following prior infection with any Omicron sublineage, as compared to non-Omicron VOCs [17], while another reported reduced risk of reinfection following prior infection with any Omicron sublineage, as compared to non-Omicron VOCs [20]	There is varying evidence regarding the risk of reinfection. One study reported protection against infection following previous BA.2 infection[19]. A recent study reported increased risk of reinfection following prior infection with any Omicron sublineage, as compared to non-Omicron VOCs[17], while another reported reduced risk of reinfection following prior infection with any Omicron sublineage, as compared to non-Omicron VOCs [20]
Impact on antibody responses	Reduced neutralizing activity reported as compared to other VOCs [21–23]	Lower neutralizing antibody titers compared to the index virus [23]	Lower neutralizing antibody titers compared to the index virus [23]	Lower neutralizing antibody titers compared to BA.1 [24,25]	Lower neutralizing antibody titers compared to BA.1 [24–26]
Impacts on diagnostics	PCR assays that include multiple gene targets maintain their accuracy to detect Omicron[27]; S gene target failure/positivity (SGTF) may be a proxy for screening. Limited to no impact on sensitivity of Ag-RDTs observed [28–31]	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[32]. Conserved neutralizing activity for three broadly neutralizing monoclonal antibodies (sotrovimab, S2X259 and S2H97) and reduced effectiveness of other monoclonal antibodies [33–35]	Reduced neutralization activity of sotrovimab and casirivimab-imdevimab [36]	Reduced neutralization activity of sotrovimab and casirivimab-imdevimab [36]	Reduced neutralization activity of sotrovimab and casirivimab-imdevimab [36]	Reduced neutralization activity of sotrovimab and casirivimab-imdevimab [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				

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



Dots represent point estimates of VE from each study; dark black horizontal lines represent median VE across all studies in stratum. All data are from a systematic review of COVID-19 VE studies; methods and summary tables of VE studies can be found on view-hub.org. Vertical panels represent VE for full primary series (grey dots) and VE for homologous or heterologous booster vaccination (other colored dots) following completion of primary series vaccination with vaccine of primary series noted in column header. All booster VE estimates are for first booster dose. Severe disease includes hospitalization; symptomatic disease includes disease of any severity level; any infection can include symptomatic and asymptomatic infection. Not shown in plot: VE against severe disease at 0.5-<3 month post primary series of Beijing CNBG-BBIBP-CorV (59%, 95% CI: 4 to 80%) 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). All vaccines included in Figure 5 are vaccines based on the ancestral SARS-CoV-2 strain; no VE data is yet available for variant-based vaccines. Additional information on vaccine performance against VOCs can also be found in Annex 3.

Since the last update on 21 September 2022, six new studies have been added to Figure 5. Two studies assessed the VE of a primary series of Pfizer BioNTech-Comirnaty against infection and symptomatic disease due to Omicron over time among adolescents in the United States and Scotland, UK, respectively, while a third evaluated VE of two and three doses of Pfizer BioNTech against infection among healthcare workers in Italy.[37–39] A fourth study assessed the VE Pfizer BioNTech-Comirnaty, Moderna-Spikevax, and Janssen-Ad26.Cov2.S against infection, hospitalization, and death due to Omicron among adults in the United States.[40] A fifth study (not yet peer-reviewed) estimated VE of two and three doses of Pfizer BioNTech-Comirnaty and of Moderna-Spikevax against emergency department/urgent care encounters and hospitalization due to the Omicron BA.4 or BA.5 sub-lineages among adults in the United States.[41] Finally, a sixth study (not yet peer-reviewed) provided evidence for the VE of three doses of Moderna-Spikevax against infection and hospitalization due to each of the Omicron BA.1, BA.2, BA.2.12.1, BA.4, and BA.5 sublineages among adults in the United States.[42]

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

To date, 49 studies from 18 countries (Argentina, Brazil, Canada, Chile, Czech Republic, Denmark, Finland, 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 with evidence for the five vaccines with more than one VE estimate shown in Figure 5 (19 studies contributed VE estimates of primary series vaccination only to the plot, six contributed estimates of the first booster vaccination only, and 24 contributed to both). Findings from these studies show reduced VE of COVID-19 primary series vaccines against the Omicron variant for all outcomes (*severe disease*, *symptomatic disease*, and *infection*) compared to those that have been observed for the original SARS-CoV-2 strain and the other four VOCs (plots of VE against other VOCs can be found on the VIEW-hub.org Resource Page). Importantly though, VE estimates against the Omicron variant remain higher for *severe disease* than the other outcomes for Omicron, 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[43]; 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. During the first three months after primary series vaccination, VE was ≥70% for 12 of 18 (67%) VE estimates for the mRNA vaccines (Moderna-Spikevax and Pfizer BioNTech-Comirnaty). Of the three vector vaccines studies available all had VE <70%: two reported VE <70% for AstraZeneca-Vaxzevria and Gamaleya-Gam-Covid-Vac, and the other reported VE <50% for Janssen-Ad26.COV2.S. Four estimates were available for inactivated vaccines: all three estimates for Sinovac-CoronaVac and the single estimate for Beijing CNBG-BBIBP-CorV (Sinopharm) were < 70%, but ≥ 50%. (The single estimates for Beijing CNBG-BBIBP-CorV (Sinopharm) and Gamaleya-Gam-Covid-Vac are not shown in the figure.) Beyond three months after vaccination with the primary series, VE was ≥70% for 17 of 46 (37%) VE estimates for the mRNA vaccines (31 [67%] had VE ≥50%); one of 13 (8%) AstraZeneca-Vaxzevria VE estimates was ≥70% (10 [77%] were ≥50%); none of

the three estimates for a single dose of the other vector-based vaccine, Janssen-Ad26.COV2.S, was ≥70% (one [33%] was ≥50%); the four VE estimates for Sinovac-CoronaVac were ≥50% but <70%.

The first booster dose vaccination improved VE against *severe disease* in all studies, and VE was ≥70% in 39 (87%) of 45 estimates evaluating VE between 14 days and three months of receipt of a booster dose (42 estimates evaluated an mRNA booster, two evaluated a Janssen-Ad26.COV2.S booster, and one evaluated a Sinovac-CoronaVac booster); one Pfizer BioNTech-Comirnaty booster dose VE and one Moderna-Spikevax booster dose VE were <50% (though confidence intervals were wide particularly for Moderna-Spikevax). At three to six months post mRNA booster, VE was ≥70% for 27 of 35 (77%) estimates (the primary series was an mRNA vaccine in 24 of the 35 estimates, AstraZeneca-Vaxzevria in eight and Sinovac-CoronaVac in three). One study found the VE to be <70% but ≥50% 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 rapidly over time. For *symptomatic disease*, only five of 20 (25%) VE estimates for the mRNA vaccines were ≥70% and only 12 (60%) were ≥50%; one (25%) of the four VE estimates for AstraZeneca-Vaxzevria was ≥70% while the remaining three estimates were <50%; the single estimate for Janssen-Ad26.COV2.S was ≥70%, and all three estimates for Sinovac (CoronaVac) were <50%. Beyond three months after vaccination, only one of 44 (2%) VE estimates was ≥50% (34 estimates evaluated mRNA vaccines, eight evaluated AstraZeneca-Vaxzevria, and two evaluated Sinovac-CoronaVac). mRNA booster vaccination after completion of a primary series of an mRNA vaccine, AstraZeneca-Vaxzevria, or Sinovac-CoronaVac improved VE against *symptomatic disease*: eight of 27 (30%) VE estimates between 14 days and three months post booster were ≥70%, although 22 (81%) were ≥50%; one (50%) of two VE estimates evaluating three doses of AstraZeneca-Vaxzevria was ≥50% but <70%; the single estimate for two doses of Janssen-Ad26.CoV2.S was ≥50% but <70%, and the single estimate for three doses of Sinovac-CoronaVac was <50%. First booster dose protection declined rapidly over time: only four of 18 (22%) estimates available at three to six months following receipt of an mRNA booster dose had VE ≥50% and none were ≥70%. Neither the single VE estimate for three doses of AstraZeneca-Vaxzevria nor the single estimate for three doses of Sinovac-CoronaVac assessed three to six months post booster vaccination was above 50%. VE against *infection* showed a similar pattern of steep waning as that against *symptomatic disease*.

Of note, two recent studies (not yet peer reviewed) among adults in the United States provided new evidence of vaccine effectiveness against Omicron sub-lineages. One study assessed VE of two and three doses of both Pfizer BioNTech-Comirnaty and Moderna-Spikevax *against emergency department/urgent care encounters* and *hospitalization* due to Omicron BA.4/BA.5 among adults and found similar magnitude of VE, as well as patterns of decreasing effectiveness over time for Omicron BA.4/BA.5 as was observed previously for BA.2/BA.2.12.1, but lower magnitude of VE than that observed for Omicron BA.1.[41] Similarly, the second study found that the VE of three doses of Moderna-Spikevax against *infection* declined more rapidly over time for BA.2, BA.2.12.1, BA.4, and BA.5 (VE ranged from 61-91% at 14-30 days with protection lost by 150 days post third dose) compared to BA.1 (VE of 86% at 14-30 days declining to 55% at 150 days post third dose); VE against *hospitalization* due to BA.4 and BA.5 combined (72%, 95% CI: 24-90%) was lower than BA.2 (82%, 95% CI: 65-91%) and BA.1 (98%, 95% CI: 96-98%) over the entire study period with a maximum potential follow-up time of approximately nine months post receipt of a third dose.[42]

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

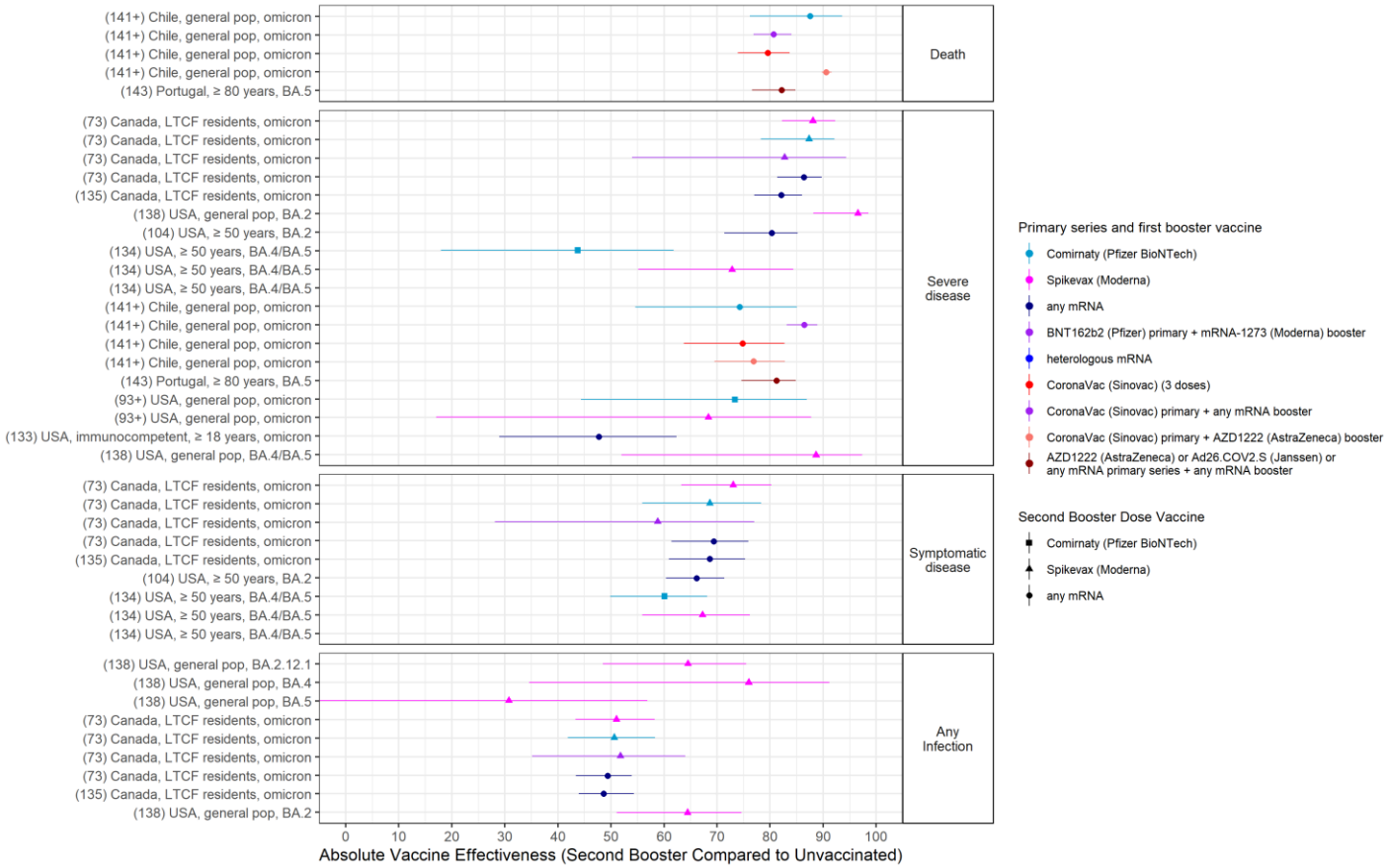
Nine studies have evaluated *absolute VE* of a second booster dose of mRNA vaccines, comparing infection and disease events among persons receiving four doses to an unvaccinated comparison group. VE of a second mRNA booster against death, severe disease, symptomatic disease, and infection due to Omicron was ≥70% among 100%

(five/five), 84% (16/19), 11% (one/nine), and 11% (one/nine) of estimates, respectively (Figure 6). Limited evidence is available on the duration of protection of a second booster dose; however, three studies found similar declines over time as has been seen with the first booster dose.[41,42,44]

To date 16 studies (see Figure 7), conducted among long-term care facility residents, older adults, healthcare workers, and adults 18 years and older have assessed *relative VE* of a second booster dose of mRNA vaccines, by comparing the risk of Omicron infection, disease, and death among persons receiving four doses to persons having received only a first booster dose of mRNA vaccines at various time points ranging from relatively recently up to nine months ago. For all outcomes, a fourth dose achieved marginal gains in VE compared to three doses (Figure 7). Relative VE of four doses of mRNA vaccine is higher for severe disease and death than for symptomatic disease and infection.

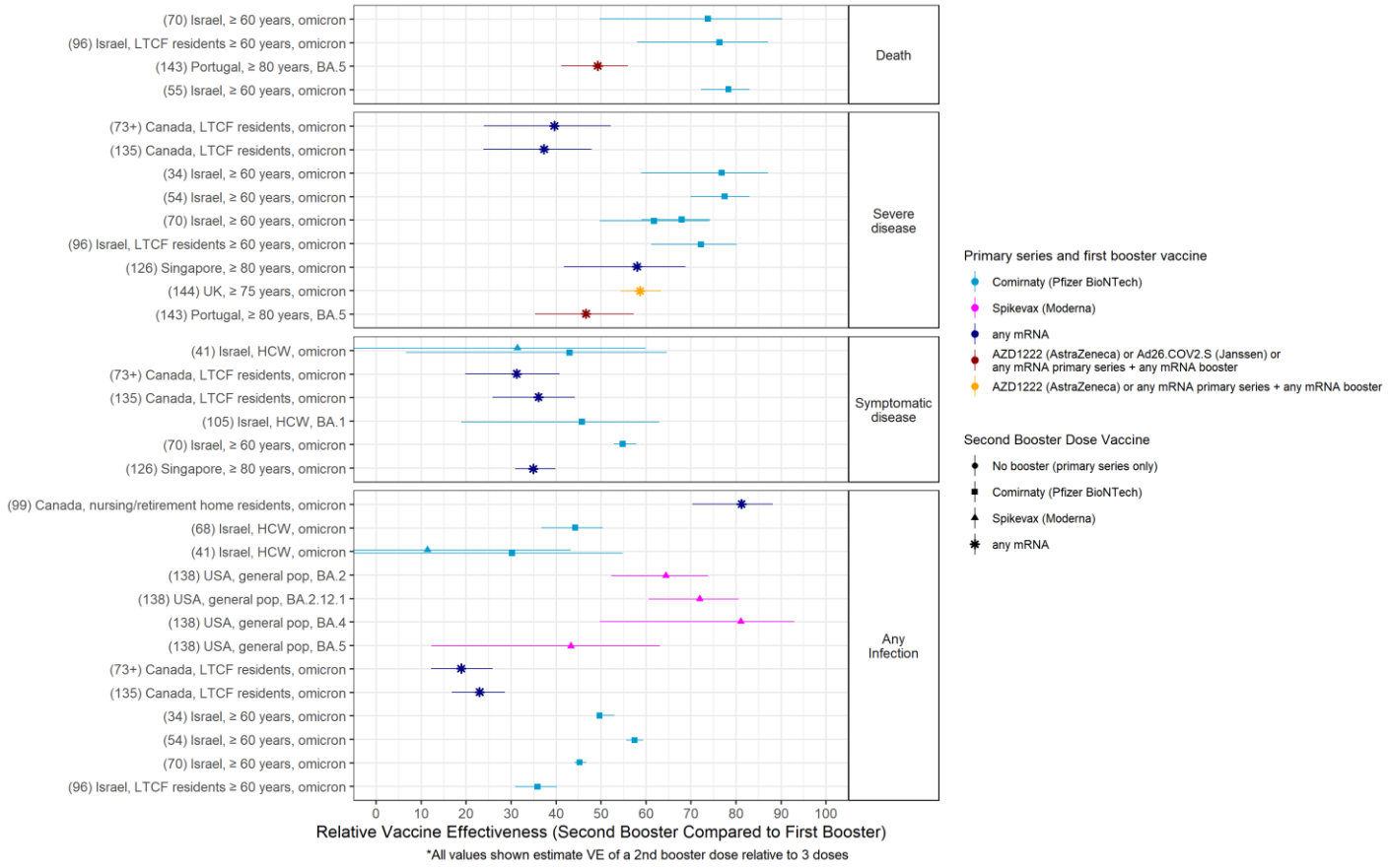
It is important to note that interpretation of relative VE is not straightforward; it cannot be translated into absolute VE or cases prevented after a second booster dose. Moreover, relative VE cannot be compared across studies due to differences in the absolute VE (which is often not reported) and epidemiological 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 29 June 2022 edition of the Weekly Epidemiological Update.

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



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

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



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

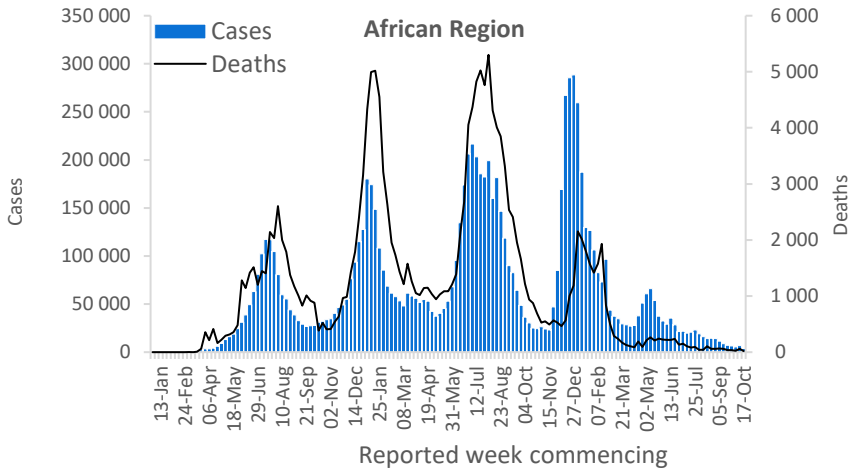
WHO regional overviews:

Epidemiological week 17 - 23 October 2022**

African Region

The Africa Region reported over 3900 new cases, a 41% decrease compared to the previous week. Six (12%) countries reported increases in the number of new cases of 20% or greater, with some of the greatest proportional increases seen in the Democratic Republic of the Congo (55 vs four new cases; +1275%), Kenya (178 vs 78 new cases; +128%) and Algeria (41 vs 29 new cases; +41%). The highest numbers of new cases were reported from South Africa (2017 new cases; 3.4 new cases per 100 000 population; -22%), Réunion (340 new cases; 38.0 new cases per 100 000; +1%) and Comoros (191 new cases; 22.0 new cases per 100 000; +3720%).

The number of new weekly deaths in the Region decreased by 72% as compared to the previous week, with 17 deaths reported. The highest numbers of new deaths were reported from South Africa (11 new deaths; <1 new death per 100 000 population; -79%), Réunion (two new deaths; <1 new death per 100 000; similar to the previous week) and Togo (two new deaths; <1 new death per 100 000; +100%).

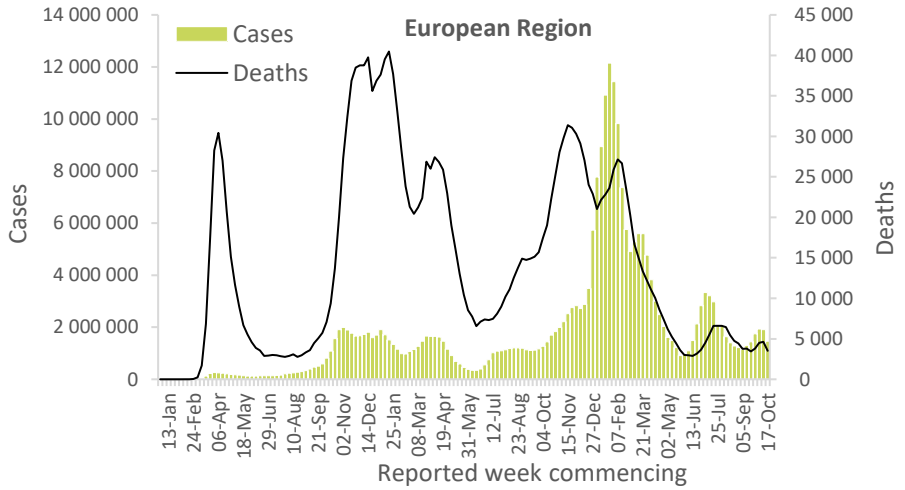


Updates from the African Region

Region of the Americas

The Region of the Americas reported over 365 000 new cases, a 2% increase compared to the previous week. Ten of 56 (18%) 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 Sint Maarten (32 vs 11 new cases; +191%), Curaçao (28 vs 16 new cases; +75%) and Paraguay (368 vs 221 new cases; +67%). The highest numbers of new cases were reported from the United States of America (255 116 new cases; 77.1 new cases per 100 000; -1%), Chile (34 497 new cases; 180.5 new cases per 100 000; +38%) and Brazil (34 180 new cases; 16.1 new cases per 100 000; +9%).

The number of new weekly deaths reported in the Region decreased by 1% as compared to the previous week, with over 3400 new deaths reported. The highest numbers of new deaths were reported from the United States of America (2538 new deaths; <1 new death per 100 000; similar to the previous week), Brazil (383 new deaths; <1 new death per 100 000; +12%) and Canada (278 new deaths; <1 new death per 100 000; +18%).

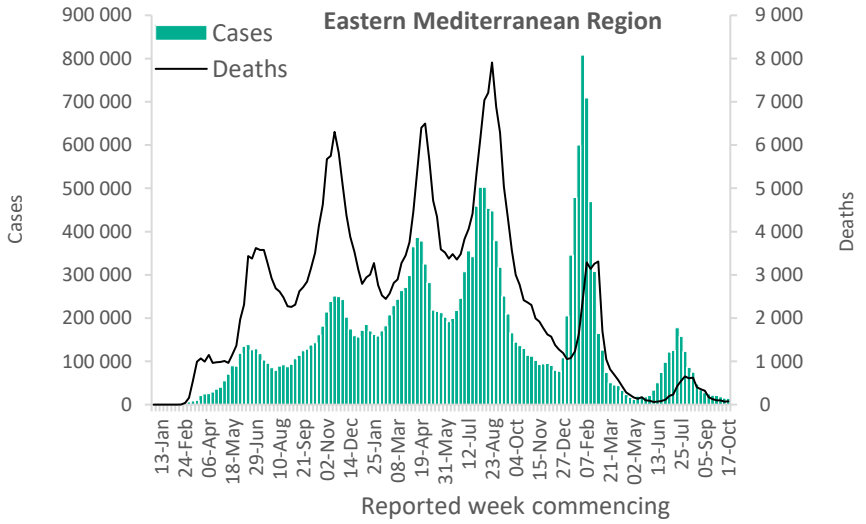


Updates from the Region of the Americas

Eastern Mediterranean Region

The Eastern Mediterranean Region reported just under 14 000 new cases, a 9% decrease as compared to the previous week. Six (27%) countries reported increases in new cases of 20% or greater, with the highest proportional increases observed in Lebanon (1083 vs 361 new cases; +200%), Morocco (181 vs 115 new cases; +57%) and Saudi Arabia (1564 vs 1102 new cases; +42%). The highest numbers of new cases were reported from Qatar (3732 new cases; 129.5 new cases per 100 000; -19%), the United Arab Emirates (2262 new cases; 22.9 new cases per 100 000; +11%), and Bahrain (2084 new cases; 122.5 new cases per 100 000; +3%).

The number of new weekly deaths increased in the Region by 9% as compared to the previous week, with 73 new deaths reported. The highest numbers of new deaths were reported from the Islamic Republic of Iran (27 new deaths; <1 new death per 100 000; -29%), Saudi Arabia (13 new deaths; <1 new death per 100 000; -7%) and Lebanon (11 new deaths; <1 new death per 100 000; +175%).

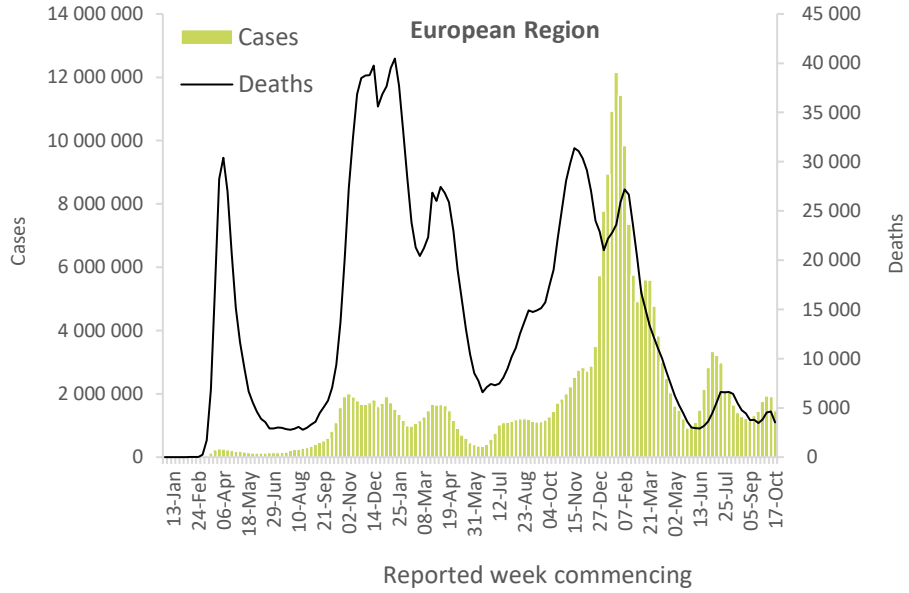


Updates from the Eastern Mediterranean Region

European Region

In the European Region, the number of new weekly cases decreased by 23% as compared to the previous week, with over 1.4 million new cases reported. Three (5%) countries reported increases in new cases of 20% or greater, with the highest proportional increases observed in Monaco (87 vs 66 new cases; +32%), Malta (184 vs 147 new cases; +25%) and Spain (25 422 vs 20 652 new cases; +23%). The highest numbers of new cases were reported from Germany (498 787 new cases; 599.7 new cases per 100 000; -23%), France (307 610 new cases; 473.0 new cases per 100 000; -22%) and Italy (252 777 new cases; 423.8 new cases per 100 000; -12%).

Over 3500 new weekly deaths were reported in the Region, a 24% decrease as compared to the previous week. The highest numbers of new deaths were reported from the Russian Federation (636 new deaths; <1 new death per 100 000; -9%), Italy (586 new deaths; 1.0 new death per 100 000; +23%) and France (484 new deaths; <1 new death per 100 000; +21%).

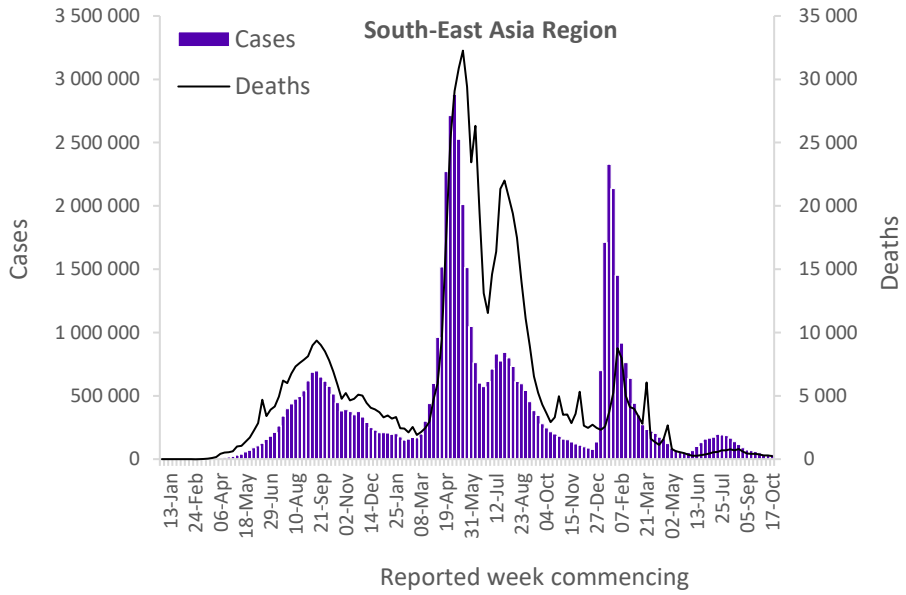


Updates from the European Region

South-East Asia Region

The South-East Asia Region reported just under 35 000 new cases, a 4% 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 (83 vs 48 new cases; +73%), Sri Lanka (73 vs 52 new cases; +40%) and the Maldives (86 vs 69; +25%). The highest numbers of new cases were reported from Indonesia (14 093 new cases; 5.2 new cases per 100 000; +18%), India (13 914 new cases; 1.0 new cases per 100 000; -17%) and Thailand (2616 new cases; 3.7 new cases per 100 000; +17%).

The Region reported over 200 deaths, a 13% decrease as compared to the previous week. The highest numbers of new deaths were reported from Indonesia (116 new deaths; <1 new death per 100 000; +7%), India (66 new deaths; <1 new death per 100 000; -31%) and Thailand (40 new deaths; <1 new death per 100 000; -25%).

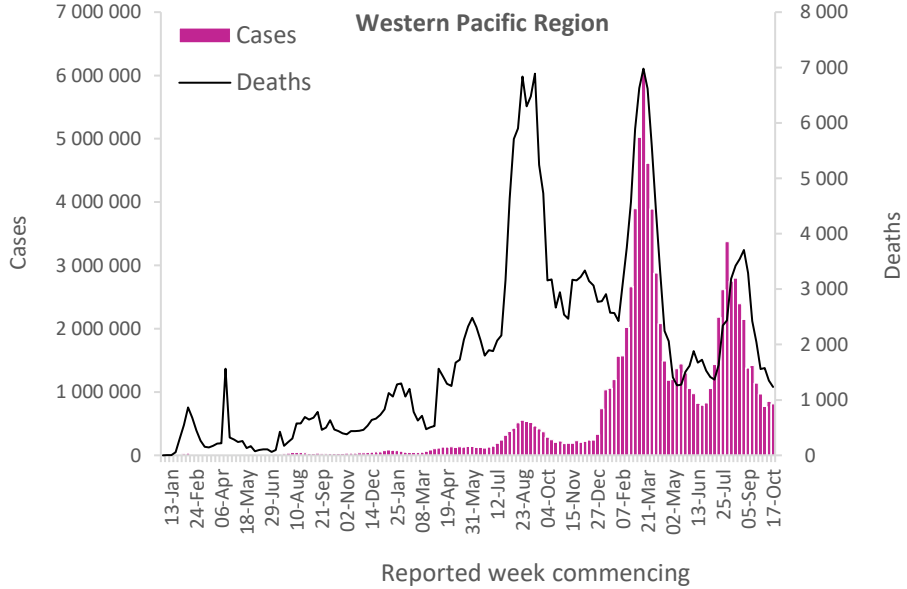


Updates from the South-East Asia Region

Western Pacific Region

The Western Pacific Region reported over 812 000 new cases, a 5% decrease as compared to the previous week. Two (6%) countries reported increases in new cases of 20% or greater, with the largest proportional increases observed in Fiji (nine vs three new cases; +200%) and Malaysia (14 525 vs 11 957 new cases; +21%). The highest numbers of new cases were reported from China (285 348 new cases; 19.4 new cases per 100 000; -13%), Japan (233 682 new cases; 184.8 new cases per 100 000; +7%) and the Republic of Korea (176 869 new cases; 345.0 new cases per 100 000; +18%).

The Region reported an 8% decrease in new weekly deaths as compared to the previous week, with over 1200 deaths reported. The highest numbers of new deaths were reported from China (469 new deaths; <1 new death per 100 000; +9%), Japan (404 new deaths; <1 new death per 100 000; -1%) and the Philippines (159 new deaths; <1 new death per 100 000; -35%).



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.

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

Annex 3. Summary of results of neutralization studies assessing primary series and booster vaccine performance against Omicron variant of concern (data updated 21 October 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	$\downarrow\downarrow_{1}$	----	----	----	----	----
	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_{55}	HNR_{8}	HNR_{1}	HNR_{1}	HNR_{1}	HNR_{3}
	Sinovac-CoronaVac	HNR_{9}	$\downarrow\downarrow\downarrow_{1}$	----	----	----	$\downarrow\downarrow\downarrow_{1}$
Vaccines without WHO EUL	Anhui ZL-Recombinant	----	----	----	----	----	----
	Gamaleya-Sputnik V	HNR_{3}	HNR_{1}	HNR_{1}	----	----	HNR_{1}
	Chumakov-Covi-Vac	HNR_{2}	----	----	----	----	----
First Booster Vaccination (Primary Series Vaccine + Booster Vaccine)							
WHO Emergency Use Listing (EUL) Qualified Booster Vaccines	AstraZeneca-Vaxzevria/SII-Covishield + AstraZeneca-Vaxzevria/SII Covishield	HNR_{2}	HNR_{2}	----	----	$\downarrow\downarrow_{1}$	$\downarrow\downarrow\downarrow_{1}$
	AstraZeneca-Vaxzevria/SII-Covishield + Moderna-Spikevax	$\downarrow_{1}$	----	----	----	----	----
	AstraZeneca-Vaxzevria/SII-Covishield + Pfizer BioNTech-Comirnaty	$\downarrow\downarrow$to$\downarrow\downarrow\downarrow_{2}$	$\downarrow\downarrow_{1}$	----	----	$\downarrow\downarrow_{1}$	----
	Beijing CNBG-BBIBP-CorV + Beijing CNBG-BBIBP-CorV	$\downarrow\downarrow$to$\downarrow\downarrow\downarrow_{4}$	$\downarrow$to$\downarrow\downarrow_{3}$	HNR_{1}	----	$\downarrow\downarrow_{1}$	$\downarrow_{4}$
	Janssen-Ad26-COV2.S + Janssen-Ad26-COV2.S	HNR_{2}	----	----	----	----	----
	Janssen-Ad26-COV2.S + Moderna-Spikevax	$\downarrow\downarrow\downarrow_{1}$	----	----	----	----	----
	Janssen-Ad26-COV2.S + Pfizer BioNTech-Comirnaty	$\downarrow$ to $\downarrow\downarrow\downarrow_{2}$	----	----	----	----	----
	Moderna-Spikevax + Moderna-Spikevax	$\downarrow$to$\downarrow\downarrow\downarrow_{10}$	$\downarrow\downarrow_{2}$	$\downarrow\downarrow_{1}$	$\downarrow_{1}$	$\downarrow\downarrow_{1}$	$\downarrow\downarrow\downarrow_{3}$
	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$\downarrow\downarrow\downarrow_{48}$	$\downarrow$to$\downarrow\downarrow\downarrow_{19}$	$\downarrow$to$\downarrow\downarrow_{5}$	$\downarrow\downarrow_{2}$	$\downarrow$to$\downarrow\downarrow_{5}$	$\downarrow\downarrow\downarrow_{10}$
	Pfizer BioNTech-Comirnaty + Janssen-Ad26-COV2.S	$\downarrow_{2}$	----	----	----	----	----
	Pfizer BioNTech-Comirnaty + Moderna-Spikevax	$\downarrow$to$\downarrow\downarrow_{3}$	----	----	$\downarrow\downarrow\downarrow_{1}$	----	$\downarrow\downarrow\downarrow_{1}$
	Sinovac-CoronaVac + Sinovac-CoronaVac	$\downarrow\downarrow$to$\downarrow\downarrow\downarrow_{7}$	$\downarrow\downarrow$ to$\downarrow\downarrow\downarrow_{5}$	HNR_{2}	----	$\downarrow\downarrow_{1}$	HNR_{4}
	Sinovac-CoronaVac + Pfizer BioNTech-Comirnaty	$\downarrow\downarrow_{5}$	$\downarrow\downarrow$to$\downarrow\downarrow\downarrow_{3}$	$\downarrow\downarrow_{1}$	----	----	$\downarrow\downarrow\downarrow_{2}$
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$\downarrow\downarrow\downarrow_{2}$	$\downarrow\downarrow_{1}$
	Sinovac-CoronaVac + Cansino-Ad5-nCoV-IH	$\downarrow\downarrow\downarrow_{1}$	----	----	----	----	----
Second Booster Vaccination (Primary Series + First Booster Vaccine + Second Booster Vaccine)							
WHO Emergency Use Listing (EUL) Qualified Booster Vaccines	Moderna-Spikevax + Moderna-Spikevax + Moderna-Spikevax	$\downarrow_{1}$	----	----	----	----	----
	Moderna-Spikevax + Moderna-Spikevax + Moderna-Spikevax Bivalent Original/Omicron BA.1	$\downarrow_{1}$	----	----	----	----	$\downarrow\downarrow_{1}$
	Pfizer BioNTech-Comirnaty + Pfizer BioNTech-Comirnaty + Pfizer BioNTech-Comirnaty	$\downarrow\downarrow\downarrow_{1}$	----	----	----	----	----
	Pfizer BioNTech-Comirnaty + Pfizer BioNTech-Comirnaty + Moderna-Spikevax	$\downarrow\downarrow\downarrow_{1}$	----	----	----	----	----

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

Additional notes for the Annex 3 table

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

Annex 4. Methods for Figure 5

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

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