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Protracted, Intermittent Outbreak of *Salmonella* Mbandaka Linked to a Restaurant — Michigan, 2008–2019

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In 2018, Michigan public health officials determined that a single restaurant in southwest Michigan was the source for a protracted, intermittent outbreak of *Salmonella* enterica serotype Mbandaka infections occurring since 2008. Isolates from 36 infected persons shared two highly related pulsed-field gel electrophoresis (PFGE) patterns and highly related whole genome sequencing (WGS) subtypes. The initial focus of the local public health investigation on food items rather than food sources (i.e., restaurants) through a questionnaire, difficulty in food history recollection among ill persons, and sporadic case identification over periods from months to years contributed to delayed source identification. The Kalamazoo County Health and Community Services Department (KHCSD) and the Michigan Department of Health and Human Services (MDHHS) collected clinical specimens, performed multiple rounds of environmental testing, and conducted multiple regulatory visits, and based on accumulated findings over 10 years, identified the restaurant source. A 2018 investigation by KCHCSD and MDHHS found that environmental samples and stool specimens from asymptomatic restaurant employees tested positive for the *Salmonella* Mbandaka outbreak strain. A complex association between the restaurant environment and employees resulted in patron illnesses. Environmental health interventions, facility renovation, asymptomatic employee exclusions, employee health monitoring, and recurrent facility environmental sampling measures were implemented. As a result of ongoing cases and environmental persistence of *Salmonella* Mbandaka, the restaurant closed permanently in 2018. Restaurant employee stool testing and environmental sampling for *Salmonella* early during the investigation of confirmed *Salmonella* cases linked to a restaurant enhances source identification. Exclusion or restriction of asymptomatic food workers with stool-positive nontyphoidal *Salmonella* should be considered part of restaurant outbreak mitigation.

Epidemiologic Investigation

In 2012, KCHCSD was notified by MDHHS about *Salmonella* Mbandaka cases occurring intermittently since 2008 that were highly related by PFGE pattern. During 2012–2014, a restaurant was not yet associated, so a hypothesis-generating questionnaire was used to ensure capture of detailed patient food histories, which included closed-ended questions about frequently eaten food items, types of restaurants visited, and animal contact. In 2014, although investigations into common suppliers among several restaurants mentioned in food histories were ongoing and other restaurants were named by cases, as more information was collected from supplementary questionnaires, KCHCSD, MDHHS, and the Michigan Department of Agriculture and Rural Development discussed the association of a single restaurant (restaurant A) based on five known, confirmed cases to date reporting a meal at restaurant A. KCHCSD gathered additional information from restaurant A

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management regarding employee health and exposures, facility and equipment, food sources, and pest control. No further epidemiologic link was established from the interview with the restaurant, but continued cleanliness and maintenance citations occurred during 2014–2018. Additional *Salmonella* Mbandaka cases in 2017 prompted development of a detailed, outbreak-specific case questionnaire that included specific questions about restaurant A. As more cases were identified, an intensive investigation began in 2018. An outbreak case was defined as a case of confirmed *Salmonella* Mbandaka with one of two closely related PFGE patterns (TDRX01.0120 and TDRX01.0127), highly related WGS subtype identified by the MDHHS Bureau of Laboratories or CDC, or probable cases with clinically compatible illness and epidemiologic linkage to a confirmed case.

During September 2008–July 2019, a total of 35 primary cases (33 confirmed and two probable) and one confirmed secondary case were identified. Patients with confirmed cases ranged in age from 1.5–90 years (mean = 57 years; median = 64 years), and 26 (72%) patients were female. Several patients reported a history of chronic gastrointestinal issues that made determination of onset date difficult. Twenty-four (67%) patients reported vomiting or diarrhea, and 12 (33%) reported urinary tract infection. Six (17%) patients were hospitalized. Approximately 40% of patients had underlying medical conditions such as diabetes or cancer. Among 19 patients with a restaurant dining history, 17 reported eating at restaurant A. Patients were routinely interviewed at the time of local health department referral and reinterviewed, often weeks later, when Mbandaka serotype was reported. Thirteen patients, retrospectively identified from early in the outbreak period, were not candidates for reinterview because their onsets preceded identifying them as part of the outbreak by >1 month.

After implementation of the outbreak-specific questionnaire in 2017, nine patients with onset during August 2017–July 2019 reported having eaten at restaurant A (Figure). To determine whether restaurant A was mentioned in the food histories of other reported foodborne illnesses, Michigan public health officials reviewed restaurant A patronage and food histories of 1,166 persons with previously reported salmonellosis, campylobacteriosis, and shigellosis cases in southwest Michigan for restaurant dining history. The only patients who reported eating at restaurant A were those associated with this outbreak; no other patients mentioned the restaurant.

Environmental and Laboratory Investigation

As part of the 2018 investigation, restaurant A employee stool specimens and environmental samples were collected in parallel and analyzed for *Salmonella*. None of the 100 employees reported symptoms at the time of sample collection or in the weeks preceding collection. MDHHS Bureau of Laboratories identified five isolates from four of 100 asymptomatic employees' stool specimens that shared the outbreak subtype. Stool cultures were collected approximately every 30 days from

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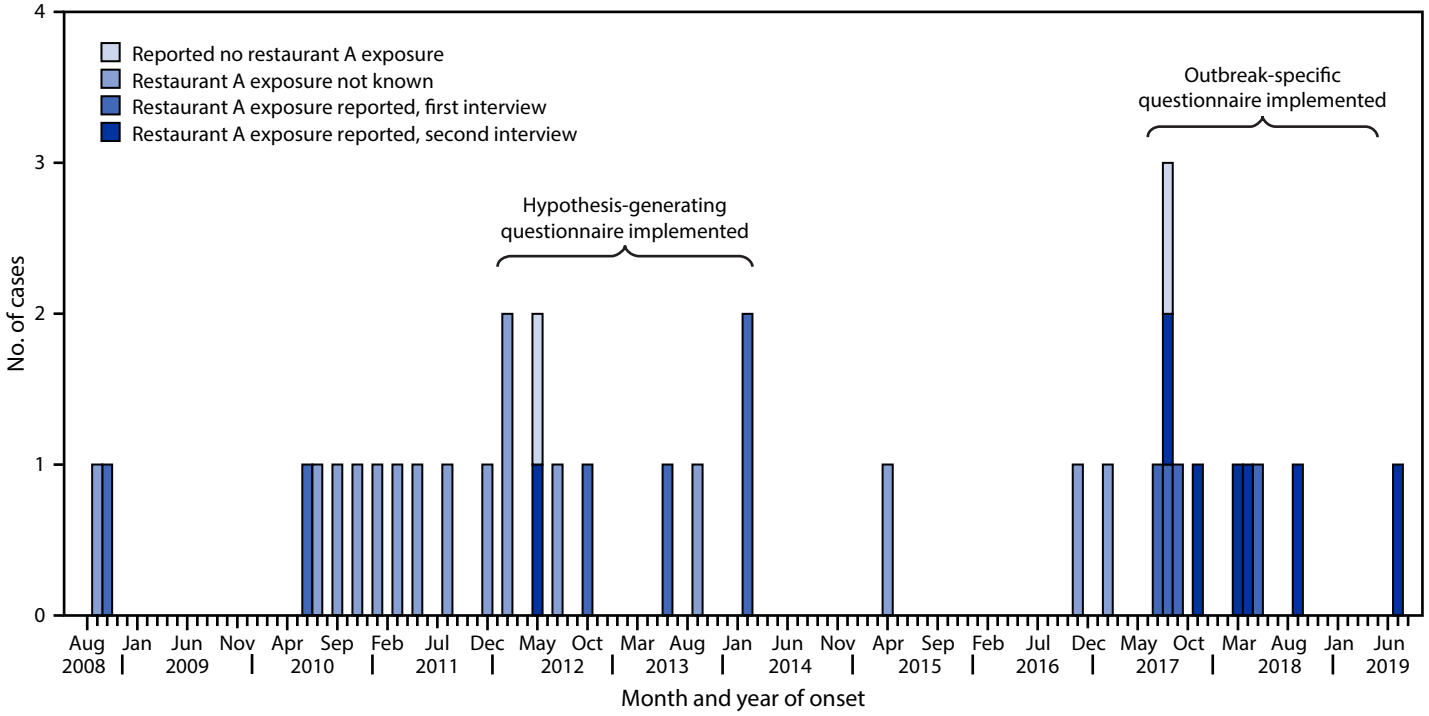
FIGURE. Cases of *Salmonella* Mbandaka outbreak subtype (N = 35), by month and year of illness onset* and restaurant A exposure — Michigan, September 2008–July 2019†



* Onset date was missing for five patients; for these cases, the date of referral to the health department was used.
† Pulsed-field gel electrophoresis was performed only on the top 20 *Salmonella* serotypes submitted to the Michigan Department of Health and Human Services Bureau of Laboratories from approximately 2009 to early 2010; the *Salmonella* Mbandaka serotype was rare and not a top 20 serotype.

asymptomatic employees with stool specimens that tested positive until a negative test result was received. A repeat stool culture was taken at least 48 hours after the first negative result. Asymptomatic employees who received positive *Salmonella* Mbandaka test results were required to have two negative stool cultures before returning to work. Because antibiotics can increase the likelihood of prolonged *Salmonella* shedding in stool, treatment was not recommended (*1*). None of the restaurant employees received antibiotics to treat asymptomatic *Salmonella* Mbandaka infection. The duration of *Salmonella* shedding among the four asymptomatic restaurant employees with positive cultures varied (range = 31–123 days).

A team of local and state public health officials collected 80 environmental samples from food and nonfood contact surfaces to be tested for *Salmonella*. *Salmonella* was isolated from 39 (49%) environmental samples. Positive samples shared the same PFGE and WGS results as the outbreak subtype (Table). Positive samples were collected throughout the restaurant kitchen, including cooking, preparation, dishwashing, storage, and employee restroom areas. Following the identification of a new case in September 2018, a second round of environmental *Salmonella* sampling was conducted. In the second round, *Salmonella* was isolated from 11 of 81 samples (14%) and shared the outbreak subtype. Positive environmental sites were generally similar, but not identical, in the two rounds. Environmental, asymptomatic employee, and symptomatic patient isolates identified by core genome multilocus sequence typing (cgMLST) revealed three clades (A, B, and C) (Table). Isolates within each clade were highly related, differing by ≤5 alleles. The clades were also considered highly related to each other, differing by ≤15 alleles. All environmental and employee isolates were in clade A; symptomatic patient isolates were identified in all three clades.

Public Health Response

In addition to routine inspections and administrative hearings in 2012 and 2014, iterative facility environmental assessments and administrative hearings during 2017–2018 addressed cleanliness, lack of active managerial control, and other foodborne illness risk factors cited at restaurant A. In addition to employee stool screening for *Salmonella* and exclusion of asymptomatic employees with *Salmonella* stool positive results, employees were also required to submit stool specimens for *Salmonella* testing if new onset of gastrointestinal symptoms occurred during the 2018 public health response. Seven employees reported symptoms, but all had

TABLE. Characteristics of *Salmonella* Mbandaka outbreak subtype isolates from symptomatic patients, asymptomatic restaurant A employees, and restaurant A environmental surfaces — Michigan, August 2008–June 2018

Source of isolate	No. of samples collected	No. (%) of isolates identified by PFGE	No. (%) of isolates identified by WGS	Isolation date or date range	Clade by cgMLST
Symptomatic patient	36	36 (100)	30 (83)	2008–2012	B
				2012–2014	C
				2015–2018	A
Asymptomatic employee*	100	5 (5)	5 (5)	Jun 2018	A
Environment (restaurant)	80	39 (49)	26 (33)	Jun 2018	A
Environment (restaurant)	81	11 (14)	10 (12)	Nov 2018	A

Abbreviations: cgMLST = core genome multilocus sequence typing; PFGE = pulsed-field gel electrophoresis; WGS = whole genome sequencing.
* Five isolates were analyzed from four asymptomatic employees.

negative *Salmonella* test results. Before the initial environmental *Salmonella* sampling event in spring 2018, the facility temporarily closed for renovations of the kitchen, flooring, walls, and major equipment. The restaurant was required to clean all facility and food contact surfaces to norovirus cleaning standards* and underwent follow-up environmental *Salmonella* sampling. In fall 2018, the facility temporarily closed for additional floor and equipment renovations with the intent of eradicating *Salmonella* from the facility. The facility again had a full norovirus standard cleaning performed before reopening. Despite kitchen renovation and environmental hygiene interventions, *Salmonella* Mbandaka continued to be detected in restaurant A. Therefore, the restaurant voluntarily and permanently closed in late 2018, and food, dishes, storage, soft goods, chairs, and tables were destroyed. The metal food production equipment was extensively cleaned, quarantined, and resampled for *Salmonella* before being redeployed. The building was deemed ineligible for food production or storage relicensure. One case of the outbreak subtype was isolated in urine 8 months after closure of the restaurant; the patient reported chronic, intermittent diarrhea after eating at restaurant A 3 weeks before it closed.

Discussion

Multiple challenges contributed to delayed source identification. Food histories were incomplete in the early cases. Initial questionnaires were inflexible and focused more on food items than on food establishments. Early cases were not initially identified as a cluster given the sporadic incidence and were hypothesized as a rare or regional PFGE pattern. Further, index of suspicion for a protracted common source early in the outbreak was low given the more typical experience of point source *Salmonella* outbreaks. Finally, restaurant management was doubtful and required intensive engagement. Both the environmental and clinical testing results were thus essential for continued mitigation efforts.

Salmonellosis outbreaks in the food industry often occur through a point source when undercooked or contaminated food products infect consumers until distribution of the foodborne vehicle ceases (*2*,*3*). In this outbreak, a complex association between the environment and employees of a single restaurant in southwest Michigan demonstrated a protracted and intermittent common source outbreak of *Salmonella* Mbandaka. A study of 23 restaurant-associated salmonellosis outbreaks found that restaurants with *Salmonella*-positive environmental samples had a higher proportion of *Salmonella*-positive food workers and longer outbreak durations than did restaurants with negative environmental samples (*4*). The nearly 11-year duration of this outbreak attests to the potential recalcitrance of *Salmonella* in restaurant environments, the importance of hygienic restaurant policies and practices, and the challenge in source identification when cases occur intermittently and without a clear foodborne vehicle. As WGS is more broadly implemented as a routine subtyping method for *Salmonella* and other bacterial enteric pathogens, increased discriminatory power might facilitate the identification of more protracted, common-source outbreaks (*5*). Whereas initially small numbers of cases might present a challenge to definitively implicating a common source, gathering as much high quality exposure data as possible, including repeated interviewing of patients with cases that are clustered in time using closed-ended questions about exposures of interest, can aid an investigation. In addition, conducting environmental assessments, environmental sampling, and employee testing for *Salmonella* are best practices that should be considered early in an investigation, particularly when a single foodborne vehicle is not apparent.

Fifteen (42%) of the 36 patients had the outbreak subtype isolated in urine; 12 (33%) patients had urinary symptoms without reporting diarrhea or vomiting. These findings are consistent with the observation that a higher proportion of *Salmonella* serogroup C1 (including Mbandaka) than of other *Salmonella* serogroups is isolated from urine (*6*,*7*). Although chronic carriage of *Salmonella* Typhi after acute infection is widely recognized, asymptomatic carriage of nontyphoidal

* https://www.cdc.gov/norovirus/about/prevention.html

Summary

What is already known about this topic?

Restaurant outbreaks of *Salmonella* with *Salmonella*-positive environmental samples might result in a higher proportion of *Salmonella*-positive food workers and longer outbreaks.

What is added by this report?

A protracted restaurant-associated outbreak of *Salmonella* Mbandaka in Michigan was identified through recursive case interviewing, asymptomatic employee testing, and environmental sampling. Multiple efforts to eradicate the organism failed, and the restaurant was permanently closed in 2018.

What are the implications for public health practice?

Coupling asymptomatic food worker testing and environmental sampling for *Salmonella* with whole genome sequencing of case isolates in suspected, protracted restaurant outbreaks of *Salmonella* enhances source identification. Exclusion or restriction of asymptomatic food workers with nontyphoidal *Salmonella* should be considered part of restaurant outbreak mitigation.

Salmonella is less well characterized but has been reported in restaurant food and hotel workers as well as in healthy adults and children (*5*,*8*,*9*).

For most of the time when the reported outbreak investigation was conducted, the restaurant was regulated under a modified version of the 2009 Food and Drug Administration (FDA) Food Code, the latest FDA Food Code that Michigan had adopted. The 2009 FDA Food Code did not include asymptomatic nontyphoidal *Salmonella* infections among the five specific foodborne pathogens[†] for which exclusion and restriction requirements are delineated. Therefore, the 2017 FDA Food Code was used for guidance because it includes asymptomatic nontyphoidal *Salmonella* infection as a food worker condition of restriction (*10*). Further adoption of the 2017 FDA Food Code will aid public health professionals in disrupting nontyphoidal *Salmonella* transmission in restaurant settings, particularly as more protracted outbreaks are identified.

[†] Norovirus, *Salmonella* Typhi, *Escherichia coli* O157:H7 or Enterohemorrhagic or Shiga toxin-producing *E. coli, Shigella* spp., and hepatitis A virus.

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Disparities in Excess Mortality Associated with COVID-19 — United States, 2020

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The COVID-19 pandemic has disproportionately affected Hispanic or Latino, non-Hispanic Black (Black), non-Hispanic American Indian or Alaska Native (AI/AN), and non-Hispanic Native Hawaiian or Other Pacific Islander (NH/PI) populations in the United States. These populations have experienced higher rates of infection and mortality compared with the non-Hispanic White (White) population (*1*–*5*) and greater excess mortality (i.e., the percentage increase in the number of persons who have died relative to the expected number of deaths for a given place and time) (*6*). A limitation of existing research on excess mortality among racial/ethnic minority groups has been the lack of adjustment for age and population change over time. This study assessed excess mortality incidence rates (IRs) (e.g., the number of excess deaths per 100,000 person-years) in the United States during December 29, 2019–January 2, 2021, by race/ethnicity and age group using data from the National Vital Statistics System. Among all assessed racial/ethnic groups (non-Hispanic Asian [Asian], AI/AN, Black, Hispanic, NH/PI, and White populations), excess mortality IRs were higher among persons aged ≥65 years (426.4 to 1033.5 excess deaths per 100,000 person-years) than among those aged 25–64 years (30.2 to 221.1) and those aged <25 years (−2.9 to 14.1). Among persons aged <65 years, Black and AI/AN populations had the highest excess mortality IRs. Among adults aged ≥65 years, Black and Hispanic persons experienced the highest excess mortality IRs of >1,000 excess deaths per 100,000 person-years. These findings could help guide more tailored public health messaging and mitigation efforts to reduce disparities in mortality associated with the COVID-19 pandemic in the United States,* by identifying the racial/ethnic groups and age groups with the highest excess mortality rates.

Data on the weekly number of deaths from all causes and from COVID-19 that occurred during December 29, 2019–January 2, 2021, were obtained from the National Vital Statistics System (NVSS).† These data included all deaths occurring in the 50 U.S. states and District of Columbia (DC) and were not limited to U.S. residents; approximately 0.2% of decedents overall were foreign residents. Deaths attributed to COVID-19 were identified with the *International Classification of Diseases, Tenth Revision, Clinical Modification* (ICD-10-CM) code U07.1, which indicated that COVID-19 was an underlying or contributing cause of death.§ Observed numbers of deaths were weighted to account for incomplete reporting by jurisdictions¶ (50 states and DC) in the most recent weeks, where the weights were estimated based on the completeness of provisional data from 2019 (*7*).

Annual population estimates from the U.S. Census Bureau** by age group and race/ethnicity for 2015–2019 were projected using seasonal autoregressive integrated moving average (sARIMA) models to obtain weekly estimates through 2020. The weekly expected numbers of deaths were estimated using sARIMA models of the all-cause mortality IRs (deaths per 100,000 person-weeks) based on 2015–2019 data multiplied by the weekly adjusted population counts for the period December 29, 2019–January 2, 2021. The resulting weekly expected numbers of deaths were subtracted from the observed numbers of deaths to generate estimates of excess deaths. The weekly population denominators were adjusted for the cumulative numbers of excess deaths in each age and racial/ethnic group occurring through each week of 2020,††

* https://www.cdc.gov/coronavirus/2019-ncov/prevent-getting-sick/prevention.html

† https://data.cdc.gov/NCHS/AH-Excess-Deaths-by-Sex-Age-and-Race/m74n-4hbs

§ Deaths from all causes excluding COVID-19 were calculated by subtracting the number of confirmed or presumed COVID-19 deaths from the total number of deaths. Deaths with confirmed or presumed COVID-19 were assigned the ICD-10-CM code U07.1 as a contributing or underlying cause of death on the death certificate. Excess deaths directly attributable to COVID-19 were calculated by subtracting the number of excess deaths from all causes excluding COVID-19 from the total number of excess deaths from all causes.

¶ Observed numbers of deaths were weighted to account for incomplete reporting of provisional death certificate data, where the weights for each jurisdiction were estimated based on the completeness of provisional data from 2019. Weights primarily affected estimates for the most recent 8 weeks, with reported and weighted counts for earlier periods being very similar.

** https://www.census.gov/data/developers/data-sets/popest-popproj/popest.html

†† sARIMA models were used to estimate weekly population counts and expected numbers of deaths for each race/ethnicity and age group. The cumulative number of excess deaths as of a given week were then subtracted from each subsequent weekly population projection to account for population changes related to the impact of the pandemic. These adjustments were made to improve the accuracy of the population projections by better accounting for smaller increases in population denominators over time because of the greater number of deaths occurring during the COVID-19 pandemic. Without adjustment, the population counts and corresponding expected numbers of deaths might have been overestimated, resulting in underestimates of excess mortality. These adjusted population counts were used to estimate the weekly expected number of deaths for each group by multiplying the expected weekly all-cause mortality IRs (estimated using historical 2015–2019 mortality and population data and sARIMA models accounting for annual temporal and seasonal trends by epidemiologic week) by the weekly adjusted population counts for the period December 29, 2019–January 2, 2021. The resulting weekly expected numbers of deaths were subtracted from the observed numbers of deaths to generate estimates of excess deaths. https://www.medrxiv.org/content/10.1101/2021.02.10.21251461v1.full-text

to account for smaller than expected population growth through the COVID-19 pandemic because of the number of excess deaths that occurred during that time.

Weekly percentage excess mortality (excess deaths as a percentage of expected deaths) and quarterly or annual excess mortality IRs (number of excess deaths per 100,000 person-quarters or person-years for 2020 overall) were estimated by age group (<25 years, 25–64 years, and ≥65 years) and race/ethnicity group (i.e., Asian, AI/AN, Black, Hispanic, NH/PI, and White populations). Persons of more than one race or for whom race and ethnicity were unknown are not shown separately because numbers were small. R statistical software (version 4.0.2; R Foundation) was used to conduct the analyses. These activities were reviewed by CDC and conducted consistent with applicable federal law and CDC policy.[§§]

Among persons aged <25 years, the percentage excess mortality was highly variable throughout 2020 for most racial/ethnic groups. Among persons aged 25–64 years, the largest percentage excess mortality occurred among Hispanic persons, with three distinct peaks of ≥75% in April, July, and December 2020. In this age group, among AI/AN persons, percentage excess mortality peaked at ≥60% during June–July and December 2020; and peaked among Black persons in April 2020 at approximately 70%, with a second smaller peak (40%) in July 2020. Among Asian persons, peaks of at least 75% occurred in April and December 2020; and among NH/PI persons, percentage excess mortality peaked in July and December 2020, at nearly 90%. Percentage excess mortality among White persons aged 25–64 years was relatively consistent (approximately 15% to 20%) during April–December 2020 (Figure 1).

Among persons aged ≥65 years, percentage excess mortality among Hispanic persons peaked at ≥90% in April, July, and December 2020. Among AI/AN and NH/PI persons in this age group, percentage excess mortality peaked at nearly 100% in December 2020, and among Asian persons, peaks of 100% and >80% were seen in April and December 2020, respectively. For Black persons aged ≥65 years, percentage excess mortality peaked in April 2020, at nearly 120%, with smaller peaks of 38% in July 2020 and 32% in December 2020. Percentage excess mortality among White persons aged ≥65 years peaked at 29% in April 2020 and 39% in December 2020 (Figure 1).

Black persons had the highest excess mortality IR among all persons aged <25 years with 14.1 excess deaths per 100,000 person-years in 2020, followed by AI/AN persons (6.5). Among adults aged 25–64 years, the highest total excess mortality IR was among AI/AN persons (221.1), followed by Black (133.4), NH/PI (124.9), Hispanic (98.5), White (51.2) and Asian persons (30.2). Quarterly excess mortality IRs among persons aged 25–64 years fell from April–June 2020 to October–December 2020 among Black persons, were relatively flat for Hispanic and Asian persons, and rose for AI/AN, NH/PI, and White persons. Among adults aged ≥65 years, the largest excess mortality IRs were seen among Black and Hispanic persons (1,033.5 and 1,007.0, respectively), followed by AI/AN (650.0), White (500.1), Asian (483.7), and NH/PI persons (426.4). Among Asian and Black adults aged ≥65 years, excess mortality IRs peaked during April–June and declined thereafter. Among Hispanic adults in this age group, excess mortality IRs were stable from April–June 2020 through October–December 2020; quarterly excess mortality IRs were highest in October–December 2020 for AI/AN, NH/PI, and White adults aged ≥65 years (Figure 2).

Among persons aged <25 years, the percentage of excess mortality directly attributed to COVID-19 during 2020 ranged from 9.8% (Black persons) to 34.3% (AI/AN persons) (Table). Among those aged 25–64 years, the percentage ranged from 46.4% (White persons) to 79.2% (NH/PI persons). Among persons aged ≥65 years, the percentage ranged from 78.7% (Black persons) to 123.8% (AI/AN persons).

Discussion

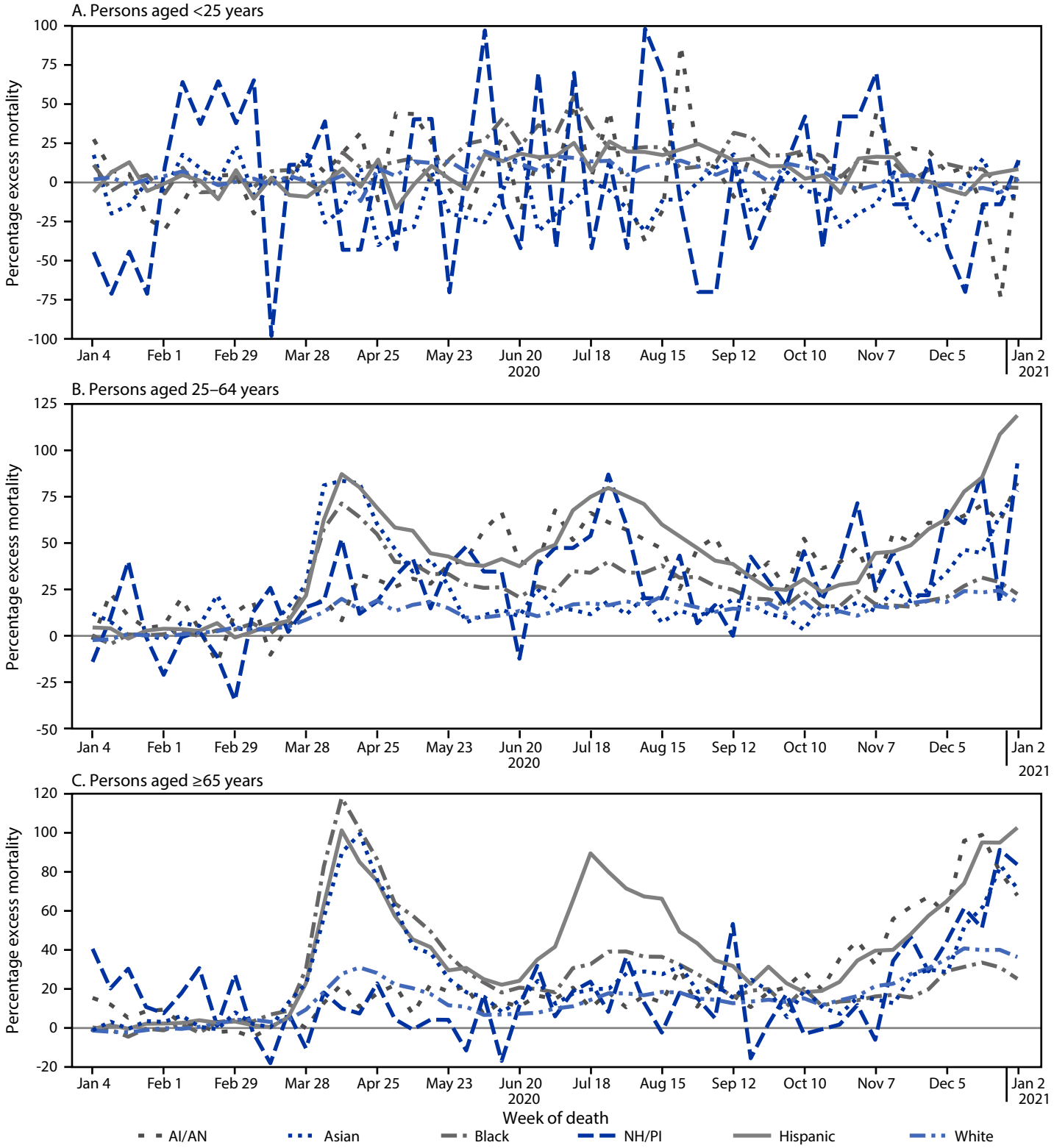
During the COVID-19 pandemic in 2020, Black and AI/AN persons had the highest excess all-cause mortality IRs among those aged <25 years and aged 25–64 years, whereas among adults aged ≥65 years, the largest excess mortality IRs occurred among Black and Hispanic persons. These findings underscore the disproportionate prevalence of excess mortality during the COVID-19 pandemic in 2020 among racial/ethnic minority groups of all ages in the United States (*1*–*5*), which have been driven, in part, by factors such as occupational risk, socioeconomic factors, housing conditions, reduced access to health care, and discrimination.[¶¶] Findings also illustrate the changing impact of the COVID-19 pandemic over time for different subgroups. Among persons aged ≥65 years, excess mortality IRs peaked during April–June 2020 for Black adults, while remaining consistently elevated among Hispanic adults, and increasing from April–June 2020 to October–December 2020 for AI/AN, NH/PI, and White adults. Additional research might help elucidate the factors that contributed to these differences over time.

Recent reports indicate that Black and AI/AN populations experienced the highest age-adjusted death rates in 2020 (*8*), and that the largest percentage excess mortality occurred among

[§§] 45 C.F.R. part 46, 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.

[¶¶] https://www.cdc.gov/coronavirus/2019-ncov/community/health-equity/race-ethnicity.html

FIGURE 1. Weekly percentage excess all-cause mortality* for persons aged <25 years (A), 25–64 years (B), and ≥65 years (C), by race/ethnicity† — United States, 2020

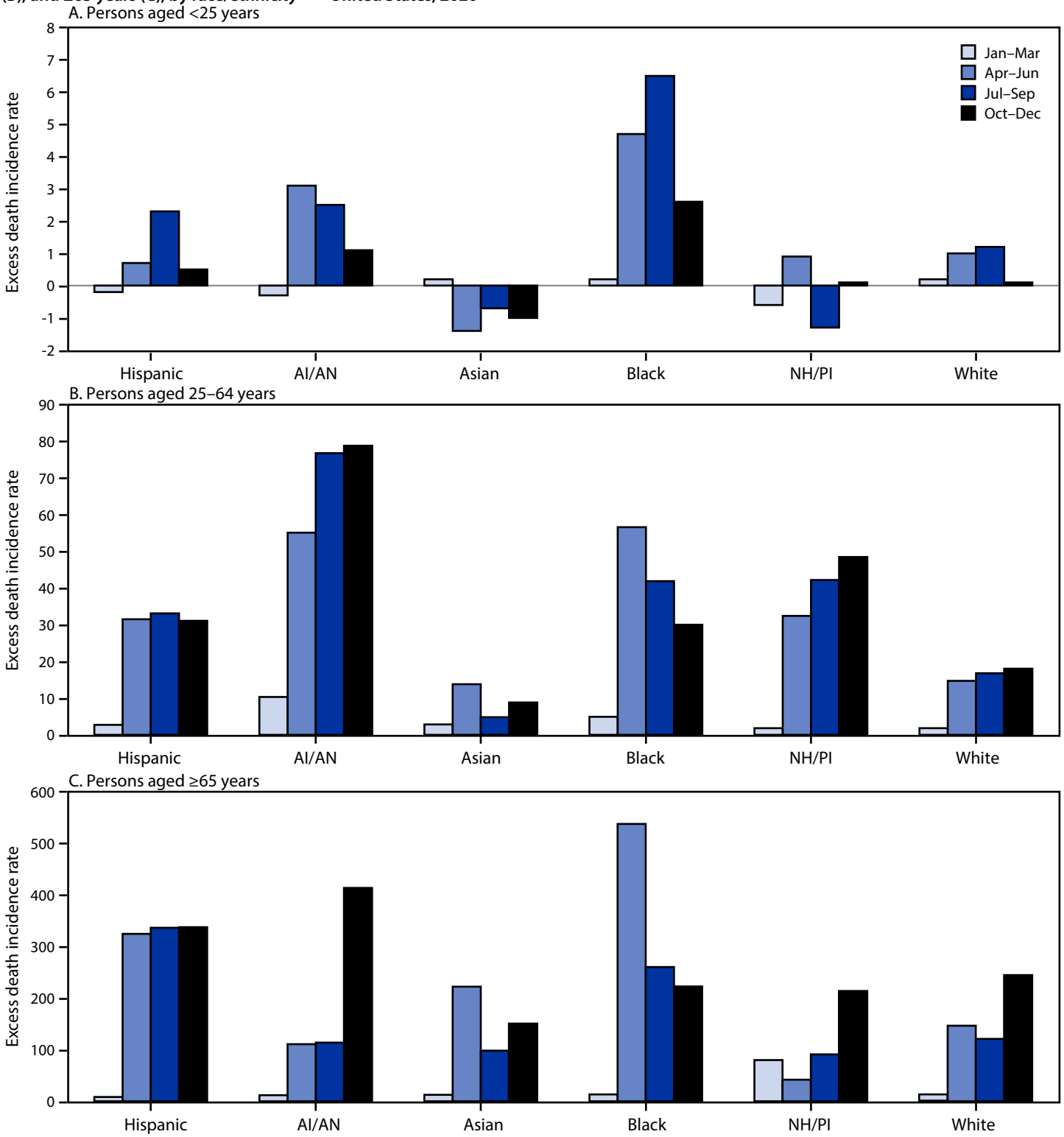


Abbreviations: AI/AN = American Indian/Alaska Native; NH/PI = Native Hawaiian/Other Pacific Islander; sARIMA = seasonal autoregressive integrated moving average.

* Weekly numbers of deaths from all causes by age group and race/ethnicity were obtained from the National Vital Statistics System. The expected numbers of deaths were estimated using sARIMA models of weekly all-cause mortality incidence rates (deaths per 100,000 population-weeks) from 2015–2019, multiplied by the weekly population projections during December 29, 2019–January 2, 2021. The percentage excess corresponds to the number of excess deaths divided by the expected number of deaths. Weeks 1–53 of 2020 are shown. The scale of the y-axis differs for each age group.

† AI/AN, Asian, Black, NH/PI, and White persons were non-Hispanic; Hispanic persons could be of any race.

FIGURE 2. Quarterly excess all-cause mortality incidence rates* and annual excess incidence rates† for persons aged <25 years (A), 25–64 years (B), and ≥65 years (C), by race/ethnicity§ — United States, 2020¶,**



Abbreviations: AI/AN = American Indian/Alaska Native; IR = incidence rates; NH/PI = Native Hawaiian/Other Pacific Islander.

* Excess deaths per 100,000 person-quarters.

† Annual excess death IRs for Hispanic, AI/AN, Asian, Black, NH/PI, and White persons were as follows: aged <25 years: 3.3, 6.5, -2.9, 14.1, -1.0 and 2.2, respectively; aged 25–64 years: 98.5, 221.1, 30.2, 133.4, 124.9, and 51.2, respectively; aged ≥65 years: 1,007.0, 650.0, 483.7, 1,033.5, 426.4, and 500.1, respectively.

§ AI/AN, Asian, Black, NH/PI, and White persons were non-Hispanic; Hispanic persons could be of any race.

¶ Weeks 1–52 (week 53 omitted to ensure each quarter consisted of 13 weeks and the four quarters summed to the total). The scale of the y-axis differs for each age group.

** Negative excess mortality IRs mean that there were fewer deaths than expected for that group.

TABLE. Total number of excess deaths* and percentage of total excess deaths that were directly attributed to COVID-19, by age group and race/ethnicity† — United States, 2020

Age group, yrs	Race/Ethnicity	No. of excess deaths (% directly attributed to COVID-19)
<25	Hispanic	857 (33.7)
	American Indian or Alaska Native	58 (34.3)
	Asian	−158 (NA)
	Black	1,983 (9.8)
	Native Hawaiian or Other Pacific Islander	−2 (NA)
	White	1,299 (13.6)
25–64	Hispanic	32,305 (77.7)
	American Indian or Alaska Native	2,950 (61.2)
	Asian	3,613 (76.8)
	Black	30,035 (57.1)
	Native Hawaiian or Other Pacific Islander	447 (79.2)
	White	54,197 (46.4)
≥65	Hispanic	52,132 (85.0)
	American Indian or Alaska Native	2,215 (123.8)
	Asian	13,554 (80.6)
	Black	55,004 (78.7)
	Native Hawaiian or Other Pacific Islander	304 (109.4)
	White	223,995 (93.2)

Abbreviations: IRs = incidence rates; NA = not applicable.

* Weekly numbers of deaths from all causes by age group and race/ethnicity were obtained from the National Vital Statistics System. The expected numbers of deaths were estimated using seasonal autoregressive integrated moving average models of weekly all-cause mortality IRs (deaths per 100,000 population-weeks) during 2015 through 2019, multiplied by the weekly population projections during December 29, 2019–January 2, 2021. The total number of excess deaths corresponded to the sum of the observed number of deaths minus the expected number of deaths during 2020. Negative numbers of excess deaths mean that fewer deaths occurred than were expected for that group; for these values, not applicable is shown for the percentage of excess deaths attributed to COVID-19. Values of >100% mean that the number of COVID-19 deaths exceeds the number of excess deaths in that group. Data include weeks 1–53 of 2020.

† Hispanic persons could be of any race; American Indian or Alaska Native, Asian, Black, Native Hawaiian or Other Pacific islander, and White persons were non-Hispanic.

racial/ethnic minority groups and persons aged 25–44 years (*6*). This study adds to the literature by describing the excess mortality IRs, which account for population size and age structure. The largest excess mortality IRs occurred among persons aged ≥65 years, with notable differences by race/ethnicity across all age groups. Although excess mortality IRs were lowest among those aged <25 years, there were substantial disparities. Of the nearly 2,000 excess deaths among Black persons aged <25 years, >90% were not directly attributed to COVID-19. Given that injury-related causes of death are typically the leading causes of death among younger age groups, these excess deaths among younger groups and related disparities might be related to increases in homicide, drug overdose, and unintentional injuries in 2020 (*9*).

The findings in this report are subject to at least four limitations. First, estimates of excess mortality might vary when different methods are used for estimating the expected numbers of deaths, and might differ from estimates calculated elsewhere. Second, race/ethnicity reported on the death certificate might be misclassified, resulting in underestimation of rates for some groups (i.e., AI/AN, Asian, and Hispanic populations) (*10*); however, data from NVSS remain one of the most complete sources of race/ethnicity data among public health surveillance systems, with data on race/ethnicity missing for <0.3% of records. Third, data are provisional and subject to change; using more recently published population estimates might also influence the results. Finally, baseline expected counts of deaths were estimated separately for each racial/ethnic group, which might understate total inequities, considering baseline differences in mortality rates by race/ethnicity. If the group with the lowest baseline mortality rates was used as the reference group to estimate excess deaths for all other racial/ethnic groups, then disparities would be even wider.

These findings highlight the importance of timely data to address inequities in social determinants of health that increase the risk for death from COVID-19 among racial/ethnic minority groups. Identifying factors that contribute to racial/ethnic disparities in mortality, either directly or indirectly attributable to COVID-19, can help guide tailored public health prevention strategies and equitable allocation of resources, including COVID-19 vaccination, to achieve greater health equity.

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Summary

What is already known about this topic?

Hispanic or Latino, non-Hispanic Black or African American (Black), and non-Hispanic American Indian or Alaska Native populations have been disproportionately affected by the COVID-19 pandemic.

What is added by this report?

Excess mortality incidence rates were higher for persons aged ≥65 years, with notable racial/ethnic disparities across all age groups. In 2020, among Black and Hispanic persons aged ≥65 years, >1,000 excess deaths per 100,000 person-years occurred compared with the number of deaths expected to occur.

What are the implications for public health practice?

These findings could help guide targeted public health messaging and mitigation efforts to reduce disparities in COVID-19–associated mortality in the United States, by identifying the racial/ethnic and age groups with the highest excess mortality rates.

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Use of Rapid Antigen Testing for SARS-CoV-2 in Remote Communities — Yukon-Kuskokwim Delta Region, Alaska, September 15, 2020–March 1, 2021

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Controlling the spread of SARS-CoV-2, the virus that causes COVID-19, in Alaska is challenging. Alaska includes many remote and isolated villages with small populations (ranging from 15 to >1,000 persons) that are accessible only by air from larger communities. Until rapid point-of-care testing became widely available, a primary challenge in the diagnosis of COVID-19 in rural Alaska was slow turnaround times for SARS-CoV-2 test results, attributable to the need to transport specimens to testing facilities. To provide more timely test results and isolation of cases, the Yukon Kuskokwim Health Corporation (YKHC) introduced Abbott BinaxNOW COVID-19 Ag rapid antigen test (BinaxNOW) on November 9, 2020, in the rural Yukon-Kuskokwim Delta region in southwestern Alaska. To evaluate the impact of implementing antigen testing, YKHC reviewed the results of 54,981 antigen and molecular tests for SARS-CoV-2 performed in the Yukon-Kuskokwim Delta during September 15, 2020–March 1, 2021. Introduction of rapid, point-of-care testing was followed by a more than threefold reduction in daily SARS-CoV-2 case rates during approximately 1 month before the introduction of COVID-19 vaccination. The median turnaround time for SARS-CoV-2 test results decreased by >30%, from 6.4 days during September 15–November 8, 2020, to 4.4 days during November 9, 2020–March 1, 2021 (p<0.001). Daily incidence decreased 65% after the introduction of BinaxNOW, from 342 cases per 100,000 population during the week of November 9 to 119 during the week of December 13 (p<0.001). These findings indicate that point-of-care rapid antigen testing can be a valuable tool in reducing turnaround times in rural communities where local access to laboratory-based nucleic acid amplification testing (NAAT) is not readily available and could thereby reduce transmission by facilitating rapid isolation of infected persons, contact tracing, and implementation of local mitigation strategies.

YKHC introduced BinaxNOW in Yukon-Kuskokwim Delta villages on November 9, 2020. BinaxNOW is a lateral flow immunoassay performed as a point-of-care test using a nasal swab, with results available in ≤15 minutes. Before the use of BinaxNOW tests, the only local testing capacity in the region was GeneXpert Express (Cepheid) SARS-CoV-2 real-time reverse transcription–polymerase chain reaction (RT-PCR) testing and Abbott ID Now COVID-19 isothermal NAAT in Bethel, Alaska. All other specimens were analyzed by RT-PCR through the Alaska state public health laboratories located in Anchorage and Fairbanks or the Alaska Native Tribal Health Consortium in Anchorage or were sent to a private out-of-state laboratory. Anchorage and Fairbanks are 397 and 522 miles, respectively, from Bethel and are accessible only by air.

Data on persons for whom SARS-CoV-2 antigen or molecular tests were performed in the Yukon-Kuskokwim Delta were obtained from electronic health records at YKHC; 54,981 records of tests performed during September 15, 2020–March 1, 2021 were reviewed. The interval from the date of specimen collection to the date of test result was used to calculate the turnaround time before (September 15–November 8, 2020) and after (November 9, 2020–March 1, 2021) introduction of BinaxNOW testing. During the period after BinaxNOW introduction, the turnaround time was calculated for NAAT and antigen testing combined. The difference in turnaround times between periods was assessed using the Wilcoxon rank-sum test. BinaxNOW testing was performed primarily on symptomatic persons or persons identified as close contacts of persons with a confirmed case of COVID-19.* The daily COVID-19 incidence (cases per 100,000 persons) was assessed, and using Poisson regression, rates were compared before and after introduction of the BinaxNOW testing. SAS (version 9.4; SAS Institute) was used to conduct analyses. Some persons who received a negative test result might have had multiple specimens collected for testing during the study period; however, these retests were not included in the regression analysis. This activity was reviewed by CDC and was conducted consistent with applicable federal law and CDC policy.†

Among 16,027 tests for SARS-CoV-2 performed via NAAT during September 15, 2020–November 8, 2020 (before BinaxNOW introduction), 1,223 (7.6%) were positive, 14,778 (92.2%) were negative, and the results for 26 (0.2%) were unknown (Table). The average turnaround

* Symptomatic persons were typically identified through clinic visits or through questionnaires used during mass testing events in villages experiencing outbreaks. Persons who received positive test results were instructed to isolate and were interviewed by a contact tracer. Symptomatic persons and selected close contacts of persons with confirmed COVID-19 who had a high pretest probability of SARS-CoV-2 infection but initially received a negative test result were retested in 3 days.

† 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.

TABLE. Number of SARS-CoV-2 tests performed and test results, by test type, and average turnaround time for receipt of test results before and after introduction of Abbott BinaxNOW COVID-19 Ag rapid antigen test — Yukon-Kuskokwim Delta region, Alaska, September 15, 2020–March 1, 2021

Time	Type of test	No. of tests	Test results, no. (%)			Average turnaround time
			Positive	Negative	Unknown	
Before BinaxNow introduction (Sep 15–Nov 8, 2020)	NAAT	16,027	1,223 (7.6)	14,778 (92.2)	26 (0.2)	5.7–7.9 days
After BinaxNow introduction (Nov 9, 2020–Mar 1, 2021)	NAAT	29,835	2,273 (7.6)	27,024 (90.6)	538 (1.8)	7 days
	BinaxNOW	9,119	1,337 (14.7)	7,782 (85.3)	0 (0)	15 mins
	All	38,954	3,610 (9.3)	34,806 (89.3)	538 (1.4)	4.4 days

Abbreviations: BinaxNOW = Abbott BinaxNOW COVID-19 Ag rapid antigen test; NAAT = nucleic acid amplification test.

time in the central hub community of Bethel was 5.7 days (range = 0.7–13.3 days), and in villages outside Bethel was 7.9 days (range = 0.8–14.6 days). The daily incidence during this time was 342 cases per 100,000 population.

During the period after introduction of BinaxNOW, November 9 through March 1, 2021, among 38,954 total tests performed including 9,119 (23.4%) using BinaxNOW and 29,835 (76.6%) using NAAT, a total of 3,610 (9.3%) were positive, 34,806 (89.4%) were negative, and the results for 538 (1.4%) were unknown. Among the 9,119 BinaxNOW tests, 1,337 (14.7%) were positive, and among 29,835 NAAT 2,273 (7.6%) were positive. BinaxNOW tests accounted for 37% of all positive test results during this period.

The median turnaround times for BinaxNOW and NAAT results were 15 minutes and 7 days, respectively; the overall median turnaround time after BinaxNOW introduction decreased to 4.4 days (range = 0.1–12.4 days) ($p<0.001$). Daily COVID-19 incidence declined to 119 during the week of December 13, 2020 ($p<0.001$) (Figure).

Discussion

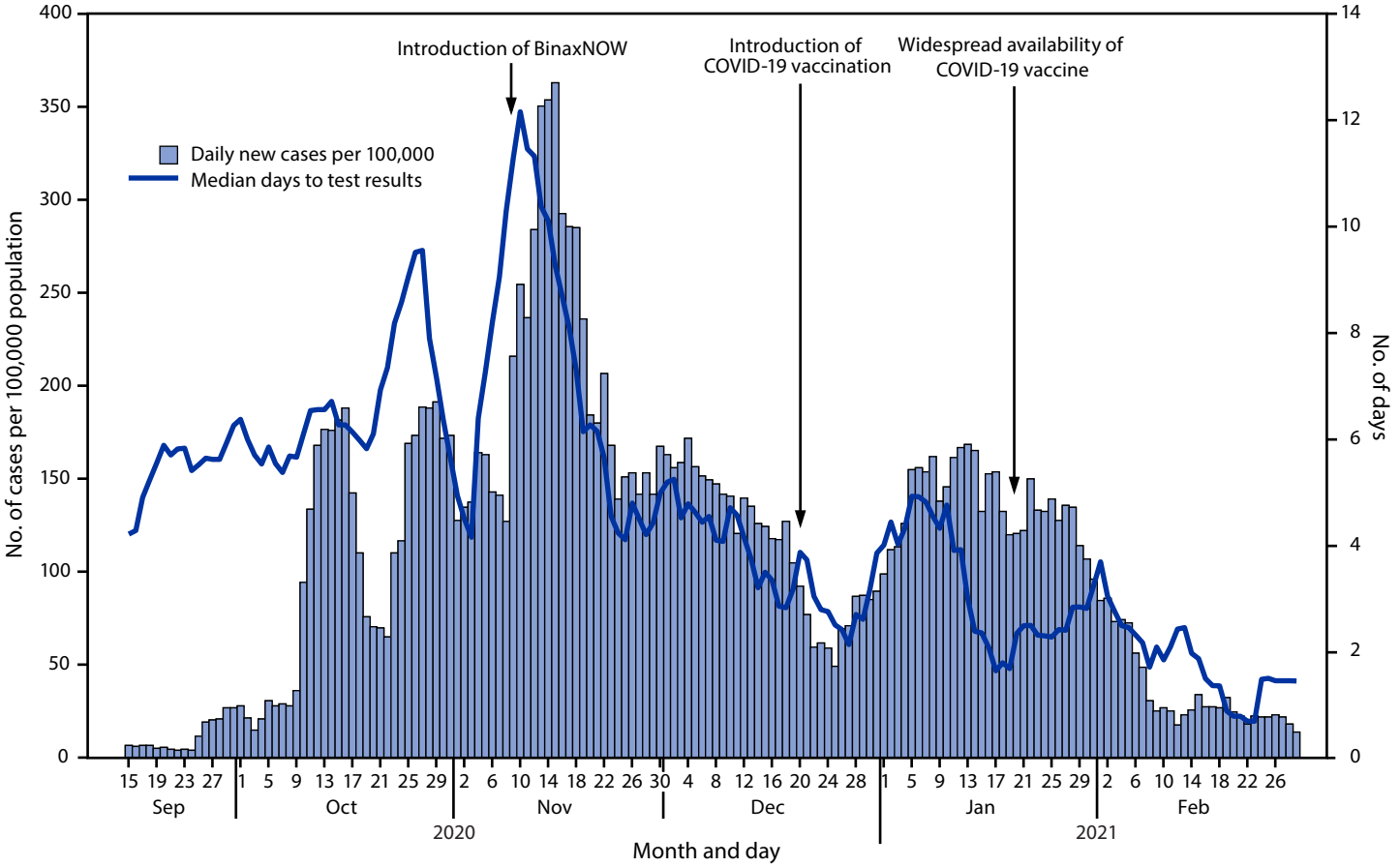
The findings from this ecologic study indicate that introduction of rapid point-of-care antigen testing in remote villages and other community settings allowed for same-day identification of infected persons, which in turn facilitated prompt isolation, contact tracing, and quarantine of close contacts. The use of rapid antigen testing also allowed for implementation of early public health interventions that might have changed the trajectory of SARS-CoV-2 outbreaks occurring in the region, such as recommending specific and tailored prevention strategies to small communities. As cases were identified, local tribal councils and governments were notified to provide situational awareness and prompt appropriate mitigation measures, including scheduled visitation with selected family members for funerals or religious ceremonies and implementation of changes in operations at local businesses to limit capacity.

The rapid identification and isolation of infected persons made possible by introduction of BinaxNOW testing in early November 2020 might have contributed to a decrease in SARS-CoV-2 transmission before the introduction COVID-19 vaccination in the region on December 17, 2020, and its availability to all Yukon-Kuskokwim Delta residents on January 19, 2021. The sharp drop in cases after February 1 was likely attributable primarily to rapidly increasing vaccination coverage rates, highlighting the importance of vaccination in preventing ongoing transmission of SARS-CoV-2. Rapid identification of cases of COVID-19 after introduction of BinaxNOW had the benefit of promptly providing infected persons with a recovery kit (equipment for home monitoring of temperature and oxygen saturation). Recovery kits were given to infected persons by the health care provider in the village who performed the test. Infected persons at higher risk for complications might have been identified sooner in the course of their illness, allowing for timely monitoring and intervention if their health status began to deteriorate.

The higher percentage of positive test results observed for BinaxNOW testing (14.7%) compared with that for NAAT (7.4%) likely occurred because the antigen tests were used for diagnostic testing of symptomatic persons and close contacts of confirmed cases, whereas the NAAT tests were usually used for screening testing. The difference in percentage of positive test results between BinaxNOW and NAAT might be due in part to the differences in sensitivity and specificity of the two types of tests. The practice of using antigen tests for symptomatic persons and those considered to be at high risk because of exposure and reserving NAAT for those at lower risk might be useful in settings in which resources are limited for NAAT tests or turnaround times are too long to implement effective isolation. Furthermore, rapid identification of persons who are contagious might have important public health implications in regions like the Yukon-Kuskokwim Delta where crowded housing and inadequate sanitation are common (*1*–*3*) and could facilitate more rapid outbreak spread. Further public health impacts in the region include the disproportionate effect COVID-19 has had on Alaska Native persons (*4*–*6*), who account for 89% of the population in the Yukon-Kuskokwim Delta region (*3*).

The findings in this report are subject to at least four limitations. First, the study is ecologic with no control region, therefore, a causal relationship cannot be inferred between

FIGURE. Daily COVID-19 incidence* and median turnaround time for test results, by week — Yukon-Kuskokwim Delta region, Alaska, September 15, 2020–March 1, 2021



Abbreviation: BinaxNOW = Abbott BinaxNOW COVID-19 Ag rapid antigen test.
* Cases per 100,000 population.

introduction of BinaxNOW and the observed reduction in numbers of cases. The extent to which other factors, such as enhanced community mitigation efforts, might have contributed to the steep decline in case counts in November is unclear. Second, antigen tests have a higher false negative rate for the presence of virus than most molecular diagnostic tests (*7*). This might have led to lower detection of cases, particularly among asymptomatic persons, because symptomatic persons who received a negative test result were typically retested in 3 days. Moreover, one of the unanticipated challenges of relying on rapid point-of-care antigen testing was that persons frequently mistook a negative antigen test result as an indication that they no longer needed to isolate until serial repeat testing was completed. Third, not all persons who had a negative antigen test result were retested, which might have decreased the false-negative error rate. Finally, the definition of turnaround time could not practically include the time from obtaining the laboratory result to the point of interaction with the person tested, and variation in responsiveness to instructions to isolate could affect the conclusion.

High vaccination coverage is necessary to reduce COVID-19–related morbidity and mortality. The findings from this study indicate that rapid point-of-care antigen testing can be a valuable tool in reducing test turnaround times in rural communities where local access to laboratory-based NAAT is not readily available. Quickly providing infected persons with a positive test result could help facilitate actions to reduce further SARS-CoV-2 transmission, including prompt isolation, contact tracing, appropriate quarantine of close contacts, and prompt initiation of treatment when warranted.

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Summary

What is already known about this topic?

Until the widespread availability of rapid point-of-care COVID-19 testing, one of the primary challenges in rural Alaska was slow turnaround times for SARS-CoV-2 laboratory-based nucleic acid amplification test results.

What is added by this report?

Introduction of rapid, point-of-care antigen testing in Alaska's remote Yukon-Kuskokwim Delta region was followed by a more than threefold reduction in daily SARS-CoV-2 case rates during approximately 1 month before the introduction of COVID-19 vaccination.

What are the implications for public health practice?

Rapid point-of-care antigen testing shortens the turn-around time and might be a valuable tool in reducing transmission of SARS-CoV-2 in rural communities by facilitating rapid isolation and quarantine.

All authors have completed and submitted the International Committee of Medical Journal Editors form for disclosure of potential conflicts of interest. No potential conflicts of interest were disclosed.

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Notes from the Field

Vitamin D–Deficient Rickets and Severe Hypocalcemia in Infants Fed Homemade Alkaline Diet Formula — Three States, August 2020–February 2021

Diane P. Calello[1,2]; Mohamed Jefri[1,2]; Melissa Yu[3]; Joseph Zarraga[3]; David Bergamo[4]; Richard Hamilton[3,5]

During August 2020–February 2021, three infants were treated in separate emergency departments in New Jersey, Pennsylvania, and Delaware for symptoms related to consumption of a nutritionally deficient homemade formula based on alkaline diet recipes, with resultant severe hypocalcemia and vitamin D–deficient rickets. Homemade infant formulas and vegan diets might be deficient in essential vitamins and nutrients as has been reported for other formulas (*1*,*2*).

Case 1. On January 29, 2021, a male infant aged 4 months experienced respiratory distress at home and became unresponsive. Emergency medical services found the infant to be pale, lethargic, tachycardic, and hypoxemic (oxygen saturation = 80% [normal ≥95%]), and transported him to the hospital, where he experienced several episodes of bradycardia and cardiac arrest despite emergency endotracheal intubation and mechanical ventilation, insertion of a central venous catheter, fluid replacement, and high-dose intravenous calcium. After the infant was successfully resuscitated, computed tomography and magnetic resonance imaging scans indicated that the infant had diffuse hypoxic brain injury. Laboratory evaluation revealed profound electrolyte abnormalities (anion gap acidosis pH: 6.67 [normal = 7.35–7.45], lactate: 8.3 mmol/L [normal = 0.22–2.98 mmol/L], serum sodium: 164 mEq/L [normal = 135–145 mEq/L], potassium: 6.9 mEq/L [normal = 3.5–5.5 mEq/L], and calcium: 4.0 mg/dL [normal = 8.8–10.8 mg/dL]). Radiographs showed diffuse bone demineralization with flaring and irregularities of long-bone metaphyses consistent with rickets. The child had been fed a homemade formula of sea moss (an intended iodine source), hemp seeds, and coconut water for approximately 1 month.

Case 2. On January 26, 2021, a male infant aged 5 months was treated in an emergency department after experiencing an episode of extremity stiffening, cyanosis, and brief apnea. Laboratory evaluation revealed that serum calcium was 4.5 mg/dL (normal = 8.8–10.8 mg/dL) with elevated alkaline phosphatase and lactate. Radiographs showed diffuse demineralization with fraying metaphyseal contours consistent with rickets. His parents reported transitioning him at age 3 months to a homemade formula made of coconut water, hemp seed hearts, dates, sea moss gel, and alkaline water. He received high-dose intravenous calcium and magnesium and was discharged home after being placed on a diet of commercial infant formula.

Case 3. On August 7, 2020, a male infant aged 9 months was evaluated after 5 days of irritability. Physical examination revealed weight and length below the third percentile, frontal bossing (prominent, protruding forehead), decreased tone (inability to sit without assistance), and gross and fine motor delays. Laboratory evaluation showed severe hypocalcemia, no detectable vitamin D, and a thyroid stimulating hormone level of 94,600 mU/L (normal = 0.5–5 mU/L). Long-bone radiographs demonstrated frayed metaphyses and tibial bowing. The patient received diagnoses of rickets and iodine deficiency. His parents reported feeding him homemade formula on an alkaline vegan diet consisting of coconut milk, dates, and sea moss, although the sea moss had been discontinued several months earlier. He was treated with iodine and calcium supplementation and was discharged to a long-term care facility.

Each of these infants had been fed a homemade formula, reported by their parents as the alkaline diet. Recipes associated with this diet, several variations of which can be found online, show it lacks essential vitamins and micronutrients such as vitamin D, calcium, and iodine. CDC and the Food and Drug Administration have issued warnings about the use of homemade infant formula.[*,†] These three cases highlight the potential for grave consequences (*1*,*2*). Parents should be cautioned to avoid this inappropriate substitute for breast milk or commercial infant formula that can cause hypovitaminosis D, hypocalcemic cardiorespiratory failure, and hypothyroidism, resulting in lasting harm and possibly death.

Human breast milk and commercial infant formula contain vitamins and micronutrients essential for growth and development (*3*). Infants fed an alternative diet can develop severe deficiencies and experience long-lasting developmental consequences. The Food and Drug Administration has advised parents and caregivers not to feed homemade formulas to infants, and guidance on choosing an infant formula is available from CDC.

[*] https://www.fda.gov/food/alerts-advisories-safety-information/fda-advises-parents-and-caregivers-not-make-or-feed-homemade-infant-formula-infants

[†] https://www.cdc.gov/nutrition/InfantandToddlerNutrition/formula-feeding/choosing-an-infant-formula.html

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Errata

Vol. 70, No. 27

In the report "Outcomes Among Patients Referred to Outpatient Rehabilitation Clinics After COVID-19 diagnosis — United States, January 2020–March 2021," on page 967, the following authors' names should have read, "Meredith **G. Dixon**, MD" and "Caitlyn **Lutfy**, MPH." On page 970, in Table 3, in the row for "Social participation ability," in the columns for "Post–COVID-19 patients," "Control patients," and "mean difference" the summary scale T-score mean standard deviations and mean differences should have read, "**46.6 (44.7 to 48.6)**," "**50.5 (50.0 to 51.1)**," and " **–4.2 (–6.4 to –2.0)**," respectively.

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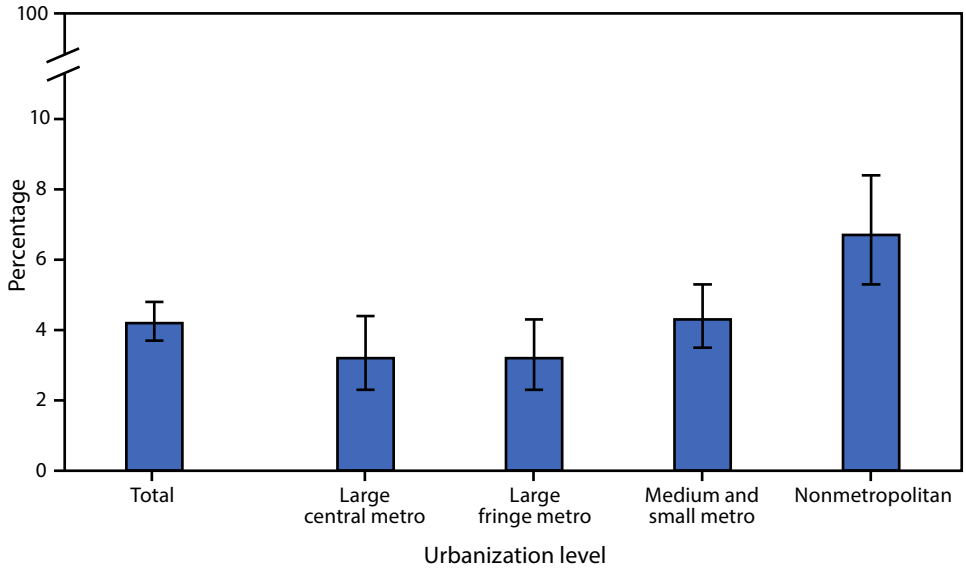
In the report "Progress Toward Hepatitis B Control — World Health Organization European Region, 2016–2019," on page 1030, in the second column, first paragraph, the last sentence should have read, "Of the 21 countries with universal HepB-BD that reported birth dose coverage to WHO,††† coverage with timely HepB-BD during 2016–2019 was ≥90% in **19–20** (90%–95%) **countries**."

QuickStats

FROM THE NATIONAL CENTER FOR HEALTH STATISTICS

Age-Adjusted Percentage* of Adults Aged ≥65 Years Who Have a Lot of Difficulty Hearing or Cannot Hear at All Even When Using Hearing Aids,† by Urbanization Level§ — National Health Interview Survey, United States, 2019¶



* Age-adjusted percentages are based on the 2000 U.S. Census standard population, using age groups 65–74, 75–84, and ≥85 years, with 95% confidence intervals indicated by error bars.
† Based on responses to the survey question, "Do you have difficulty hearing, even when using your hearing aid(s)? Would you say no difficulty, some difficulty, a lot of difficulty, or are you unable to do this?"
§ Urbanization level is determined by the Office of Management and Budget's February 2013 delineation of metropolitan statistical areas (MSAs), in which each MSA must have at least one urbanized area of ≥50,000 inhabitants. Areas with <50,000 inhabitants are grouped into the nonmetropolitan category.
¶ Estimates are based on household interviews of a sample of the civilian, noninstitutionalized U.S. population.

In 2019, 4.2% of U.S. adults aged ≥65 years had a lot of difficulty hearing or could not hear at all even when using hearing aids. Percentages were highest in nonmetropolitan areas (6.7%). The differences between percentages in large central (3.2%), large fringe metropolitan (3.2%), and medium and small metropolitan (4.3%) areas were not statistically significant.

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

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