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Routine Vaccination Coverage — Worldwide, 2022

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Abstract

In 2020, the World Health Assembly endorsed the Immunization Agenda 2030 (IA2030), the 2021–2030 global strategy that envisions a world where everyone, everywhere, at every age, fully benefits from vaccines. This report reviews trends in World Health Organization and UNICEF immunization coverage estimates at global, regional, and national levels through 2022 and documents progress toward improving coverage with respect to the IA2030 strategy, which aims to reduce the number of children who have not received the first dose of a diphtheria-tetanus-pertussis–containing vaccine (DTPcv1) worldwide by 50% and to increase coverage with 3 diphtheria-tetanus-pertussis–containing vaccine doses (DTPcv3) to 90%. Worldwide, coverage ≥1 dose of DTPcv1 increased from 86% in 2021 to 89% in 2022 but remained below the 90% coverage achieved in 2019. Estimated DTPcv3 coverage increased from 81% in 2021 to 84% in 2022 but also remained below the 2019 coverage of 86%. Worldwide in 2022, 14.3 million children were not vaccinated with DTPcv1, a 21% decrease from 18.1 million in 2021, but an 11% increase from 12.9 million in 2019. Most children (84%) who did not receive DTPcv1 in 2022 lived in low- and lower-middle–income countries. COVID-19 pandemic–associated immunization recovery occurred in 2022 at the global level, but progress was unevenly distributed, especially among low-income countries. Urgent action is needed to provide incompletely vaccinated children with catch-up vaccinations that were missed during the pandemic, restore national vaccination coverage to prepandemic levels, strengthen immunization programs to build resiliency to withstand future unforeseen public health events, and further improve coverage to protect children from vaccine-preventable diseases.

Introduction

The Expanded Program on Immunization was established by the World Health Organization (WHO) in 1974 to ensure that every infant in the world received vaccines against diphtheria, tetanus, pertussis, poliomyelitis, measles, and tuberculosis (*1*). Since then, immunization programs have broadened to include many additional vaccines.* In 2020, the World Health Assembly endorsed the Immunization Agenda 2030 (IA2030), the 2021–2030 global strategy that envisions a world where everyone, everywhere, at every age, fully benefits from vaccines. A central target of IA2030 is reducing the number of children who have not received the first dose of a diphtheria-tetanus-pertussis–containing vaccine (DTPcv1) (zero-dose children) by 50% by 2030 (*2*). Initial IA2030 implementation was disrupted by the COVID-19 pandemic, and global vaccination coverage declined to the lowest levels in more than a decade, resulting in a 40% increase in the number of zero-dose children during 2019–2021, with fewer vaccinations administered in

*Additional vaccines recommended by WHO based on region or population risk group. https://cdn.who.int/media/docs/default-source/immunization/immunization_schedules/table_1_feb_2023_english.pdf

Continuing Education examination available at https://www.cdc.gov/mmwr/mmwr_continuingEducation.html

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2021 compared with 2020 (*3*). This report updates a previous report, reviews global vaccination coverage trends through 2022, and highlights signs of global but uneven immunization program recovery in 2022 (*4*,*5*).

Methods

WHO and UNICEF produce Estimates of National Immunization Coverage (WUENIC) at the national, regional, and global level based on review of country-specific data, including administrative and survey-based coverage[†] (*6*,*7*). This report examines trends in coverage with vaccines received from routine immunization programs through 2022, across all WHO countries, as well as aggregated trends at WHO regional and global levels.[§] Trends in vaccine coverage are also examined by World Bank economic classification.[¶] Reviewed vaccines include those typically provided by a national routine immunization program during the first year of life: Bacille Calmette-Guérin (BCG); DTPcv1, a third DTPcv dose (DTPcv3); a hepatitis B birth dose (HepB-BD) and third dose (HepB3); a third dose of *Haemophilus influenzae* type b vaccine (Hib3); a first dose of measles-containing vaccine (MCV1); a third pneumococcal conjugate vaccine dose (PCV3); a third polio vaccine dose (Pol3); rotavirus vaccine last dose (Rota, last); and a first rubella-containing vaccine dose (RCV1). Reviewed vaccines provided beyond the first year of life include the second dose of measles-containing vaccine (MCV2), and first and last doses of HPV vaccine (HPV, first; HPV, last).[**] Zero-dose children represent those who lack access to or are never reached by immunization services (*2*). Children who receive DTPcv1 but not DTPcv3 are considered incompletely vaccinated.[††] DTPcv1-to-DTPcv3 and DTPcv1-to-MCV1 dropout rates were calculated as the

[†] Administrative coverage with a given vaccine is calculated as the number of doses administered in a specified target group divided by the estimated target population. Doses administered during routine immunization visits are counted, but doses administered during supplementary immunization activities (mass campaigns) usually are not. Survey-based vaccination coverage is calculated as the proportion of persons in a target age group who had received a vaccine dose. During surveys, a representative sample of households is visited, and caregivers of children in a specified target age group (e.g., 12–23 months) are interviewed. Vaccination dates are transcribed from the child's home-based record or health facility records, and if documented evidence is unavailable, recorded based on caregiver recall.

[§] Years 2021 and 2022 are reported for the pandemic period: 2021, because immunization coverage in 2021 was worse than 2020; and 2022, as the most recent update.

[¶] Economic classification is based on gross national income (GNI) per capita, calculated using the World Bank Atlas method (https://datahelpdesk.worldbank.org/knowledgebase/articles/906519-world-bank-country-and-lending-groups). Low-income economies are defined as those with GNI in U.S. dollars per capita in 2022 of <$13,845; lower-middle–income, $1,136–$4,465; upper-middle–income, $4,466–$13,845; and high-income, >$13,845. For all years shown, Cook Islands and Niue are excluded in this classification because of lack of available GNI estimates. For 2021 and 2022, data for Venezuela were also excluded as temporarily unclassified pending release of revised national accounts statistics.

[**] Vaccines provided during the first year of life versus after the first year of life are based on WHO routine immunization schedule (https://cdn.who.int/media/docs/default-source/immunization/immunization_schedules/table_1_feb_2023_english.pdf?sfvrsn). The age at which a specific vaccine is delivered might vary among different country routine immunization schedules based on its associated country-specific disease incidence.

[††] Incompletely vaccinated children might also be referred to as undervaccinated children.

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percentage of children who received DTPcv1 but not DTPcv3 or MCV1, respectively.[§§] This activity was reviewed by CDC, deemed not research, and was conducted consistent with applicable federal law and CDC policy.[¶¶]

Results

Diphtheria-Tetanus-Pertussis–Containing Vaccines

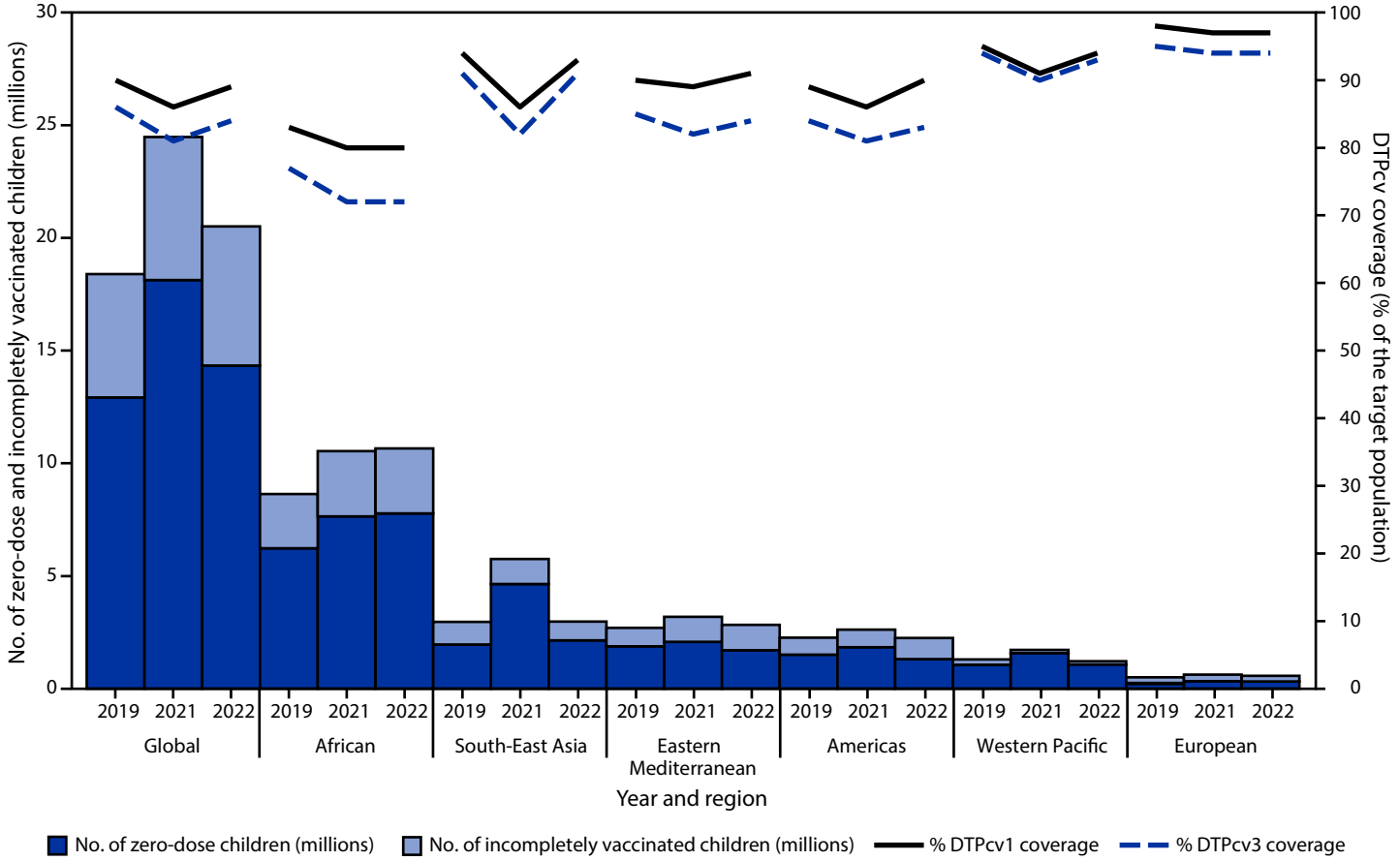
WHO and UNICEF estimates of global DTPcv1 coverage increased from 86% in 2021 to 89% in 2022, but remained below 2019 coverage (90%) (Figure). Similarly, estimated DTPcv3 coverage increased from 81% in 2021 to 84% in 2022, but remained below the 2019 level (86%). During 2021 and 2022, DTPcv1 and DTPcv3 coverage improved in all WHO regions except the African Region (AFR), where DTPcv1 and DTPcv3 coverage stagnated at 80% and 72%, respectively, and remained below 2019 coverage (83% and 77%, respectively). During both 2021 and 2022, in the European Region, DTPcv1 and DTPcv3 coverage remained ≥97% and ≥94%, respectively. The South-East Asia Region experienced the most recovery from 2021 to 2022, with DTPcv1 coverage increasing from 86% to 93%, and DTPcv3 coverage increasing from 82% to 91%. Among the 194 WHO countries, 73 (38%) experienced at least a 5% decline in DTPcv3 coverage from 2019 to 2021; among these 73 countries, only 15 (21%) achieved DTPcv3 coverage in 2022 that equaled or exceeded that in 2019.

In 2022, the number of zero-dose children (14.3 million) decreased 21%, from 18.1 million in 2021, but was still 11% higher than the 12.9 million in 2019. Only AFR reported an increase in zero-dose children from 2021 to 2022 (2.6%; from 7.6 million to 7.8 million) (Figure) (Table 1). During 2021 and 2022, the number of incompletely vaccinated children (those

[§§] DTPcv1-to-DTPcv3 dropout = ([number of children vaccinated with DTPcv1] – [number of children vaccinated with DTPcv3]) / (number of children vaccinated with DTPcv1) x 100%. DTPcv1-to-MCV1 dropout = ([number of children vaccinated with DTPcv1] – [number of children vaccinated with MCV1]) / (number of children vaccinated with DTPcv1) x 100%.

[¶¶] 45 C.F.R. part 46.102(l)(2), 21 C.F.R. part 56; 42 U.S.C. Sect. 241(d); 5 U.S.C. Sect. 552a; 44 U.S.C. Sect. 3501 et seq.

FIGURE. Estimated number of zero-dose and incompletely vaccinated children* and estimated coverage with first and third dose of diphtheria-tetanus-pertussis–containing vaccine, by World Health Organization Region — worldwide, 2019, 2021, and 2022



Abbreviations: DTPcv1 = first dose of diphtheria-tetanus-pertussis–containing vaccine; DTPcv3 = third dose of diphtheria-tetanus-pertussis–containing vaccine.

* Zero-dose children are surviving children who lack documentation of receipt of any dose of DTPcv by age 12 months (i.e., DTPcv1). Incompletely vaccinated children are those who received at least DTPcv1 but not DTPcv3.

TABLE 1. Numbers and global percentages of surviving infants who did not receive the first dose of diphtheria-tetanus-pertussis–containing vaccine (zero-dose children),* by World Health Organization Region, World Bank economic classification, and Gavi, the Vaccine Alliance eligibility — worldwide, 2019, 2021, and 2022

Year/Characteristic	Global	WHO Region†						Income classification§				Among Gavi-eligible countries¶
		AFR	AMR	EMR	EUR	SEAR	WPR	Low	Lower-middle	Upper-middle	High	
2019												
No. of countries	**194**	47	35	21	53	11	27	26	54	52	59	57
No. of surviving infants (millions)	**134.3**	37.0	14.0	18.1	10.5	33.3	21.4	23.0	64.6	35.0	12.0	74.3
Global % of surviving infants	—	27.5	10.4	13.5	7.8	24.8	15.9	17.1	48.1	26.0	9.0	55.3
No. of zero-dose children (millions)	**12.9**	6.2	1.5	1.9	0.3	2.0	1.1	3.9	6.8	2.2	0.3	9.0
Global % of zero-dose children	—	48.2	11.7	14.6	2.0	15.2	8.3	29.8	52.5	16.7	2.3	69.4
2021												
No. of countries	**194**	47	35	21	53	11	27	26	54	52	59	57
No. of surviving infants (millions)	**130.5**	38.1	13.6	18.2	10.2	32.8	17.6	24.0	64.5	30.7	11.8	75.2
Global % of surviving infants	—	29.2	10.4	14.0	7.8	25.1	13.5	18.4	49.4	23.5	9.1	57.7
No. of zero-dose children (millions)	**18.1**	7.6	1.8	2.1	0.3	4.6	1.6	4.9	9.9	3.1	0.3	12.4
Global % of zero-dose children	—	42.1	10.2	11.5	1.8	25.6	8.7	27.2	54.4	17.2	1.7	68.3
2022												
No. of countries	**194**	47	35	21	53	11	27	26	54	52	59	57
No. of surviving infants (millions)	**130.6**	38.6	13.6	18.2	10.1	32.7	17.4	23.3	64.5	30.4	11.8	75.7
Global % of surviving infants	—	29.5	10.4	14.0	7.7	25.0	13.4	17.8	49.4	23.3	9.0	58.0
No. of zero-dose children (millions)	**14.3**	7.8	1.3	1.7	0.3	2.1	1.1	4.7	7.3	1.9	0.3	10.2
Global % of zero-dose children	—	54.3	9.1	12.0	2.2	15.0	7.5	33.1	50.8	13.4	1.9	71.4

Abbreviations: AFR = African Region; AMR = Region of the Americas; DTPcv = diphtheria-tetanus-pertussis–containing vaccine; DTPcv1 = first dose of DTPcv; EMR = Eastern Mediterranean Region; EUR = European Region; GNI = gross national income; SEAR = South-East Asia Region; USD = U.S. dollars; WHO = World Health Organization; WPR = Western Pacific Region.

* Zero-dose children are surviving children who lack documentation of receipt of a dose of DTPcv1 by age 12 months. The 2022 WHO and UNICEF estimates of national immunization coverage used the 2022 World Population Prospect from the United Nations Population Division for estimates of national immunization coverage and for calculations of regional and global vaccination coverage figures. Estimates of live births and surviving infants in the 2022 World Population Prospect changed from previous years.

† Included countries are WHO countries.

§ Economic classification is based on 2022 GNI per capita, calculated using the World Bank Atlas method in USD (https://datahelpdesk.worldbank.org/knowledgebase/articles/906519-world-bank-country-and-lending-groups). Categorization is based on the World Bank's economic classification for 2022, in which low-income economies are defined as those with GNI in USD per capita of ≤$1,135; lower middle-income economies, GNI = $1,136–$4,465; upper middle-income, GNI = $4,466–$13,845; and high-income, GNI >$13,845. For all years shown, Cook Islands and Niue are excluded in this classification because of lack of available GNI estimates. For 2021 and 2022, data for Venezuela were also excluded as temporarily unclassified pending release of revised national accounts statistics.

¶ Gavi is a public-private global health partnership that aims to increase access to immunization in poor countries. Eligibility is defined as a country's average 3-year GNI per capita in USD. As GNI increases, a country moves through Gavi's different eligibility phases until reaching the transition phase in which GNI exceeds the eligibility threshold (https://www.gavi.org/types-support/sustainability/eligibility). Gavi operates on a 5-year strategic period. For Gavi 4.0 (2016–2020), the number of countries decreased to 68 with the same GNI per capita threshold. For Gavi 5.0 (2021–2025), the number of countries remained at 57 but average 3-year GNI per capita threshold was increased to ≤$1,630. For analysis, this report retrospectively looks back at the current 57 Gavi-funded countries to compare across years.

who had started, but not completed the 3-dose DTPcv series) worldwide remained relatively unchanged (6.3 and 6.2 million, respectively), but higher than the number in 2019 (5.5 million) (Figure). In 2022, most (84%) zero-dose children lived in low- and lower-middle–income countries, and 71% lived in countries eligible for support from Gavi, the Vaccine Alliance (Table 1).

Measles–Containing Vaccines

From 2021 to 2022, global MCV1 coverage increased from 81% to 83% yet remained below the 2019 coverage level (86%). MCV1 coverage in all regions was lower in 2022 than in 2019, except for the Eastern Mediterranean Region, where it had returned to the 2019 prepandemic level (83%).

Among all 194 WHO countries, 115 (59%) reported lower MCV1 coverage in 2022 than in 2019. Global MCV2 coverage increased from 71% in 2019 to 74% in 2022, principally reflecting the introduction of MCV2 in 11 countries, mostly in AFR, during 2019–2022 (Table 2).

Other Vaccines

Global coverage with the following childhood vaccines increased from 2021 to 2022, but coverage levels in 2022 remained lower than those in 2019: BCG (87%), HepB3 (84%), Pol3 (84%), and RCV1 (68%) remained lower than in 2019 (89%, 86%, 87%, and 69%, respectively). As a result of recent vaccine introductions, coverage with the following vaccines increased from 2019 to 2022: HPV, first (19% to 21%); HPV, last (14% to 15%); PCV3 (51% to 60%); and Rota, last (40% to 51%). Coverage remained relatively unchanged from 2012 to 2022 for HepB-BD (from 44% to 45%) and Hib3 (74% to 76%).

TABLE 2. Estimated vaccination coverage, by World Health Organization Region, vaccine, and dose in series — worldwide, 2022

Vaccine	Countries with vaccine in schedule,* no. (%)	Coverage, %						
			WHO Region†,§,¶					
		Global	AFR	AMR	EMR	EUR	SEAR	WPR
BCG	155 (80)	**87**	80	87	90	93	91	92
DTPcv1	194 (100)	**89**	80	90	91	97	93	94
DTPcv3	194 (100)	**84**	72	83	84	94	91	93
HepB-BD	103 (53)	**45**	18	65	32	42	58	80
HepB3	190 (98)	**84**	72	83	84	91	91	93
Hib3	193 (99)	**76**	72	83	84	93	91	32
HPV, first**	130 (67)	**21**	33	68	2	37	5	5
HPV, last††	130 (67)	**15**	22	52	0	32	3	3
MCV1	194 (100)	**83**	69	84	83	93	92	92
MCV2	188 (97)	**74**	45	76	78	91	85	91
PCV3	157 (81)	**60**	68	78	55	83	58	23
Pol3	194 (100)	**84**	71	82	85	94	91	91
RCV1	173 (89)	**68**	36	84	42	93	92	92
Rota, last§§	120 (62)	**51**	51	74	58	31	68	4

Abbreviations: AFR = African Region; AMR = Region of the Americas; BCG = Bacille Calmette-Guérin vaccine; DTPcv1 = first dose of diphtheria-tetanus-pertussis–containing vaccine; DTPcv3 = third dose of diphtheria-tetanus-pertussis–containing vaccine; EMR = Eastern Mediterranean Region; EUR = European Region; HepB-BD = birth dose of hepatitis B vaccine; HepB3 = third dose of hepatitis B vaccine; Hib3 = third dose of *Haemophilus influenzae* type b vaccine; HPV, first = first dose of human papillomavirus vaccine; HPV, last = final dose of HPV vaccine; MCV1 = first dose of measles-containing vaccine; MCV2 = second dose of measles-containing vaccine; PCV3 = third dose of pneumococcal conjugate vaccine; Pol3 = third dose of polio vaccine; RCV1 = first dose of rubella-containing vaccine; Rota, last = final dose of rotavirus vaccine series; SEAR = South-East Asia Region; WPR = Western Pacific Region; WHO = World Health Organization.

* Vaccination coverage is reported among the 194 WHO countries. By WHO Region, this includes 47 countries in AFR; 35 countries in AMR; 21 countries in EMR; 53 countries in EUR; 11 countries in SEAR; and 27 countries WPR. Vaccine coverage does not include countries recommending vaccines for special groups only.

† https://www.who.int/about/who-we-are/regional-offices

§ https://www.who.int/teams/immunization-vaccines-and-biologicals/policies/who-recommendations-for-routine-immunization---summary-tables

¶ Vaccine coverage for all vaccines (except for BCG and HepB-BD) is based on 194 WHO countries (global) or all WHO countries in the specified region. BCG coverage is based on 157 countries that have BCG in the national schedule for all infants. HepB-BD is reported for countries that are able to distinguish vaccine administration within 24 hours of birth. Administrative coverage is the number of vaccine doses administered to those in a specified target group divided by the estimated target population. During vaccination coverage surveys, a representative sample of households are visited, and caregivers of children in a specified target group (e.g., caregivers of children aged 12–23 months) are interviewed. Dates of vaccination are transcribed from the child's home-based record, from health facility records, or based on caregiver recall. Survey-based vaccination coverage is calculated as the proportion of persons in a target age group who received a vaccine dose.

** Estimates are based on HPV, first dose coverage among females. Number of doses to complete the HPV series depends on the age of the recipient and whether the country has a 1- versus 2-dose HPV immunization policy.

†† Estimates are based on HPV, last dose coverage among females. https://www.who.int/teams/immunization-vaccines-and-biologicals/policies/position-papers/human-papillomavirus-(hpv)

§§ Number of doses to complete the rotavirus vaccine series varies from 2 to 3, depending on the vaccine product.

Vaccination Dropout Rates

In 2022, the DTPcv1-to-DTPcv3 dropout rate (the percentage of children who received DTPcv1 but did not receive DTPcv3) was higher among low-income countries (12%) than among lower-middle–income (5%), upper-middle–income (3%), or high-income (3%) countries. Global DTPcv1-to-MCV1 dropout (the percentage of children who received DTPcv1 but did not receive MCV1) increased from 5% (6.3 million children) in 2019, to 7% (7.6 million) in 2022. In 2022, low-income countries reported the highest DTPcv1-to-MCV1 dropout (17%), substantially higher than that in lower-middle–income (5%), upper-middle–income (3%), and high-income countries (5%) (Supplementary Figure, https://stacks.cdc.gov/view/cdc/134102).

Discussion

Recovery of global childhood coverage with multiple vaccines occurred from 2021 to 2022; however, recovery was uneven across countries, and some countries have yet to regain 2019 prepandemic coverage levels (*4*). Global distribution of zero-dose and incompletely vaccinated children in 2022 highlights equity issues in immunization coverage and ongoing challenges faced by many low- and lower-middle–income countries. Faster-growing birth cohorts in low- and lower-middle–income countries*** compared with those in upper-middle and high-income countries (*8*) might affect coverage recovery, because some of these countries have vaccinated a similar number of children in 2022 and 2019 in the context of substantially larger 2022 birth cohorts. Although coverage increased from 2021 to 2022 in lower-middle–income countries, where nearly one half of the world's zero-dose children live, low-income countries experienced higher DTPcv1-to-DTPcv3 dropout rates and little change in the number of zero-dose children, reflecting an uneven recovery.

*** Annual population growth rate (%) is highest in West and Central Africa (2.7%), sub-Saharan Africa (2.6%), and Eastern and Southern Africa (2.5%). Global projected population growth rate during 2020–2030 is also highest among these African countries (https://www.unicef.org/media/108161/file/SOWC-2023-full-report-English.pdf). Among the 26 low-income countries and 54 lower-middle–income countries, 20 (77%) and 19 (35%) are in AFR, respectively.

Summary

What is already known about this topic?

The COVID-19 pandemic negatively affected global childhood immunization programs, resulting in lower childhood vaccination coverage.

What is added by this report?

From 2021 to 2022, global coverage with the first dose of diphtheria-tetanus-pertussis–containing vaccine increased from 86% to 89%, and with the first dose of measles-containing vaccine from 81% to 84%, but neither returned to 2019 prepandemic coverage levels of 90% and 86%, respectively. Coverage recovery was unevenly distributed across regions and countries and slower among low-income countries.

What are the implications for public health practice?

Strategies to provide catch-up vaccination throughout childhood have the potential to address heightened risks for vaccine-preventable disease outbreaks resulting from years of low vaccination coverage.

The COVID-19 pandemic affected immunization programs worldwide and resulted in millions of children missing vaccine doses and substantial increases in the numbers of zero-dose and incompletely vaccinated children. As these children age out of the usual target age range for their country's routine immunization program, they might experience limited opportunities for catch-up vaccination unless countries adopt catch-up vaccination schedules and strategies for older children. Declines in vaccination coverage among current and older age cohorts can result in immunity gaps and increased risk for outbreaks of vaccine-preventable diseases (*3*). Decreasing vaccinations for measles from 2019 to 2022, especially among low-income countries, contributed to an increase in measles outbreaks in 2022 (*3*). Many countries are implementing catch-up vaccination activities; however, because most national assessments have not typically estimated coverage beyond the usual recommended age range for administration of a given vaccine, it is unclear how effectively pandemic-associated immunity gaps among children older than the recommended age for receipt of a particular vaccine are being reduced through national catch-up vaccination efforts.

To reduce the number of zero-dose children and decrease the number of vaccine-preventable disease outbreaks worldwide (e.g., diphtheria, measles, polio, and yellow fever) will require sustained improvement in immunization coverage and progress toward reaching equity in access across all countries, not only regaining 2019 immunization coverage levels that declined during the pandemic, but also improving immunization coverage beyond 2019 prepandemic levels (*2*). Achieving these goals will require targeted, country-specific strategies, because zero-dose and undervaccinated children tend to live predominantly in low- and lower-middle–income countries and underserved communities; this includes the urban poor and those living in remote rural or conflict-affected settings (*9*). WHO and UNICEF recommend that countries enhance their immunization programs to bolster resiliency against public health events such as the COVID-19 pandemic. Building a resilient program requires actions that include strengthening the health care workforce capacity, ensuring reliable vaccine supply chains, and building community demand and confidence in vaccines. Sustainable program funding and use of immunization data for action will also be needed to identify and reach unvaccinated and undervaccinated children with all recommended and catch-up vaccination opportunities across the lifespan (*3*,*8*).

Limitations

The findings in this report are subject to at least six limitations. First, for 12 countries (2.2% of the global birth cohort) that did not report 2022 immunization coverage data by July 23, 2023, WUENIC reflects the 2021 estimated coverage (*10*). Second, data quality limitations might have resulted in inaccurate estimates of administrative coverage in some countries. Third, selection and recall bias might affect survey-based estimates of coverage (*7*). Fourth, coverage estimates do not include statistical uncertainty. Fifth, because of COVID-19 pandemic–related disruptions in survey implementation, 2022 estimates are less guided by survey data than are estimates for previous years in this report. Finally, population estimates used to calculate the number of zero-dose and incompletely vaccinated children are subject to inaccuracies.

Implications for Public Health Practice

The disruptions in daily living and health services during the COVID-19 pandemic set back decades of progress in global immunization activities. Although some recovery was seen in 2022 at the global level, progress was uneven across countries, especially among low- and lower-middle–income countries. Urgent action is needed to provide catch-up vaccination to incompletely vaccinated children, restore national vaccination coverage, and strengthen immunization programs to build the resiliency to withstand future public health events.

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Early Detection and Surveillance of the SARS-CoV-2 Variant BA.2.86 — Worldwide, July–October 2023

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Abstract

Early detection of emerging SARS-CoV-2 variants is critical to guiding rapid risk assessments, providing clear and timely communication messages, and coordinating public health action. CDC identifies and monitors novel SARS-CoV-2 variants through diverse surveillance approaches, including genomic, wastewater, traveler-based, and digital public health surveillance (e.g., global data repositories, news, and social media). The SARS-CoV-2 variant BA.2.86 was first sequenced in Israel and reported on August 13, 2023. The first U.S. COVID-19 case caused by this variant was reported on August 17, 2023, after a patient received testing for SARS-CoV-2 at a health care facility on August 3. In the following month, eight additional U.S. states detected BA.2.86 across various surveillance systems, including specimens from health care settings, wastewater surveillance, and traveler-based genomic surveillance. As of October 23, 2023, sequences have been reported from at least 32 countries. Continued variant tracking and further evidence are needed to evaluate the full public health impact of BA.2.86. Timely genomic sequence submissions to global public databases aided early detection of BA.2.86 despite the decline in the number of specimens being sequenced during the past year. This report describes how multicomponent surveillance and genomic sequencing were used in real time to track the emergence and transmission of the BA.2.86 variant. This surveillance approach provides valuable information regarding implementing and sustaining comprehensive surveillance not only for novel SARS-CoV-2 variants but also for future pathogen threats.

Introduction

CDC uses a diverse, multicomponent surveillance approach to track the emergence of new and potentially significant SARS-CoV-2 variants across the United States and globally. These surveillance systems include genomic, wastewater, traveler-based, and digital public health surveillance, which complement other traditional public health surveillance systems (Box). The implementation of a multicomponent approach optimizes timely collection of the best available data, because each individual surveillance method might not capture all COVID-19 cases, and not all specimens will undergo genomic sequencing.

Each surveillance component provides distinct information, that, when considered together, enable robust situational awareness for early warning signals and support epidemiologic characterization if more widespread transmission is established. The SARS-CoV-2 variant BA.2.86, first detected in August 2023, has more than 30 mutations in the spike protein compared with other currently circulating variants. This sequence divergence of BA.2.86 suggested potentially reduced antibody protection from previous SARS-CoV-2 infection and vaccination, especially before early laboratory-based evaluations were conducted. Consequently, CDC is actively monitoring BA.2.86 to guide public health actions and surveillance efforts (*1*). Continued variant tracking and further evidence, such as real-word evaluations, are needed to understand the full public health impact of BA.2.86. This report highlights the use of a diverse, multicomponent surveillance system for early warning, and describes how this approach has informed the response to the SARS-CoV-2 BA.2.86 variant.

Methods

Surveillance System Data

Data from four early warning surveillance systems were analyzed in this report: 1) National SARS-CoV-2 genomic surveillance,[†] 2) Traveler-based Genomic Surveillance (TGS), 3) the National Wastewater Surveillance System (NWSS), and 4) digital public health surveillance. National SARS-CoV-2 genomic surveillance comprises three different sequence sources that are combined and modeled to create weighted estimates of variant proportions for every 2-week period. These data are also used to create Nowcast estimates, which are

[*] These authors contributed equally to this report.

[†] National SARS-CoV-2 genomic surveillance comprises three genomic sequencing sources of data from respiratory virus specimen collection: 1) national SARS-CoV-2 strain surveillance, 2) commercial contract laboratory sequencing, and 3) sequences from public health, academic, and clinical laboratories that are tagged as baseline surveillance in public genomic data repositories. https://www.cdc.gov/coronavirus/2019-ncov/variants/cdc-role-surveillance.html

BOX. Components of SARS-CoV-2 surveillance* — United States, 2023

Vital records
- NVSS

Health care facilities
- NREVSS
- NHSN
- NSSP
- Unified Hospital Data Set
- NVSN
- COVID-NET
- National SARS-CoV-2 genomic surveillance

Community
- ICATT
- National SARS-CoV-2 genomic surveillance

Traveler
- TGS

Wastewater
- NWSS
- Academic, private, and local jurisdictional wastewater surveillance activities

Digital
- News media
- Social media
- Global public health partner reports
- Public genomic data repositories
- GISAID

Abbreviations: COVID-NET = COVID-19–Associated Hospitalization Surveillance Network; GISAID = Global Initiative on Sharing All Influenza Data; ICATT = Increasing Community Access to Testing; NHSN = National Healthcare Safety Network; NREVSS = National Respiratory and Enteric Virus Surveillance System; NSSP = National Syndromic Surveillance Program; NVSN = New Vaccine Surveillance Network; NVSS = National Vital Statistics System; NWSS = National Wastewater Surveillance System; TGS = Traveler-based Genomic Surveillance Program.

* More detailed clinical and epidemiologic data are available from vital records and health care facilities and other more traditional surveillance systems; however, these data are less timely. Data from community, travel, wastewater, and digital surveillance are less illness- and infection-specific but are timelier and can provide early warning.

model-based projections of variant proportions for the most recent 2-week period (*2*). CDC's TGS program collects nasal swab samples from volunteer international travelers arriving at six major U.S. international airports (*3*) from more than 135 countries.[§] CDC's NWSS operates across 50 states and two U.S. territories covering sewer sheds that service 40% of the U.S. population[¶] (*4*). SARS-CoV-2 sequences from global genomic surveillance systems are uploaded to the National Center for Biotechnology's Information Sequence Read Archive (NCBI SRA)** and Global Initiative on Sharing All Influenza Data (GISAID).[††] Digital public health surveillance includes monitoring of global public genomic data repositories such as NCBI and GISAID and also includes monitoring other digital content such as news media, social media, and global event-based and public health partner reports.[§§]

Analyses

For this analysis, BA.2.86 reports from digital public health surveillance were collected and confirmed by a CDC team. Sequences in public databases and corresponding metadata were examined daily from NCBI and GISAID. These data were analyzed using descriptive statistics and used for geographic and temporal mapping. A more detailed data analysis was conducted using sequences reported during the first 2 weeks after the emergence of the BA.2.86 variant to describe the earliest available data in more detail. In addition, differences in lag time between specimen collection and reporting dates were calculated and compared using global repository metadata. Analyses were conducted in R (version 4.1.3; R Foundation). Early public health actions that were taken as a result of these early warning surveillance data are also described in this report to illustrate how these data were used in real time. This activity was reviewed by CDC, deemed not research, and conducted consistent with applicable federal law and CDC policy.[¶¶]

Results

Tracking BA.2.86 Emergence

The first global BA.2.86 case was submitted to GISAID from Israel on Sunday, August 13, 2023 (Table). The next day the second and third BA.2.86 cases were reported by Denmark; these two cases were not epidemiologically linked to one another. On August 17, the United States reported the fourth BA.2.86 case (in Michigan), and on the same day, NWSS reported the first U.S. BA.2.86 detection in an Ohio wastewater sample, which had been collected on July 30. During the following 10 days, nine additional BA.2.86 cases

[§] CDC TGS program operates in Los Angeles (LAX), Newark (EWR), New York (JFK), San Francisco (SFO), Seattle (SEA), and Washington D.C./Dulles (IAD) airports. https://wwwnc.cdc.gov/travel/page/travel-genomic-surveillance

[¶] CDC National Wastewater Surveillance System operates in all 50 U.S. states, District of Columbia, and two territories (Puerto Rico and Guam). https://www.cdc.gov/nwss/wastewater-surveillance.html

** https://www.ncbi.nlm.nih.gov/sra

[††] https://gisaid.org/

[§§] Digital public health surveillance manual formal data collection included structured data pulls from public genomic repositories. Manual informal data collection methods included monitoring social media, such as X, for updated genomic surveillance news.

[¶¶] 45 C.F.R. part 46.102(l)(2), 21 C.F.R. part 56; 42 U.S.C. Sect.241(d); 5 U.S.C.0 Sect.552a; 44 U.S.C. Sect. 3501 et seq.

TABLE. Reported global detections of the SARS-CoV-2 BA.2.86 variant in the 2 weeks after initial report* (N = 14) — worldwide, August 13–26, 2023

Specimen source/Country	Collection date	Report date	Interval, days†	Surveillance component
Respiratory specimens				
Israel	Jul 31	Aug 13	13	Digital public health
Denmark	Jul 24	Aug 14	21	Digital public health
Denmark	Jul 31	Aug 14	14	Digital public health
United States (Michigan)	Aug 3	Aug 17	14	Respiratory specimen genomic
United Kingdom (England)	Aug 13	Aug 18	5	Digital public health
Denmark	Aug 7	Aug 19	12	Digital public health
United States/Japan	Aug 10	Aug 21	11	Traveler-based genomic
South Africa	Jul 24	Aug 22	29	Digital public health
South Africa	Jul 28	Aug 22	25	Digital public health
Denmark	Aug 14	Aug 25	11	Digital public health
United States (Ohio)	Jul 29	Aug 26	28	Respiratory specimen genomic
Wastewater				
United States (Ohio)	Jul 30	Aug 17	18	Wastewater genomic
Switzerland	Aug 4	Aug 23	19	Wastewater genomic
Denmark	Missing	Aug 25	—	Wastewater genomic

* August 13, 2023.
† Number of days from respiratory specimen or wastewater sample collection to public report.

were reported. Additional countries reporting respiratory cases included the United Kingdom and South Africa, and Switzerland and Denmark reported wastewater detections. On August 10, BA.2.86 was detected in a sample collected from a TGS participant traveling from Japan arriving at Dulles International Airport (near the District of Columbia) (*5*) and confirmed on August 20 (Figure). On August 26, Ohio reported a case from a patient sample collected on July 29. The patient had been in the same area where the first wastewater detection was reported 9 days earlier. Although systematic case investigations were not conducted, at least one of the early U.S. cases was confirmed to have no history of international travel.

The earliest respiratory specimen collection date for a BA.2.86 detection was collected in Denmark on July 24 (the second global reported BA.2.86 detection); the earliest U.S. specimen collection date was July 29 (the second U.S. reported BA.2.86 detection). Among the 11 BA.2.86 sequence detections reported in the 2 weeks after the first reported detection, the median lag time between specimen collection and sequence reporting for respiratory detections was 14 days (range = 5–29 days), including the TGS sample, for which the lag time from collection to reporting was 10 days. The median lag time from two of the three earliest wastewater detections to sequence reporting was 18 days (the collection date was missing for the third specimen).***

After these initial 14 detections, BA.2.86 was detected through respiratory or wastewater samples in at least 32 countries worldwide, across five continents. As of October 23, using publicly available data from 945 specimens in GISAID, the median lag time from specimen collection date to report date is 15 days (range = 4–53 days) (Supplementary Figure 1, https://stacks.cdc.gov/view/cdc/134230). As of October 23, 2023, BA.2.86 accounted for <1% of circulating variants in the United States (Supplementary Figure 2, https://stacks.cdc.gov/view/cdc/134231).†††

Public Health Response

Data related to the early detection of BA.2.86 enabled rapid risk communication, viral isolation and characterization, and cross-coordination for public health action. Rapid risk communication was released through timely, web-based Respiratory Virus Updates§§§ (weekly updates on the respiratory illness season) to alert public health partners and the public. Early detection of BA.2.86 through genomic surveillance also facilitated collaborations between sequencing laboratories and CDC. Residual virus samples were shared with CDC laboratories for isolation in viral culture, early characterization, and laboratory-based neutralization studies to better understand the potential impact of immune escape. High-quality, rapidly generated BA.2.86 sequences facilitated the understanding of the wide geographic distribution of the lineage and aided early laboratory-based and computer-modeled studies predicting immune escape.

Discussion

Despite decreased SARS-CoV-2 sequencing resulting from changing COVID-19 testing practices, U.S. genomic surveillance systems detected BA.2.86, a novel SARS-CoV-2 lineage circulating at very low levels. Using multiple surveillance systems enhanced early detection, tracking, and characterization of emerging SARS-CoV-2 variants. The first U.S. detection of BA.2.86 was identified through a health care facility

*** https://twitter.com/SSI_dk/status/1695027179711533235

††† https://covid.cdc.gov/covid-data-tracker/#variant-proportions
§§§ https://www.cdc.gov/respiratory-viruses/whats-new/index.html

FIGURE. SARS-CoV-2 BA.2.86 variant detection in respiratory specimens and wastewater samples, by country — worldwide, August 26 (A) and October 23, 2023 (B)

Summary

What is already known about this topic?

Early detection of emerging SARS-CoV-2 variants is critical to assessing risk, providing clear and timely communication messages, and coordinating public health action. CDC tracks SARS-CoV-2 variants using multiple approaches, including genomic, wastewater, traveler-based, and digital public health surveillance.

What is added by this report?

The SARS-CoV-2 variant BA.2.86 was first reported in August 2023. CDC used a multicomponent surveillance approach to track its global spread. It has been reported in 32 countries as of October 23, 2023.

What are the implications for public health practice?

An early warning multicomponent surveillance approach can provide valuable actionable information not only for novel SARS-CoV-2 variants but also for future pathogen threats.

specimen that was sent to CDC by the state laboratory for isolation and further characterization. Successful virus isolation at CDC allowed for the sharing of BA.2.86 isolates with other laboratories. TGS detected BA.2.86 in a sample from a traveler returning to the United States who was likely infected while abroad (*5*). NWSS facilitated BA.2.86 early warning in additional areas, and wastewater surveillance was a leading indicator in Ohio where BA.2.86 was identified 9 days before a respiratory sequence was reported in the same area.

Specimen collection dates support that BA.2.86 was likely beginning to circulate in the United States before the end of July 2023. Currently, BA.2.86 has not become predominant but is likely circulating across the United States at low levels. Preliminary laboratory research findings indicate that existing antibodies from previous SARS-CoV-2 infection or vaccination are effective in neutralizing BA.2.86 but real-world human outcome data are also needed to better understand the impacts of preexisting immunity[¶¶¶,****] (*6*).

Early warning of SARS-CoV-2 variant detection enables timely assessments of risk, mobilization of resources, clear and timely communication, and coordinated public health action (*7*). The complementary surveillance systems provided critical data and specimens for culture, treatment effectiveness evaluation, and will facilitate the development of other treatments, as needed. Integrating pathogen genomic sequencing throughout the different surveillance system components added important molecular resolution for tracking variant emergence and transmission dynamics. Digital public health surveillance can provide a signal to enhance and focus other surveillance systems toward detection of new variants. Global information-sharing and partnerships for early warning also played an important role; these systems and partnerships are crucial in light of the decrease in specimen sequencing.

Other existing surveillance systems[††††] might become critical to monitoring the impacts of BA.2.86. If circulation increases, epidemiologic data related to relative transmissibility, disease severity, and vaccine and therapeutic effectiveness will be important to understanding this variant's impact on human health. If BA.2.86 exceeds 1% of circulating variants within the United States, it will be reported through CDC's Nowcast estimates over time and by region. If BA.2.86 circulation expands to represent a significant proportion of circulating variants in the United States, other complementary COVID-19 surveillance systems that capture detailed laboratory- and patient-level data can be tracked in parallel to understand epidemiologic impacts. If new data become available that result in heightened concern, CDC can launch epidemiologic field studies on transmissibility and severity.

Limitations

The findings of this report are subject to at least five limitations. First, data analyzed from complementary surveillance systems included varying levels of geographic, epidemiologic, clinical, and demographic information. Links between surveillance data and epidemiologic and clinical data necessary to guide action are often missing, limiting the level of analysis performed. In addition, unequal levels of global sequencing capacity and funding also limit understanding of geographic spread. Second, digital public health surveillance methods employed both informal and formal manual data gathering, which was resource-intensive. Third, global genomic surveillance is limited by the variable lag times between specimen collection and reporting, which can impact real-time actionability. Fourth, standardized national methods for genomic sequence (or partial sequence) data reporting into different public repositories are lacking; this limitation is especially apparent for wastewater sequences. Finally, data quality, reporting, and aggregation standards are needed for multicomponent pathogen genomic surveillance.

¶¶¶ https://www.biorxiv.org/content/10.1101/2023.09.04.556272v1

**** https://www.biorxiv.org/content/10.1101/2023.09.07.556636v1#:~:text=The%20pseudovirus%20assay%20showed%20that,due%20to%20the%20increased%20infectivity

†††† These surveillance systems include National Syndromic Surveillance Program (https://www.cdc.gov/nssp/overview.html) capturing emergency department visits, National Respiratory and Enteric Virus Surveillance System (https://www.cdc.gov/surveillance/nrevss/index.html) capturing proportion of COVID nucleic acid amplification test/polymerase chain reaction test positivity, National Hospital Sentinel Network (https://www.cdc.gov/nhsn/index.html) capturing hospitalization data, Unified Hospital Data Set, New Vaccine Surveillance Network (https://www.cdc.gov/surveillance/nvsn/index.html), and COVID-19–Associated Hospitalization Surveillance Network (https://www.cdc.gov/coronavirus/2019-ncov/covid-data/covid-net/purpose-methods.html).

Implications for Public Health and Preparedness

The emergence of BA.2.86 has highlighted the importance of early detection through multiple, complementary surveillance systems involving diverse approaches, populations, and specimen types. These systems can be further improved by addressing timeliness, improving understanding of both the strengths and limitations of each system, and increasing cross-public health coordination and action. Leveraging, maintaining, and prioritizing these robust, multipurpose public health surveillance systems require sustained financial resources.

Early detection data are more actionable as the lag time between specimen collection and reporting of results decreases, and when more clinical and epidemiologic data are available. Innovations in pathogen testing and genomic sequencing, capacity building, and reporting systems can support earlier public health action. New technology is also needed from the private sector to offer less expensive, targeted, and more sustainable products (e.g., cheaper, faster diagnostic tests) to support the future of public health surveillance. Continuous, automated data scraping[§§§§] for early warning signs (e.g., robust event-based surveillance) can more efficiently alert health authorities of global events to guide preparation measures. Complementary surveillance systems in place for early warning can be used for other known and novel public health threats. As public health and surveillance advancements continue, the deployment of multiple innovations to strengthen early warning, preparedness, and response will be critical.

[§§§§] Data scraping is the process of extracting data from the Internet.

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Notes from the Field:

Early Identification of the SARS-CoV-2 Omicron BA.2.86 Variant by the Traveler-Based Genomic Surveillance Program — Dulles International Airport, August 2023

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During August 13–14, 2023, a new SARS-CoV-2 Omicron subvariant with a large number of mutations compared with previously circulating BA.2 variants (>30 amino acid differences in its spike protein) was identified by genomic sequencing in Denmark and Israel and subsequently designated BA.2.86 (*1*,*2*). Given near-simultaneous detections in multiple countries, including the United States, further information was needed regarding geographic spread of BA.2.86. Since January 2022, submissions to SARS-CoV-2 sequence repositories have declined by 95%,* substantially decreasing global capacity to monitor new variants. To fill gaps in global surveillance, CDC's Traveler-based Genomic Surveillance (TGS) program was developed to provide early warning of new variants entering the United States by collecting samples from arriving international travelers (*3*).

Investigation and Outcomes

The TGS program anonymously collects two nasal swab samples from consenting international travelers arriving at six major U.S. airports.† Participants complete a brief questionnaire that collects information including travel history, COVID-19 vaccination status, and previous COVID-19 history. One sample collected from each traveler is pooled together with up to nine other travelers' samples and tested for SARS-CoV-2 using reverse transcription–polymerase chain reaction. If a pooled sample tests positive, it undergoes viral genomic sequencing. The second nasal samples from each traveler in that pool are then tested for SARS-CoV-2, and positive individual samples are sequenced. Select positive individual samples are sent to CDC laboratories for virus isolation and characterization. This activity was reviewed by CDC, deemed not research, and was conducted consistent with applicable federal law and CDC policy.§

On August 17, 2023, genomic sequencing identified BA.2.86 in a pooled sample of swabs from 10 TGS participants collected on August 10 at Dulles International Airport near the District of Columbia. Testing and sequencing of the individual samples confirmed the presence of BA.2.86 in one individual sample on August 20. The sample was collected from a U.S. resident returning from a 15–30-day trip to Japan; health authorities in Japan were notified upon confirmation. The traveler reported no previous COVID-19 infection and had last received a COVID-19 vaccine dose in October 2022. This sequence was the second publicly reported BA.2.86 sequence in the United States and the seventh reported globally,¶ preceding the first BA.2.86 sequence submission reported from Japan by 17 days.** The TGS sample was sent to a CDC laboratory, but virus isolation was not successful. Phylogenetic analyses indicated that the TGS sample contained distinct genetic differences from other BA.2.86 sequences collected in August 2023 (Figure), consistent with BA.2.86 circulation and divergence from BA.2.86.1 viruses several months before detection (*4*,*5*).

Preliminary Conclusions and Actions

As a component of comprehensive U.S. SARS-CoV-2 genomic surveillance, TGS detected the BA.2.86 variant within days of its first identification globally, highlighting its importance for the detection of variants entering the United States. This identification provided important context regarding BA.2.86 geographic spread and diversity. Although virus isolation was not successful in this case, continued surveillance and sample collection are important to enable rapid laboratory characterization of variant sensitivity to antibody neutralization and antiviral drugs. Early variant detection among travelers and laboratory characterization of new variants are essential components of CDC's respiratory illness surveillance, especially as global sequencing volumes decline.

* https://gisaid.org/hcov-19-variants-dashboard/

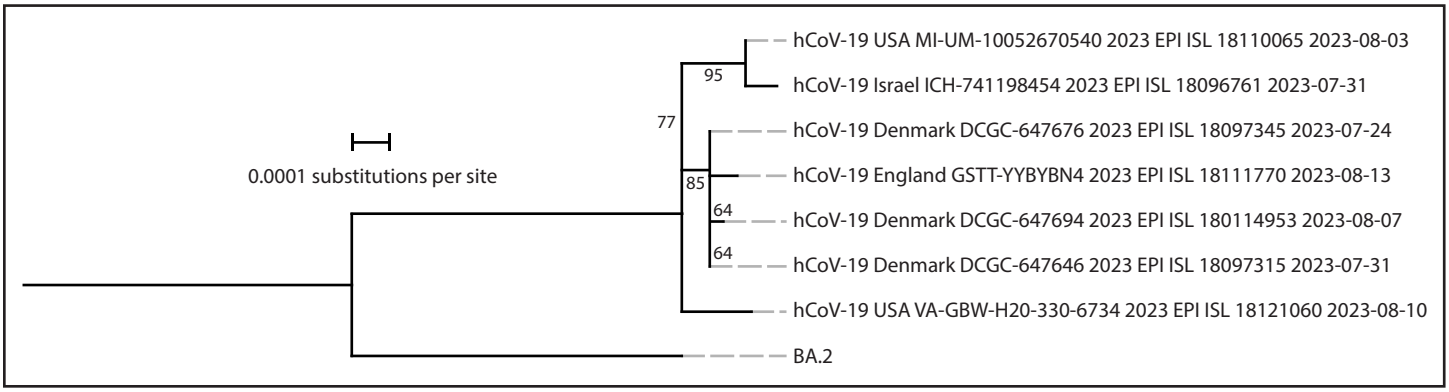
† Newark Liberty International Airport, Newark, New Jersey; John F. Kennedy International Airport, New York, New York; Dulles International Airport, near the District of Columbia; Seattle-Tacoma International Airport, Seattle, Washington; San Francisco International Airport, San Francisco, California; and Los Angeles International Airport, Los Angeles, California. https://wwwnc.cdc.gov/travel/page/travel-genomic-surveillance

§ 45 C.F.R. part 46.102(l)(2), 21 C.F.R. part 56; 42 U.S.C. Sect. 241(d); 5 U.S.C. Sect. 552a; 44 U.S.C. Sect. 3501 et seq.

¶ The TGS sequence was submitted to the Global Initiative on Sharing All Influenza Data (GISAID) repository on August 21, 2023 (accession number EPI_ISL_18121060), and raw sequencing reads were submitted to the National Center for Biotechnology Information Sequence Read Archive on August 23, 2023 (accession number SRX21474168).

** A BA.2.86 sequence from Japan (sample collection date August 24, 2023) was submitted to GISAID on September 7, 2023 (accession number EPI_ISL_18233521). This sequence had mutations that differed from the TGS sample, and unlike the TGS sample, this sequence was assigned to the BA.2.86.1 sublineage.

FIGURE. Phylogeny of SARS-CoV-2 Omicron BA.2.86 samples available on Global Initiative on Sharing All Influenza Data* as of August 21, 2023 (seven genomes) and ancestral BA.2 sequences†,§,¶, — worldwide, August 2023**



Abbreviation: GISAID = Global Initiative on Sharing All Influenza Data.

* https://gisaid.org

† Consensus genome sequences from BA.2.86 GISAID submissions on or before August 21, 2023, were aligned and mutational profiles were generated using Nextclade (version 2.14.1; https://joss.theoj.org/papers/10.21105/joss.03773). Consensus reference genomes for BA.2 were available at https://github.com/corneliusroemer/ncov-simplest/tree/main/data. A maximum likelihood phylogenetic tree was generated using iqTREE software (version 1.6.12) with 1,000 bootstraps. Using the iqTREE model finder tool, the HKY+F+I model was selected as the most appropriate model according to Bayesian Information Criterion. The maximum likelihood tree was visualized and annotated using iTOL (version 6; https://academic.oup.com/nar/article/49/W1/W293/6246398). Branch labels indicate confidence in phylogenetic placement as a percentage.

§ https://academic.oup.com/bioinformatics/article/34/23/4121/5001388

¶ https://academic.oup.com/mbe/article/32/1/268/2925592

** The BA.2.86 sample identified through the Traveler-based Genomic Surveillance program (hCoV-19 USA VA-GBW-H20-330-6734 2023 EPI ISL 18121060 2023-08-10) was collected at Dulles International Airport on August 10, 2023.

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Erratum

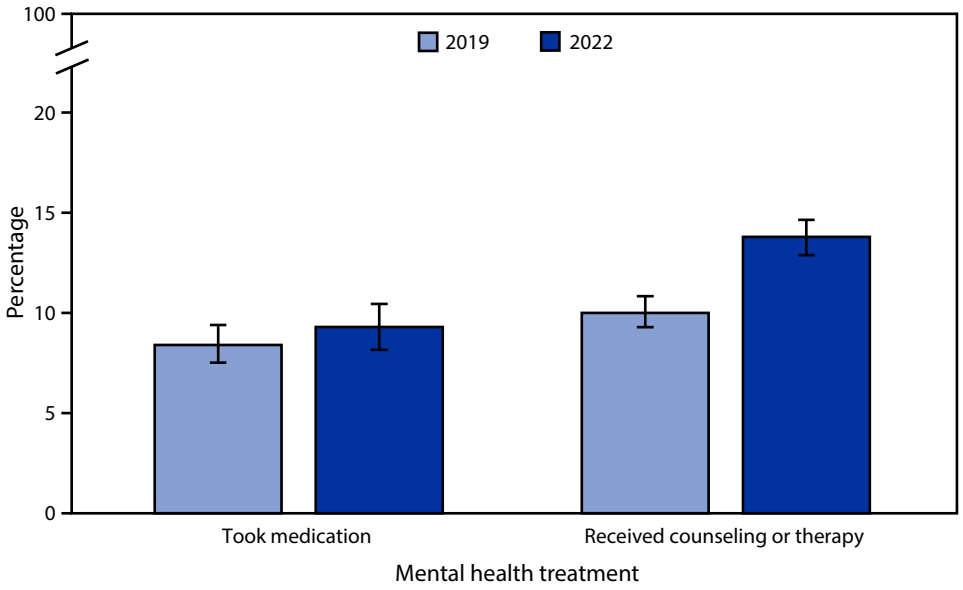
Vol. 72, No. RR-2

In the *MMWR* Recommendations and Reports, "Prevention and Control of Seasonal Influenza with Vaccines: Recommendations of the Advisory Committee on Immunization Practices — United States, 2023–24 Influenza Season," on page 15, in the first paragraph, the second sentence should have read, "Examples include AS01B (in Shingrix, recombinant zoster subunit vaccine) (*146*), AS01E (in **Arexvy**, respiratory syncytial virus vaccine) (*147*) MF59 (in Fluad Quadrivalent [aIIV4]) (*56*), and cytosine phosphoguanine oligodeoxynucleotide (in Heplisav-B, a recombinant hepatitis B surface antigen vaccine) (*148*)." In addition, on page 25, reference 147 should have read, "**Arexvy** [Package insert]. Durham, NC: GlaxoSmithKline; 2023."

QuickStats

FROM THE NATIONAL CENTER FOR HEALTH STATISTICS

Percentage* of Children and Adolescents Aged 5–17 Years Who Took Medication for Their Mental Health or Received Counseling or Therapy from a Mental Health Professional During the Past 12 Months,† by Year — National Health Interview Survey,§ United States, 2019 and 2022



* With 95% CIs indicated by error bars.
† Based on a positive response to one or both of these questions: "During the past 12 months, did [child's name] receive counseling or therapy from a mental health professional, such as a psychiatrist, psychologist, psychiatric nurse, or clinical social worker?" and "During the past 12 months, did [child's name] take any prescription medication to help with [his/her] emotions, concentration, behavior, or mental health?" Children and adolescents could have both taken medication for their mental health and received counseling or therapy.
§ Estimates are based on household interviews of a sample of the civilian, noninstitutionalized U.S. population.

The percentage of children and adolescents aged 5–17 years who took medication for their mental health during the past 12 months did not change significantly from 2019 (8.4%) to 2022 (9.3%). The percentage of children and adolescents who received counseling or therapy during the past 12 months increased from 10.0% in 2019 to 13.8% in 2022. In both 2019 and 2022, the percentage of children and adolescents who received counseling or therapy was higher than the percentage of those who took medication for their mental health.

Source: National Center for Health Statistics, National Health Interview Survey, 2019 and 2022. https://www.cdc.gov/nchs/nhis/index.htm

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