COVID-19 Weekly Epidemiological Update

Edition 101 published 20 July 2022

In this edition:

Global overview

Data as of 17 July 2022

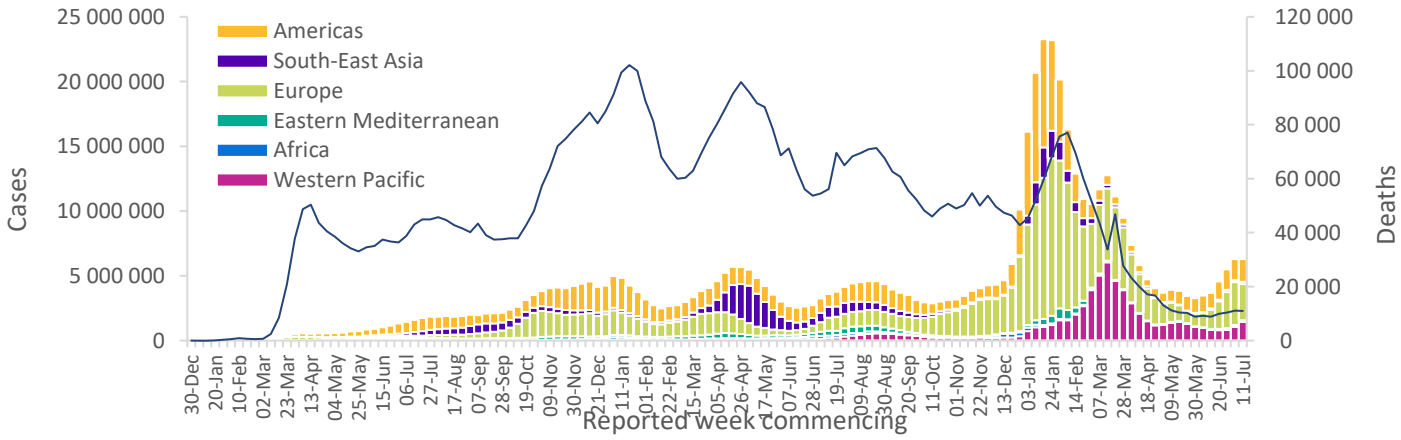
Globally, during the week of 11 to 17 July 2022, the number of weekly cases plateaued, with just under 6.3 million new cases after an increasing trend for the past five weeks (Figure 1). The reported number of new weekly deaths is increasing with 11 000 fatalities reported.

At the regional level, the number of new weekly cases increased in the Western Pacific Region (+37%), the Region of the Americas (+9%) and the South-East Asia Region (+5%), while it decreased in the African Region (-27%) and the European Region (-16%). The number of new weekly cases in the Eastern Mediterranean Region was similar to the figure reported during the previous week. The number of new weekly deaths increased in the South-East Asia Region (+20%), the Eastern Mediterranean Region (+15%) and the Region of the Americas (+7%), while it decreased in the African Region (-39%) and the European Region (-14%). The number of new weekly deaths in the Western Pacific Region was similar to the figure reported during the previous week.

As of 17 July 2022, over 559 million confirmed cases and over 6.3 million deaths have been reported globally.

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 is continuously updated to incorporate regular changes made by countries retrospectively.

Figure 1. COVID-19 cases reported weekly by WHO Region, and global deaths, as of 17 July 2022**



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

At the country level, the highest numbers of new weekly cases were reported from the United States of America (866 479 new cases; +18%), France (757 830 new cases; -15%), Italy (718 925 new cases; +9%), Germany (602 930 new cases; -3%), and Japan (559 111 new cases; +107%). The highest numbers of new weekly deaths were reported from the United States of America (2345 new deaths; +5%), Brazil (1 751 new deaths; +7%), Italy (784 new deaths; +37%), Spain (610 new deaths; -1%), and China (576 new deaths; -17%).

Table 1. Newly reported and cumulative COVID-19 confirmed cases and deaths, by WHO Region, as of 17 July 2022**

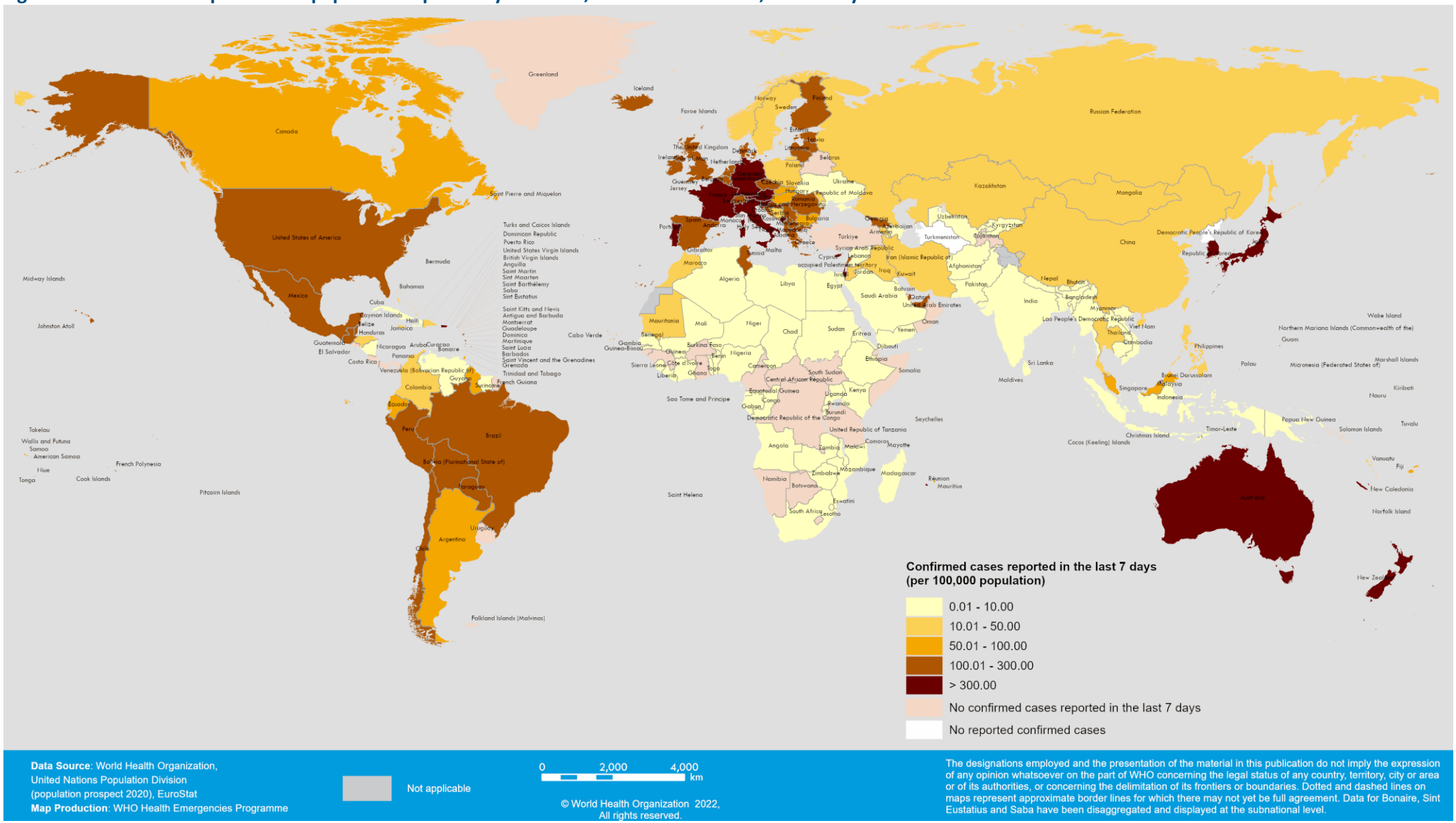
WHO Region	New cases in last 7 days (%)	Change in new cases in last 7 days *	Cumulative cases (%)	New deaths in last 7 days (%)	Change in new deaths in last 7 days *	Cumulative deaths (%)
Europe	2 785 259 (44%)	-16%	235 432 245 (42%)	3 311 (30%)	-14%	2 036 904 (32%)
Americas	1 756 694 (28%)	9%	167 081 979 (30%)	5 470 (50%)	7%	2 775 646 (44%)
Western Pacific	1 444 382 (23%)	37%	66 933 896 (12%)	1 366 (12%)	-3%	241 684 (4%)
South-East Asia	173 854 (3%)	5%	58 967 419 (11%)	538 (5%)	20%	791 164 (12%)
Eastern Mediterranean	120 859 (2%)	-1%	22 288 922 (4%)	228 (2%)	15%	344 024 (5%)
Africa	15 409 (<1%)	-27%	9 175 098 (2%)	87 (1%)	-39%	173 861 (3%)
Global	**6 296 457 (100%)**	**0%**	**559 880 323 (100%)**	**11 000 (100%)**	**-1%**	**6 363 296 (100%)**

**Percent change in the number of newly confirmed cases/deaths in the past seven days, compared to seven days prior*
**See *Annex 1: Data, table, and figure notes*

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

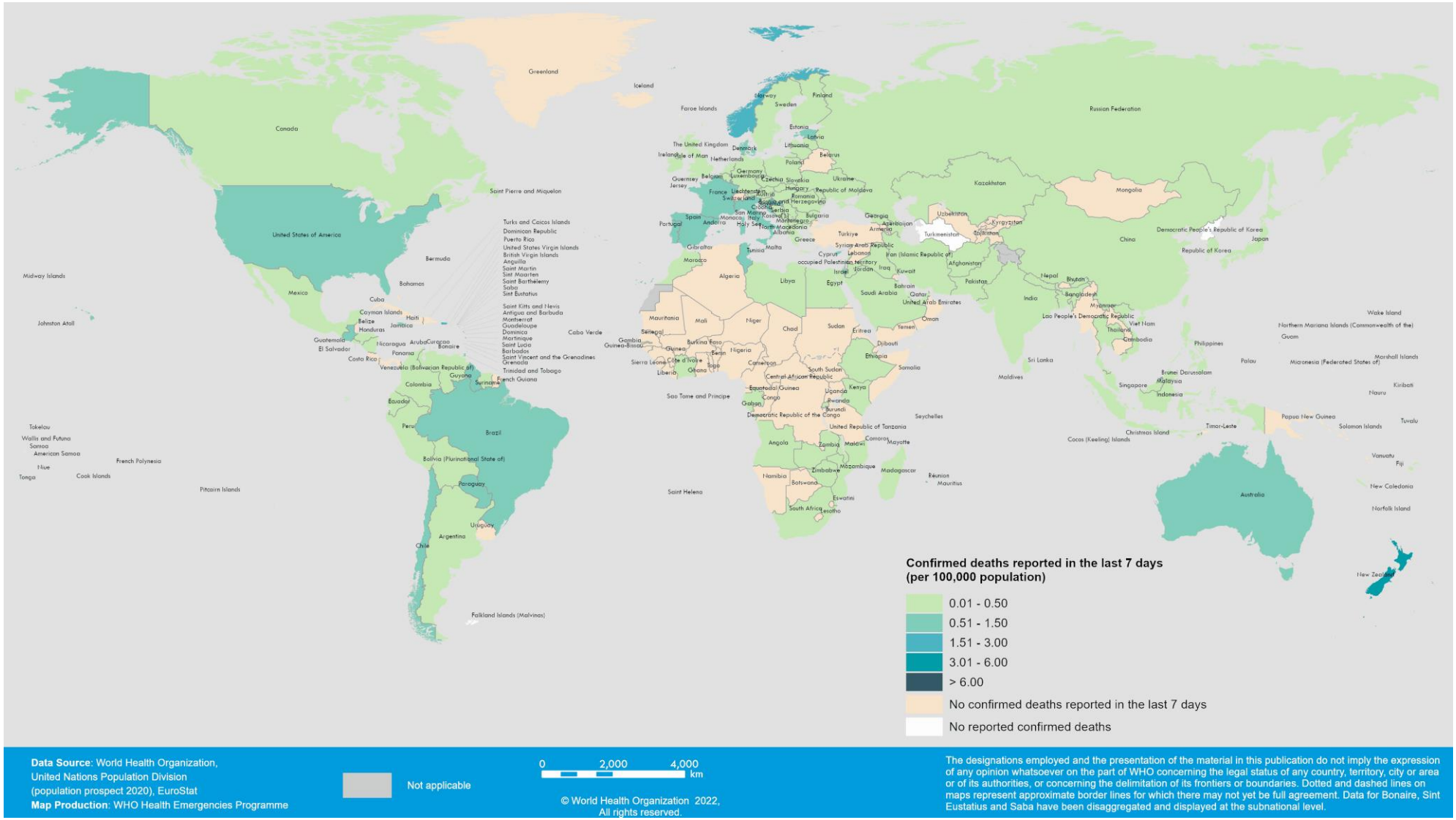
- WHO COVID-19 Dashboard
- WHO COVID-19 Weekly Operational Update and previous editions of the Weekly Epidemiological Update
- WHO COVID-19 detailed surveillance data dashboard

Figure 2. COVID-19 cases per 100 000 population reported by countries, territories and areas, 11 - 17 July 2022*



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

Figure 3. COVID-19 deaths per 100 000 population reported by countries, territories and areas, 11 - 17 July 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 13 June to 13 July 2022, 200 845 SARS-CoV-2 sequences were collected and submitted to GISAID. Among these sequences, the Omicron VOC remains the dominant variant circulating globally, accounting for 95.4% (191 648) of sequences. The remaining 4.4% (8876) sequences are awaiting PANGO lineage designations and 0.2% (321) are Delta and several recombinants.

Among Omicron sequences, as of epidemiological week 27 (4 to 10 July 2022), BA.2 represents 2.61%, while BA.2.12.1 represents 4.51%, BA.4 represents 10.57%, and BA.5 represents 53.59%. Comparing to the proportion of Omicron sequences collected during epidemiological weeks 26 (27 June to 3 July), BA.2 declined from 3.84% to 2.61%, BA.2.12.1 declined from 10.59% to 4.51%, BA.4 declined from 13.21% to 10.57% while BA.5 increased from 51.84% to 53.59%. Based on the data downloaded from GISAID on 18 July 2022, BA.5 has been reported in 100 countries and continues to drive an increase in cases, hospitalisations and ICU admissions.

Several subvariants of Omicron have emerged and some of these are being monitored by WHO[i]. BA.2.75 is an Omicron subvariant under monitoring, with earliest sequences reported from May 2022. BA.2.75 has nine additional mutations in the spike compared to BA.2. There is no evidence yet of the extent to which these mutations impact on transmissibility and disease severity compared to other circulating lineages. As of 18 July, 250 sequences of BA.2.75 from 15 countries have been reported on GISAID.

Current trends describing the circulation of Omicron subvariants should be interpreted with due consideration of the limitations of SARS-CoV-2 surveillance systems, including differences in sequencing capacity and sampling strategies between countries, as well as changes in sampling strategies and reductions in testing and sequences being conducted and shared from countries around the world.

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

[i] WHO tracking SARS-CoV-2 Variants

Figure 4. Panel A and B: The number and percentage of SARS-CoV-2 sequences, as of 18 July 2022

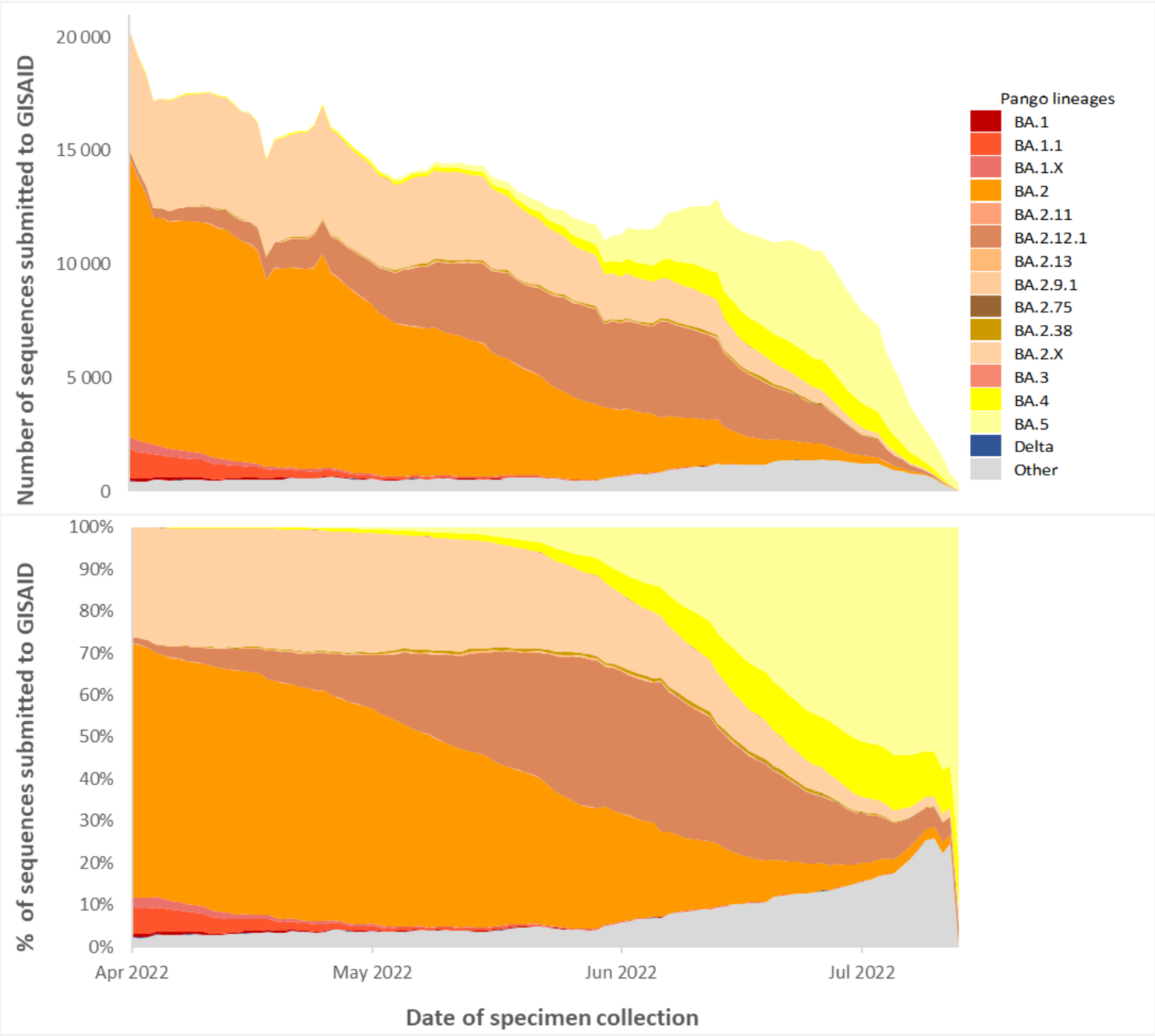


Figure 4 Panel A shows the number and **Panel B** the percentage of all circulating variants since 1 April 2022. Omicron sister-lineages and additional Omicron VOC descendent lineages under further monitoring (VOC-VUM) are shown. BA.1.X and BA.2.X include all BA.1 and BA.2 pooled descendent lineages, except those already shown in the figure above. Source: SARS-CoV-2 sequence data and metadata from GISAID, as of 18 July 202

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

A.

			Last 4 weeks by collection date (%)[b]			
Lineage	**Countries**	**Sequences[a]**	**2022-24**	**2022-25**	**2022-26**	**2022-27**
BA.1	177	482 065	0.01	0.01	0.01	0.00
BA.1.1	183	997 165	0.05	0.02	0.02	0.02
BA.1.X*	179	899 907	0.04	0.03	0.02	0.01
BA.2	153	1 141 038	9.83	6.61	3.84	2.61
BA.2.11	23	815	0.02	0.02	0.00	0.01
BA.2.12.1	95	225 356	22.86	15.83	10.59	4.51
BA.2.13	48	3 737	0.32	0.21	0.14	0.12
BA.2.38	56	6 533	0.89	0.51	0.22	0.16
BA.2.75	15	250	0.09	0.14	0.08	0.05
BA.2.9.1	16	767	0.01	0.00	0.01	0.00
BA.2.X*	147	547 294	9.14	6.05	3.19	2.39
BA.3	42	1 146	0.05	0.02	0.01	0.01
BA.4	88	49 813	11.47	12.15	13.21	10.57
BA.5	100	139 680	34.67	45.07	51.84	53.59
Delta[#]	203	4 362 456	0.01	0.04	0.01	0.00
Other[C]	210	2 776 891	10.54	13.30	16.82	25.95

[a] Data source: sequences and metadata from GISAID, data published on 18 July 2022.

[b] Relative proportions in %.

* BA.1.X and BA.2.X include all BA.1 and BA.2 pooled descendent lineages, except those already shown in the table above.

[#] Previously circulating VOC.

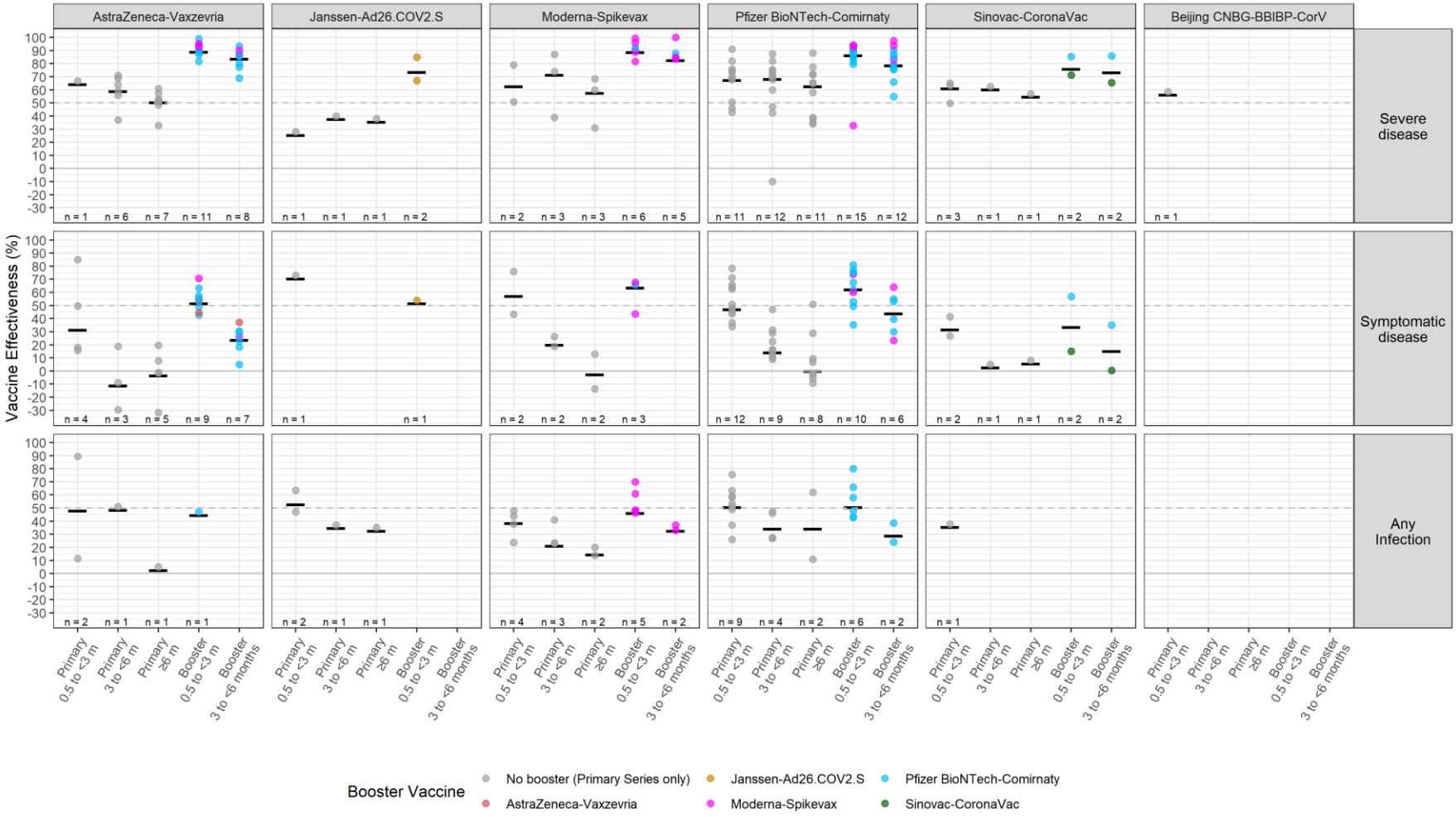
[c] Other includes all omicron lineages which are not listed in the table above as well as sequences which are awaiting PANGO lineage designations (presumed Omicron).

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

Public health domain of impact	Omicron (B.1.1.529)	Omicron sublineages			
		BA.1	BA.2	BA.4	BA.5
Transmissibility	Growth advantage and increased transmissibility compared to Delta [ii]	Lower growth advantage compared to BA.2[1], BA.4 and BA.5 [2]	Lower growth advantage 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 despite contrasting evidence. Earlier studies reported lower severity compared to Delta. [3–7] However, more recent studies in different settings reported similar [8,9] or increased severity[10] compared to Delta.[3–7,11] [12]	No difference in disease severity compared to BA.2, BA.4 and BA.5 [13]	No difference in disease severity compared to BA.4 and BA.5[13]	Currently available evidence does not suggest a difference in disease severity compared to BA.2 and BA.5 [13]	Currently available evidence does not suggest a difference in disease severity compared to BA.2 and BA.4[13]
Risk of reinfection	Reduced risk of Omicron reinfection among individuals previously infected with a different SARS-CoV-2 variant compared to naïve individuals[14,15]	Reduced risk of reinfection with BA.1 after infection with BA.2[15]	Reduced risk of reinfection following infection with BA.1 [15]	Protection against infection following previous BA.2 infection [16]	Protection against infection following previous BA.2 infection [16]
Impact on antibody responses	Reduction in neutralizing activity reported as compared to other VOCs[17–19]	Lower neutralising antibody titers compared to the index virus[19]	Lower neutralising antibody titers compared to the index virus[19]	Lower neutralizing antibody titres (7.6-fold) compared to BA.1 [20,21]	Lower neutralising antibody titres (7.5-fold) compared to BA.1 [20,21]
Impacts on diagnostics	PCR assays that include multiple gene targets maintain their accuracy to detect Omicron[22]; S gene target failure/positivity (SGTF) may be a proxy for screening. Limited to no impact on sensitivity of Ag-RDTs observed[23–26]	S gene target failure	The majority will be S gene target positive	S gene target failure.	S gene target failure.
Impact on treatment	No difference in the effectiveness of antiviral agents (polymerase and protease inhibitors) against the Omicron variant[27]. Conserved neutralizing activity for three broadly neutralizing monoclonal antibodies (sotrovimab, S2X259 and S2H97) and a reduced effectiveness of other monoclonal antibodies[28–31]	Reduced efficacy of cilgavimab[32] and casirivimab-imdevimab[33]	Reduced neutralising activity of sotrovimab, bamlanivimab, casirivimab, etesevimab, imdevimab and tixagevimab [34]	Reduced neutralising activity of sotrovimab, bamlanivimab, casirivimab, etesevimab, imdevimab and tixagevimab. Increased resistance to cilgavimab compared to BA.2[34]	Reduced neutralising activity of sotrovimab, bamlanivimab, casirivimab, etesevimab, imdevimab and tixagevimab. Increased resistance to cilgavimab compared to BA.2[34]
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				

[ii] 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 are provided in text.

Figure 5 summarises 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 3.

Since the last update, one new study (not yet peer reviewed) has been added to the figure. The study assessed the VE of two and three doses of Pfizer BioNTech-Comirnaty against emergency department admissions and hospitalization due to Omicron BA.1 and BA.2 sub-lineages over time among adults 18 years and older in the United States of America.[35]

For more information on the methods for Figure 5 refer to Annex 4.

Interpretation of the results of absolute VE for the Omicron variant

To date, 34 studies from 14 countries (Argentina, Brazil, Canada, Chile, Czech Republic, Denmark, Finland, Norway, Israel, Qatar, South Africa, the United Kingdom, the United States of America, and Zambia) have collectively assessed the protection of six vaccines against the Omicron variant (12 studies contributed VE estimates of primary series vaccination, four contributed to estimates of first booster vaccination only, and 18 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*) than has been observed for the other four VOCs. Importantly though, VE estimates against the Omicron variant remain higher for *severe disease* than the other outcomes, in the majority of studies. The first booster vaccination substantially improves VE for all outcomes and for all combinations of schedules with estimates available for both primary series and booster vaccination. VE declines more with time after the first booster vaccination for symptomatic disease and infection than it does for severe disease[36]; 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 of the primary series showed little decline over six months. VE was ≥70% during the first three months after primary series vaccination for seven of 13 (54%) VE estimates for the mRNA vaccines (Moderna-Spikevax and Pfizer BioNTech-Comirnaty). Of the two vector vaccines studies 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%] were ≥ 50%); the single estimate for Beijing CNBG-BBIBP-CorV (Sinopharm) was <70% but ≥50%. Beyond three months after vaccination VE was ≥70% for 13 of 33 (39%) VE estimates for the mRNA vaccines (23 [70%] had VE ≥50%); one of 13 (8%) AstraZeneca-Vaxzevria VE estimates was ≥70% (9 [69%] were ≥50%); neither of the two estimates for the other vector-based vaccine, Janssen-Ad26.COV2.S, was ≥50%; the two 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 36 (95%) of 38 estimates evaluating VE between 14 days and three months of receipt of a booster dose (35 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 <50%, and one Janssen-Ad26.COV2.S booster dose had VE <70%. At three to six months post mRNA booster, VE was ≥70% for 25 of 28 (89%) estimates (the primary series was an mRNA vaccine in 19 of the 28 estimates, AstraZeneca-Vaxzevria in eight and Sinovac-CoronaVac in one). 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 substantially over time. For *symptomatic disease*, only three of 14 (21%) VE estimates for the mRNA vaccines were ≥70% and only seven (50%) 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 35 (3%) VE estimates was ≥50% (25 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*: six of 23 (26%) VE estimates between 14 days and three months post booster were ≥70% (18 [78%] were ≥50%); one (50%) of two VE estimates evaluating three doses of AstraZeneca-Vaxzevria was ≥50% but <70%, as was the single estimate for three doses of Janssen-Ad26.COV2.S, and the single estimate for three doses of Sinovac-CoronaVac was <50%. However, first booster dose protection declined rapidly over time: only four of 15 (27%) estimates available at three to six months following receipt of an mRNA booster dose had VE ≥50% and none were ≥70%. Neither the single 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 waning as that against *symptomatic disease.*

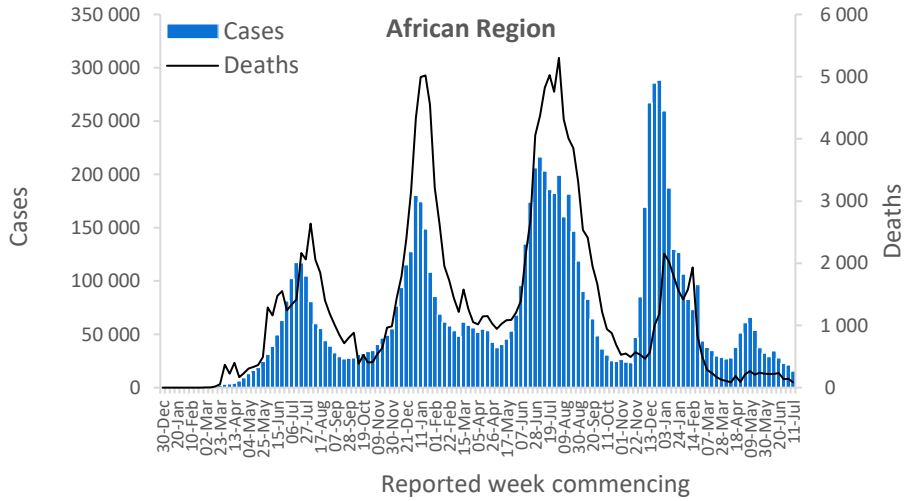
WHO regional overviews:

Epidemiological week 11 - 17 July 2022**

African Region

The African Region reported a decline in the number of new weekly cases, with over 15 000 new cases reported, a 27% decrease as compared to the previous week. Seven (14%) countries reported an increase in the number of new cases of 20% or greater, with the greatest proportional increases seen in Burundi (451 vs 169 new cases; +167%), Senegal (263 vs 133 new cases; +98%), and Eritrea (40 vs 23 new cases; +74%). The highest numbers of new cases were reported from Réunion (3599 new cases; 402 new cases per 100 000 population; +25%), South Africa (2482 new cases; 4.2 new cases per 100 000; +25%), and Zambia (1200 new cases; 6.5 new cases per 100 000; -17%).

The number of new weekly deaths in the Region decreased by 39% as compared to the previous week, with just under 90 new deaths reported. The highest numbers of new deaths were reported from South Africa (42 new deaths; <1 new death per 100 000 population; -34%), Ethiopia (10 new deaths; <1 new death per 100 000; -23%), and Réunion (six new deaths; <1 new death per 100 000; -14%).

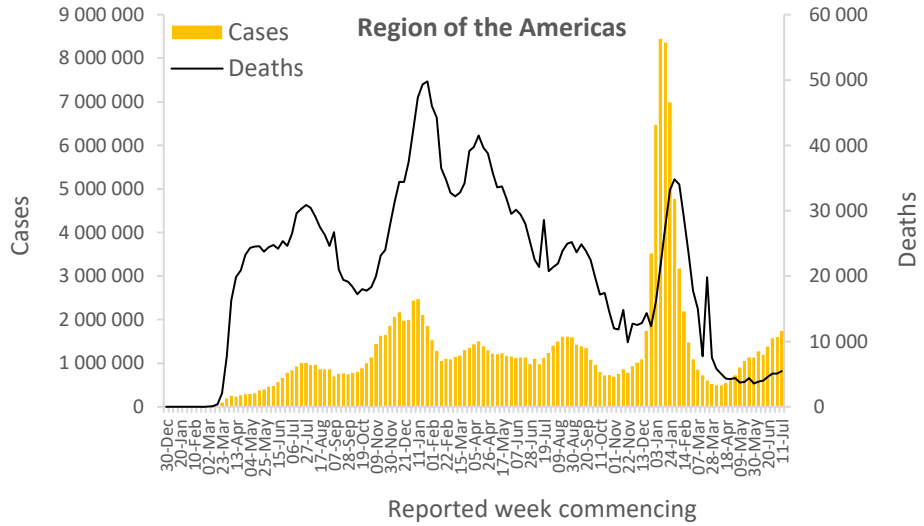


Updates from the African Region

Region of the Americas

The Region of the Americas reported over 1.7 million new cases, a 9% increase as compared to the previous week. Eighteen of 56 (32%) 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 Sint Eustatius (69 vs 18 new cases; +283%), Peru (67194 vs 32889 new cases; +104%), and Saint Vincent and the Grenadines (114 vs 56 new cases; +104%). The highest numbers of new cases were reported from the United States of America (866 479 new cases; 261.8 new cases per 100 000; +18%), Brazil (419 273 new cases; 197.2 new cases per 100 000; +6%), and Mexico (141 241 new cases; 109.5 new cases per 100 000; -20%).

The number of new weekly deaths reported in the Region increased by 7% as compared to the previous week, with over 5000 new deaths reported. The highest numbers of new deaths were reported from the United States of America (2345 new deaths; <1 new death per 100 000; +5%), Brazil (1751 new deaths; <1 new death per 100 000; +7%), and Mexico (315 new deaths; <1 new death per 100 000; +32%).

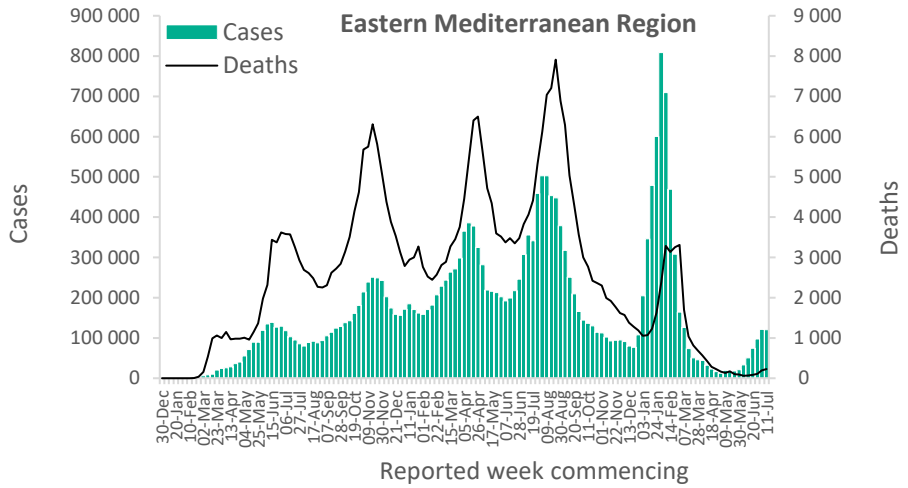


Updates from the Region of the Americas

Eastern Mediterranean Region

After an increasing trend over the past two months, the Eastern Mediterranean Region reported over 120 000 new weekly cases, a figure similar to last week's figure. Six (27%) countries reported increases in the number of new cases of 20% or greater, with some of the highest proportional increases observed in Libya (453 vs 51 new cases; +788%, partly due to batch reporting), the Islamic Republic of Iran (25 126 vs 8761 new cases; +187%), and Jordan (2135 vs 1329 new cases; +61%). The highest numbers of new cases were reported from the Islamic Republic of Iran (25 126 new cases; 29.9 new cases per 100 000; +187%), Tunisia (20 903 new cases; 176.9 new cases per 100 000; +50%), and Iraq (19 217 new cases; 47.8 new cases per 100 000; -34%).

The number of new weekly deaths in the Region increased by 15% as compared to the previous week, with over 200 new deaths reported. The highest numbers of new deaths were reported from Tunisia (75 new deaths; <1 new death per 100 000; +32%), the Islamic Republic of Iran (57 new deaths; <1 new death per 100 000; +46%), and Morocco (27 new deaths; <1 new death per 100 000; -23%).

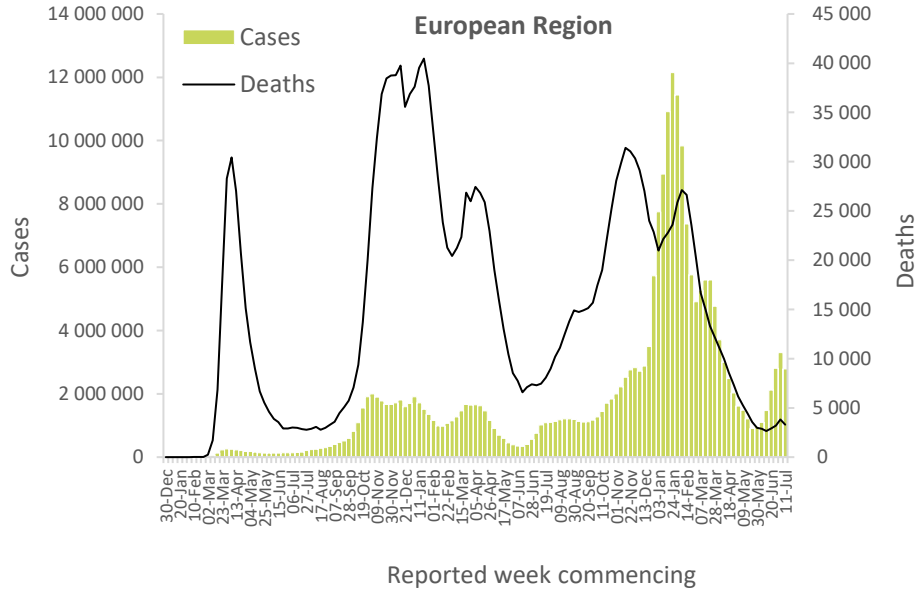


Updates from the Eastern Mediterranean Region

European Region

The European Region reported over 2.7 million new weekly cases, a 16% decrease from the previous week. Twenty (33%) countries in the Region reported increases in new cases of 20% or greater, with the highest proportional increases observed in Kyrgyzstan (485 vs 78 new cases; +522%), Romania (34 582 vs 7726 new cases; +348%), and Kazakhstan (7190 vs 2293 new cases; +214%). The highest numbers of new cases were reported from France (757 830 new cases; 1165.2 new cases per 100 000; -15%), Italy (718 925 new cases; 1205.4 new cases per 100 000; +9%), and Germany (602 930 new cases; 725.0 new cases per 100 000; -3%).

Over 3000 new weekly deaths were reported in the Region, a 14% decrease as compared to the previous week. The highest numbers of new deaths were reported from Italy (784 new deaths; 1.3 new deaths per 100 000; +37%), Spain (610 new deaths; 1.3 new deaths per 100 000; -1%), and France (530 new deaths; <1 new death per 100 000; +30%).

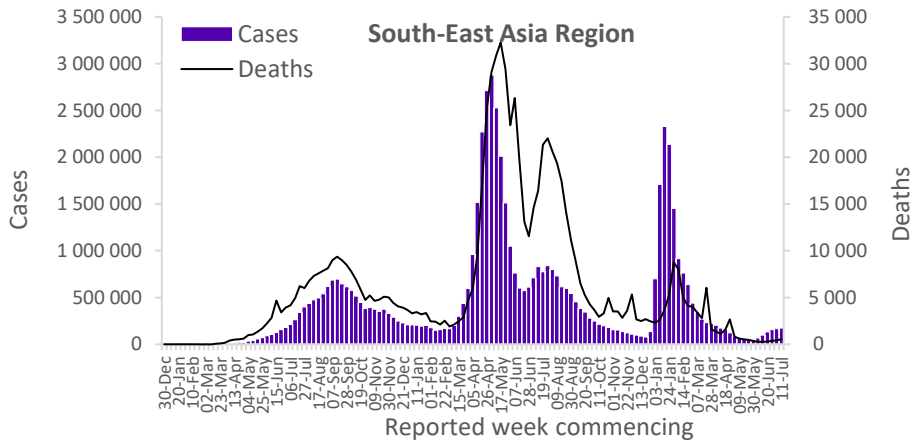


Updates from the European Region

South-East Asia Region

The South-East Asia Region has been reporting an increasing trend in cases since early June, with over 173 000 new cases reported, a 5% increase as compared to the previous week. Three of 10 countries (30%) for which data were available showed increases in the number of new cases of 20% or greater, with the greatest proportional increases observed in Nepal (1091 vs 516 new cases; +111%), Sri Lanka (175 vs 106 new cases; +65%) and Indonesia (23 648 vs 17 388; +36%). The highest numbers of new cases were reported from India (127 948 new cases; 9.3 new cases per 100 000; +6%), Indonesia (23 648 new cases; 8.6 new cases per 100 000; +36%), and Thailand (13 986 new cases; 20 new cases per 100 000; -6%).

The number of new weekly deaths in the Region increased by 20% as compared to the previous week, with over 500 new deaths reported. The highest numbers of new deaths were reported from India (281 new deaths; <1 new death per 100 000; +23%), Thailand (161 new deaths; <1 new death per 100 000; +19%), and Indonesia (58 new deaths; <1 new death per 100 000; +38%).

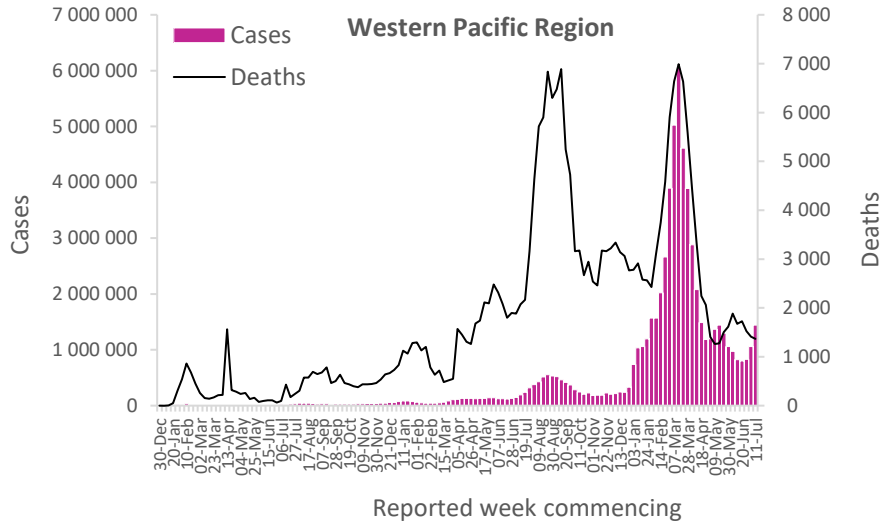


Updates from the South-East Asia Region

Western Pacific Region

The Western Pacific Region reported over 1.4 million new cases, a 37% increase as compared to the previous week. Fourteen (42%) countries reported increases in new cases of 20% or greater, with some of the largest proportional increases observed in the Lao People's Democratic Republic (149 vs 55 new cases; +171%), Japan (559 111 vs 269 760 new cases; +107%), and the Republic of Korea (249 912 vs 122 234 new cases; +104%). The highest numbers of new cases were reported from Japan (559 111 new cases; 442.1 new cases per 100 000; +107%), the Republic of Korea (249 912 new cases; 487.5 new cases per 100 000; +104%), and Australia (229 874 new cases; 901.5 new cases per 100 000; -11%).

The Region reported over 1300 new weekly deaths, similar to the figure reported during the previous week. The highest numbers of new deaths were reported from China (576 new deaths; <1 new death per 100 000; -17%), Australia (293 new deaths; 1.1 new deaths per 100 000; -1%), and Japan (164 new deaths; <1 new death per 100 000; +52%).



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] Since 21 May 2022, data for COVID-19 cases and deaths in Northern Ireland was no longer included in the United Kingdom updates.
[3] 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.

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 11 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_{10}	HNR_{1}	----	----	----
	Beijing CNBG-BBIBP-CorV	HNR_{7}	HNR_{2}	HNR_{1}	HNR_{1}	HNR_{1}
	Bharat-Covaxin	$\downarrow\downarrow_{1}$	----	----	----	----
	Cansino-Convidecia	----	----	----	----	----
	Janssen-Ad26-COV2.S	HNR_{6}	----	----	----	----
	Moderna-Spikevax	$\downarrow\downarrow\downarrow_{10}$	HNR_{2}	----	----	----
	Novavax-Nuvaxovid/SII - Covavax	----	----	----	----	----
	Pfizer BioNTech-Comirnaty	HNR_{47}	$\downarrow\downarrow\downarrow_{2}$	----	HNR_{1}	HNR_{1}
	Sinovac-CoronaVac	$\downarrow\downarrow\downarrow_{1}$	----	----	----	----
Vaccines without WHO EUL	Anhui ZL-Recombinant	----	----	----	----	----
	Gamaleya-Sputnik V	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_{1}	----	----	----	----
	Janssen-Ad26-COV2.S + Pfizer BioNTech-Comirnaty	$\downarrow_{1}$	----	----	----	----
	Moderna-Spikevax + Moderna-Spikevax	$\downarrow$to$\downarrow\downarrow\downarrow_{9}$	$\downarrow\downarrow_{1}$	$\downarrow\downarrow_{1}$	$\downarrow\downarrow_{1}$	$\downarrow\downarrow\downarrow_{1}$
	Moderna-Spikevax + Pfizer BioNTech-Comirnaty	$\downarrow\downarrow\downarrow_{1}$	----	----	----	----
	Pfizer BioNTech-Comirnaty + Pfizer BioNTech-Comirnaty	$\downarrow$to$\downarrow\downarrow\downarrow_{40}$	$\downarrow$to$\downarrow\downarrow_{13}$	$\downarrow$to$\downarrow\downarrow\downarrow_{3}$	$\downarrow$to$\downarrow\downarrow_{4}$	$\downarrow\downarrow$to$\downarrow\downarrow\downarrow_{5}$
	Pfizer BioNTech-Comirnaty + Janssen-Ad26-COV2.S	$\downarrow_{2}$	----	----	----	----
	Pfizer BioNTech-Comirnaty + Moderna-Spikevax	$\downarrow$to$\downarrow\downarrow_{2}$	----	----	----	----
	Sinovac-CoronaVac + Sinovac-CoronaVac	HNR_{6}	$\downarrow\downarrow_{2}$	$\downarrow\downarrow_{1}$	$\downarrow\downarrow_{1}$	$\downarrow\downarrow_{1}$
	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 summarised in the table do not incorporate uncertainty intervals around the fold reductions which can vary substantially across studies when reported.

Annex 4. Methods for Figure 5

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

References

1. Campbell F, Archer B, Laurenson-Schafer H, et al. Increased transmissibility and global spread of SARS-CoV-2 variants of concern as at June 2021. *Eurosurveillance*. 2021;26(24):2100509.

2. UK Health Security Agency. SARS-CoV-2 variants of concern and variants under investigation in England. Technical briefing 43. 24 June 2022. https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/1086494/Technical-Briefing-43-28.06.22.pdf

3. Ferguson N, Ghani A, Hinsley W, Volz E. *Report 50: Hospitalisation Risk for Omicron Cases in England*. Imperial College London; 2021. Accessed December 23, 2021. https://www.imperial.ac.uk/media/imperial-college/medicine/mrc-gida/2021-12-22-COVID19-Report-50.pdf

4. Ulloa AC, Buchan SA, Daneman N, Brown KA. Estimates of SARS-CoV-2 Omicron Variant Severity in Ontario, Canada. *JAMA*. Published online February 17, 2022. doi:10.1001/jama.2022.2274

5. Lewnard JA, Hong VX, Patel MM, Kahn R, Lipsitch M, Tartof SY. *Clinical Outcomes among Patients Infected with Omicron (B.1.1.529) SARS-CoV-2 Variant in Southern California*. Epidemiology; 2022. doi:10.1101/2022.01.11.22269045

6. Nyberg T, Twohig KA, Harris RJ, et al. Risk of hospital admission for patients with SARS-CoV-2 variant B.1.1.7: cohort analysis. *BMJ*. 2021;373:n1412. doi:10.1136/bmj.n1412

7. Wolter N, Jassat W, Walaza S, et al. *Early Assessment of the Clinical Severity of the SARS-CoV-2 Omicron Variant in South Africa*. Infectious Diseases (except HIV/AIDS); 2021. doi:10.1101/2021.12.21.21268116

8. Gunadi, Hakim MS, Wibawa H, et al. *Comparative Analysis of the Outcomes of COVID-19 between Patients Infected with SARS-CoV-2 Omicron and Delta Variants: A Retrospective Cohort Study*. Public and Global Health; 2022. doi:10.1101/2022.04.30.22274532

9. Strasser Z, Hadavand A, Murphy S, Estiri H. *SARS-CoV-2 Omicron Variant Is as Deadly as Previous Waves After Adjusting for Vaccinations, Demographics, and Comorbidities*. In Review; 2022. doi:10.21203/rs.3.rs-1601788/v1

10. Grint DJ, Wing K, Gibbs HP, et al. *Accident and Emergency (AE) Attendance in England Following Infection with SARS-CoV-2 Omicron or Delta*. Infectious Diseases (except HIV/AIDS); 2022. doi:10.1101/2022.05.03.22274602

11. Wang Z, Schmidt F, Weisblum Y, et al. mRNA vaccine-elicited antibodies to SARS-CoV-2 and circulating variants. *Nature*. Published online February 2021. https://www.ncbi.nlm.nih.gov/pubmed/33567448

12. Nyberg T, Ferguson NM, Nash SG, et al. Comparative analysis of the risks of hospitalisation and death associated with SARS-CoV-2 omicron (B.1.1.529) and delta (B.1.617.2) variants in England: a cohort study. *The Lancet*. 2022;399(10332):1303-1312. doi:10.1016/S0140-6736(22)00462-7

13. Faust JS, Renton B, Chen AJ, et al. *The Uncoupling of All-Cause Excess Mortality from Covid-19 Cases and Associated Hospitalizations in Late Winter and Spring of 2022 in a Highly Vaccinated State*. Epidemiology; 2022. doi:10.1101/2022.07.07.22277315

14. Chang CC, Vlad G, Vasilescu ER, et al. *Previous SARS-CoV-2 Infection or a Third Dose of Vaccine Elicited Cross-Variant Neutralizing Antibodies in Vaccinated Solid Organ Transplant Recipients*. Infectious Diseases (except HIV/AIDS); 2022. doi:10.1101/2022.04.13.22273829

15. Carazo S, Skowronski DM, Brisson M, et al. *Protection against Omicron Re-Infection Conferred by Prior Heterologous SARS-CoV-2 Infection, with and without MRNA Vaccination*. Infectious Diseases (except HIV/AIDS); 2022. doi:10.1101/2022.04.29.22274455

16. Altarawneh HN, Chemaitelly H, Ayoub HH, et al. *Protection of SARS-CoV-2 Natural Infection against Reinfection with the Omicron BA.4 or BA.5 Subvariants*. Epidemiology; 2022. doi:10.1101/2022.07.11.22277448

17. Bowen JE, Sprouse KR, Walls AC, et al. *Omicron BA.1 and BA.2 Neutralizing Activity Elicited by a Comprehensive Panel of Human Vaccines*. Immunology; 2022. doi:10.1101/2022.03.15.484542

18. Iketani S, Liu L, Guo Y, et al. Antibody evasion properties of SARS-CoV-2 Omicron sublineages. *Nature*. 2022;604(7906):553-556. doi:10.1038/s41586-022-04594-4

19. Yu J, Collier A ris Y, Rowe M, et al. *Comparable Neutralization of the SARS-CoV-2 Omicron BA.1 and BA.2 Variants*. Infectious Diseases (except HIV/AIDS); 2022. doi:10.1101/2022.02.06.22270533

20. Hachmann NP, Miller J, Collier A ris Y, et al. *Neutralization Escape by the SARS-CoV-2 Omicron Variants BA.2.12.1 and BA.4/BA.5*. Infectious Diseases (except HIV/AIDS); 2022. doi:10.1101/2022.05.16.22275151

21. Cao Y, Yisimayi A, Jian F, et al. *BA.2.12.1, BA.4 and BA.5 Escape Antibodies Elicited by Omicron Infection*. Immunology; 2022. doi:10.1101/2022.04.30.489997

22. Metzger CM, Lienhard R, Seth-Smith HM. PCR performance in the SARS-CoV-2 Omicron variant of concern? *Swiss Med Wkly*. 2021;151(49-50). doi:10.4414/smw.2021.w30120

23. Drain PK, Bemer M, Morton JF, et al. *Accuracy of Rapid Antigen Testing across SARS-CoV-2 Variants*. Infectious Diseases (except HIV/AIDS); 2022. doi:10.1101/2022.03.21.22272279

24. Soni A, Herbert C, Filippaios A, et al. *Comparison of Rapid Antigen Tests' Performance between Delta (B.1.61.7; AY.X) and Omicron (B.1.1.529; BA1) Variants of SARS-CoV-2: Secondary Analysis from a Serial Home Self-Testing Study*. Infectious Diseases (except HIV/AIDS); 2022. doi:10.1101/2022.02.27.22271090

25. Bayart JL, Degosserie J, Favresse J, et al. Analytical Sensitivity of Six SARS-CoV-2 Rapid Antigen Tests for Omicron versus Delta Variant. Published online 2022:9.

26. Bekliz M, Perez-Rodriguez F, Puhach O, et al. *Sensitivity of SARS-CoV-2 Antigen-Detecting Rapid Tests for Omicron Variant*. Infectious Diseases (except HIV/AIDS); 2021. doi:10.1101/2021.12.18.21268018

27. Takashita E, Kinoshita N, Yamayoshi S, et al. Efficacy of Antiviral Agents against the SARS-CoV-2 Omicron Subvariant BA.2. *N Engl J Med*. Published online March 9, 2022:NEJMc2201933. doi:10.1056/NEJMc2201933

28. Planas D, Saunders N, Maes P, et al. *Considerable Escape of SARS-CoV-2 Variant Omicron to Antibody Neutralization*. Immunology; 2021. doi:10.1101/2021.12.14.472630

29. VanBlargan LA, Errico JM, Halfmann PJ, et al. *An Infectious SARS-CoV-2 B.1.1.529 Omicron Virus Escapes Neutralization by Several Therapeutic Monoclonal Antibodies*. Microbiology; 2021. doi:10.1101/2021.12.15.472828

30. Cameroni E, Saliba C, Bowen JE. Broadly neutralizing antibodies overcome SARS-CoV-2 Omicron antigenic shift. Published December 14, 2021. Accessed December 23, 2021. https://www.biorxiv.org/content/10.1101/2021.12.12.472269v1

31. Roche. Ronapreve does not retain neutralising activity against the Omicron variant. Published 2021. Accessed December 17, 2021. https://www.roche.com/dam/jcr:dfe6dcb4-d787-45d6-9b1d-ffc17d667e4c/2021216_Roche%20statement%20on%20Ronapreve%20Omicron.pdf

32. Arora P, Kempf A, Nehlmeier I, et al. Augmented neutralisation resistance of emerging omicron subvariants BA.2.12.1, BA.4, and BA.5. *The Lancet Infectious Diseases*. Published online June 2022:S1473309922004224. doi:10.1016/S1473-3099(22)00422-4

33. WHO: Therapeutics and COVID-19: living guideline. https://www.who.int/publications/i/item/WHO-2019-nCoV-therapeutics-2022.4

34. Yamasoba D, Kosugi Y, Kimura I, et al. *Sensitivity of Novel SARS-CoV-2 Omicron Subvariants, BA.2.11, BA.2.12.1, BA.4 and BA.5 to Therapeutic Monoclonal Antibodies*. Microbiology; 2022. doi:10.1101/2022.05.03.490409

35. Tartof SY, Slezak JM, Puzniak L, et al. BNT162b2 Effectiveness and Durability Against BA.1 and BA.2 Hospital and Emergency Department Admissions in a Large US Health System: A Test-Negative Design. Published online June 30, 2022. doi:10.2139/ssrn.4150500

36. Higdon MM, Baidya A, Walter KK, et al. Duration of effectiveness of vaccination against COVID-19 caused by the omicron variant. *The Lancet Infectious Diseases*. 2022;0(0). doi:10.1016/S1473-3099(22)00409-1