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Health-Related Workplace Absenteeism Among Full-Time Workers — United States, 2017–18 Influenza Season

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During an influenza pandemic and during seasonal epidemics, more persons have symptomatic illness without seeking medical care than seek treatment at doctor's offices, clinics, and hospitals (*1*). Consequently, surveillance based on mortality, health care encounters, and laboratory data does not reflect the full extent of influenza morbidity. CDC uses a mathematical model to estimate the total number of influenza illnesses in the United States (*1*). In addition, syndromic methods for monitoring illness outside health care settings, such as tracking absenteeism trends in schools and workplaces, are important adjuncts to conventional disease reporting (*2*). Every month, CDC's National Institute for Occupational Safety and Health (NIOSH) monitors the prevalence of health-related workplace absenteeism among full-time workers in the United States using data from the Current Population Survey (CPS) (*3*). This report describes the results of workplace absenteeism surveillance analyses conducted during the high-severity 2017–18 influenza season (October 2017–September 2018) (*4*). Absenteeism increased sharply in November, peaked in January and, at its peak, was significantly higher than the average during the previous five seasons. Persons especially affected included male workers, workers aged 45–64 years, workers living in U.S. Department of Health and Human Services (HHS) Region 6* and Region 9,† and those working in management, business, and financial; installation, maintenance, and repair; and production and related occupations. Public health authorities and employers might consider results from relevant absenteeism surveillance analyses when developing prevention messages and in pandemic preparedness planning. The most effective ways to prevent influenza transmission in the workplace include vaccination and nonpharmaceutical interventions, such as staying home when sick, covering coughs and sneezes, washing hands frequently, and routinely cleaning frequently touched surfaces (*5*).

CPS is a monthly national survey of approximately 60,000 households conducted by the U.S. Census Bureau for the Bureau of Labor Statistics. The survey collects information on employment, demographics, and other characteristics of the civilian, noninstitutionalized population aged ≥16 years; CPS is the nation's primary source of labor force statistics. Data on all sample household members are collected from a single respondent by trained interviewers using a standardized questionnaire during in-person or telephone interviews (*3*). During July 2016–June 2018, the response rates ranged from 84% to 88%.§

A full-time worker is defined as an employed person who reports usually working ≥35 hours per week. Health-related

*HHS Region 6 includes the states of Arkansas, Louisiana, New Mexico, Oklahoma, and Texas. https://www.hhs.gov/about/agencies/iea/regional-offices/index.html.

†HHS Region 9 includes the states of Arizona, California, Hawaii, and Nevada. https://www.hhs.gov/about/agencies/iea/regional-offices/index.html.

§https://www.census.gov/programs-surveys/cps/technical-documentation/methodology/non-response-rates.html.

INSIDE

Continuing Education examination available at https://www.cdc.gov/mmwr/cme/conted_info.html#weekly.

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workplace absenteeism is defined as working <35 hours during the reference week because of the worker's own illness, injury, or other medical issue. Because CPS questions refer to 1 week of each month, absenteeism during the other weeks is not measured. These 1-week measures are intended to be representative of all weeks of the month during which they occur.

Each month, NIOSH updates an influenza season–based time series of the prevalence of health-related workplace absenteeism among full-time workers with the previous month's estimate (i.e., with a 1-month lag). Point estimates and 95% confidence intervals (CIs) are calculated and compared with an epidemic threshold defined as the 95% upper confidence limit of a baseline established using data from the previous five seasons, aggregated by month (*6*). Estimates with lower 95% confidence limits that exceed the epidemic threshold are considered significantly elevated. Estimates by sex, age group, geographic region (HHS Regions[¶]), and specific occupational group[**] are also calculated.

[¶] HHS Regions are used for consistency with geographic regions used in CDC's ILI surveillance. https://www.cdc.gov/flu/weekly/overview.htm.

[**] Occupational groups correspond to the CPS Major Occupational Group recodes, which are groupings of Census Occupation Codes (https://www2.census.gov/programs-surveys/cps/methodology/Occupation%20Codes.pdf). The Census Occupation Codes are, in turn, based on the 2010 Standard Occupational Classification codes promulgated by the Bureau of Labor Statistics (https://www.bls.gov/soc/2018/home.htm).

Using these data, health-related workplace absenteeism prevalence during the high-severity 2017–18 influenza season (October 2017–September 2018) was analyzed. All analyses were weighted using the CPS composite weight, and estimates of all standard errors were adjusted to account for the complex design of the CPS sample. Analyses were performed using SAS software (version 9.4; SAS Institute).

The prevalence of health-related workplace absenteeism among full-time workers was 1.7% (95% CI = 1.6%–1.8%) in October 2017, increased sharply beginning in November, peaked in January 2018 at 3.0% (95% CI = 2.8%–3.2%), and declined steadily thereafter to a low of 1.4% (95% CI = 1.3%–1.5%) in July before gradually increasing again in August and September (Table). The January absenteeism peak significantly exceeded the epidemic threshold (Figure 1). Absenteeism remained elevated in February, but not significantly. Peak absenteeism in the 2017–18 influenza season exceeded that of any of the five previous seasons except the 2012–13 season (Figure 2).

The epidemic threshold was significantly exceeded for the following subgroups: male workers in January and February; workers aged 45–64 years in January and February; workers in HHS Region 6 in January and February and in Region 9 in December and March; and workers in management, business, and financial occupations and installation, maintenance, and repair occupations in January and in production and related

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TABLE. Monthly prevalence of health-related workplace absenteeism* among full-time workers† during the 2017–2018 influenza season, by sex, age group, U.S. Department of Health and Human Services (HHS) region§ and occupational group — Current Population Survey, United States, October 2017–September 2018

	Weighted % (95% CI)											
	2107			2018								
Characteristic	Oct	Nov	Dec	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep
Overall	**1.7 (1.6–1.8)**	**1.8 (1.6–1.9)**	**2.3 (2.1–2.4)**	**3.0 (2.8–3.2)¶**	**2.7 (2.5–2.9)**	**2.2 (2.0–2.3)**	**2.0 (1.8–2.1)**	**1.8 (1.6–1.9)**	**1.7 (1.6–1.8)**	**1.4 (1.3–1.5)**	**1.6 (1.4–1.8)**	**1.9 (1.7–2.0)**
Sex												
Male	1.4 (1.3–1.5)	1.4 (1.2–1.5)	1.9 (1.7–2.1)	2.6 (2.4–2.9)¶	2.3 (2.1–2.4)¶	1.9 (1.7–2.1)	1.7 (1.5–1.8)	1.3 (1.2–1.5)	1.5 (1.3–1.6)	1.2 (1.0–1.4)	1.5 (1.3–1.7)	1.6 (1.3–1.8)
Female	2.1 (1.9–2.4)	2.3 (2.0–2.5)	2.8 (2.5–3.0)	3.6 (3.3–3.8)	3.2 (2.9–3.5)	2.5 (2.4–2.7)	2.3 (2.1–2.5)	2.4 (2.1–2.7)	2.1 (1.9–2.3)	1.7 (1.5–1.9)	1.8 (1.6–2.0)	2.2 (2.0–2.4)
Age group (yrs)												
16–24	1.8 (1.3–2.3)	1.7 (1.2–2.3)	2.0 (1.4–2.6)	3.2 (2.4–4.1)	2.4 (1.7–3.0)	1.6 (0.9–2.2)	1.7 (1.1–2.3)	2.2 (1.7–2.8)	1.5 (1.1–1.8)	1.4 (1.0–1.7)	1.1 (0.8–1.5)	2.0 (1.5–2.4)
25–44	1.5 (1.4–1.6)	1.6 (1.4–1.7)	2.0 (1.8–2.2)	2.5 (2.3–2.7)	2.4 (2.2–2.6)	2.0 (1.8–2.1)	1.6 (1.4–1.8)	1.5 (1.3–1.7)	1.5 (1.3–1.7)	1.2 (1.0–1.4)	1.5 (1.2–1.7)	1.7 (1.5–1.9)
45–64	1.8 (1.6–2.0)	1.9 (1.7–2.0)	2.6 (2.3–2.8)	3.4 (3.1–3.7)¶	3.0 (2.8–3.3)¶	2.4 (2.2–2.7)	2.2 (2.0–2.4)	1.8 (1.6–2.0)	1.9 (1.8–2.1)	1.5 (1.3–1.7)	1.7 (1.5–2.0)	1.9 (1.7–2.1)
≥65	3.0 (2.3–3.6)	2.6 (1.8–3.4)	3.1 (2.2–4.1)	4.6 (3.8–5.4)	3.4 (2.5–4.3)	3.2 (2.3–4.1)	4.2 (3.3–5.0)	3.2 (2.3–4.0)	2.8 (1.5–4.0)	2.6 (1.9–3.2)	2.7 (2.0–3.3)	2.7 (1.9–3.4)
HHS region§												
Region 1	1.5 (1.1–1.8)	1.7 (1.2–2.2)	2.1 (1.6–2.5)	3.0 (2.5–3.6)	2.4 (1.7–3.2)	1.5 (1.3–1.7)	2.2 (1.9–2.5)	1.5 (0.9–2.1)	1.9 (1.6–2.2)	1.7 (1.2–2.2)	1.8 (1.3–2.2)	2.0 (1.6–2.4)
Region 2	1.4 (1.1–1.7)	1.3 (0.8–1.8)	1.9 (1.6–2.1)	2.2 (1.6–2.8)	2.0 (1.6–2.5)	2.1 (1.5–2.7)	1.6 (0.8–2.4)	1.4 (1.0–1.7)	1.3 (1.2–1.4)	1.0 (0.7–1.3)	1.3 (0.2–2.5)	1.0 (0.7–1.3)
Region 3	1.5 (1.3–1.8)	1.5 (1.1–1.9)	2.6 (1.8–3.4)	2.8 (2.0–3.5)	3.2 (2.6–3.8)	2.1 (1.6–2.6)	2.4 (2.0–2.7)	1.9 (1.4–2.3)	1.9 (1.5–2.2)	1.6 (1.2–2.1)	1.3 (1.2–1.5)	2.1 (1.4–2.8)
Region 4	1.7 (1.4–2.0)	1.6 (1.4–1.8)	2.0 (1.6–2.4)	2.7 (2.3–3.1)	2.3 (1.9–2.7)	1.9 (1.8–2.0)	1.7 (1.6–1.9)	1.6 (1.4–1.8)	1.6 (1.4–1.8)	1.2 (0.9–1.5)	1.6 (1.3–1.9)	1.5 (1.2–1.9)
Region 5	1.8 (1.6–2.1)	2.1 (1.9–2.2)	2.2 (1.6–2.7)	3.2 (2.5–3.8)	3.0 (2.4–3.5)	2.3 (1.8–2.8)	2.2 (1.7–2.7)	1.8 (1.6–2.0)	1.9 (1.6–2.1)	1.3 (1.0–1.6)	1.6 (1.1–2.2)	2.1 (1.8–2.4)
Region 6	1.7 (1.6–1.8)	1.8 (1.5–2.1)	2.1 (1.8–2.3)	3.3 (3.1–3.6)¶	2.7 (2.4–2.9)¶	2.1 (1.6–2.5)	1.8 (1.5–2.1)	1.8 (1.0–2.6)	1.8 (1.4–2.2)	1.3 (0.8–1.7)	1.6 (1.3–1.9)	1.9 (1.6–2.1)
Region 7	2.2 (1.6–2.7)	2.3 (1.3–3.2)	2.3 (2.1–2.5)	2.7 (2.3–3.2)	3.0 (2.6–3.4)	2.5 (1.5–3.5)	2.4 (1.7–3.2)	1.8 (1.5–2.1)	2.2 (1.6–2.8)	1.9 (1.5–2.2)	1.6 (1.1–2.0)	1.6 (0.9–2.3)
Region 8	1.6 (0.9–2.4)	1.4 (1.2–1.6)	2.0 (1.2–2.8)	2.7 (2.4–3.0)	3.2 (1.8–4.6)	1.9 (1.5–2.3)	1.9 (1.7–2.1)	1.6 (1.2–2.1)	1.3 (1.2–1.5)	1.6 (1.3–1.9)	1.5 (0.8–2.2)	1.6 (0.9–2.3)
Region 9	1.7 (1.3–2.0)	1.9 (1.3–2.4)	2.7 (2.6–2.8)¶	3.5 (2.9–4.1)	2.6 (2.1–3.2)	2.7 (2.5–2.8)¶	1.7 (1.5–1.9)	2.1 (1.5–2.6)	1.6 (1.5–1.8)	1.6 (1.2–1.9)	1.8 (1.6–2.0)	2.2 (1.6–2.8)
Region 10	2.4 (2.1–2.6)	1.7 (1.4–2.0)	3.4 (2.0–4.7)	4.0 (3.1–4.8)	2.7 (2.4–3.1)	2.8 (2.2–3.4)	2.1 (1.5–2.6)	2.4 (1.9–2.8)	1.8 (0.7–2.9)	1.9 (1.3–2.5)	1.9 (1.4–2.5)	2.3 (2.1–2.5)
Occupational group												
Management, business and financial	1.2 (1.0–1.4)	1.3 (1.0–1.6)	1.7 (1.4–2.1)	2.6 (2.4–2.9)¶	2.1 (1.8–2.3)	1.7 (1.3–2.2)	1.6 (1.3–1.9)	1.4 (1.1–1.6)	1.2 (0.9–1.4)	1.0 (0.7–1.2)	1.1 (0.9–1.3)	1.2 (0.9–1.4)
Professional and related	1.8 (1.5–2.1)	1.6 (1.4–1.8)	2.0 (1.8–2.2)	2.8 (2.6–3.1)	2.6 (2.3–3.0)	1.8 (1.5–2.1)	1.8 (1.6–2.1)	1.6 (1.3–1.8)	1.4 (1.1–1.7)	1.2 (1.0–1.5)	1.4 (1.1–1.6)	1.6 (1.3–1.9)
Service	2.2 (1.9–2.6)	2.3 (1.8–2.7)	3.1 (2.6–3.5)	3.4 (2.8–4.0)	2.9 (2.5–3.3)	2.7 (2.2–3.2)	2.3 (1.9–2.7)	2.0 (1.7–2.4)	2.1 (1.8–2.3)	1.7 (1.4–2.0)	2.0 (1.6–2.4)	2.4 (2.0–2.8)
Sales and related	1.5 (1.1–1.9)	1.7 (1.3–2.1)	1.9 (1.4–2.4)	2.7 (2.3–3.1)	2.0 (1.5–2.4)	1.8 (1.3–2.2)	1.5 (1.1–1.8)	1.7 (1.2–2.1)	1.6 (1.1–2.1)	1.3 (1.0–1.5)	1.4 (0.9–1.8)	1.5 (1.1–1.9)
Office and administrative support	1.9 (1.5–2.3)	2.0 (1.5–2.4)	2.5 (2.1–3.0)	3.2 (2.6–3.8)	2.5 (2.1–2.9)	2.7 (2.1–3.3)	2.5 (2.1–3.0)	2.5 (2.0–3.0)	2.4 (2.0–2.8)	1.8 (1.5–2.2)	2.0 (1.6–2.4)	2.6 (2.0–3.1)
Farming, fishing and forestry	2.1 (0.7–3.4)	1.2 (0.2–2.3)	3.3 (1.4–5.2)	3.7 (1.2–6.2)	4.1 (2.4–5.7)	2.3 (0.9–3.7)	3.1 (1.1–5.2)	2.5 (0.0–6.2)	2.0 (0.0–4.2)	1.4 (0.3–2.5)	0.6 (0.0–1.4)	1.7 (0.0–3.6)
Construction and extraction	1.2 (0.8–1.5)	1.5 (1.1–1.8)	2.4 (1.8–3.0)	3.4 (2.8–3.9)	3.3 (2.5–4.0)	2.8 (2.1–3.4)	1.5 (1.0–2.1)	1.8 (1.1–2.5)	1.7 (1.1–2.3)	1.7 (1.0–2.4)	2.0 (1.4–2.5)	2.6 (1.8–3.4)
Installation, maintenance and repair	2.0 (1.2–2.7)	2.6 (1.7–3.4)	2.2 (1.5–2.9)	4.3 (3.3–5.2)¶	2.3 (1.4–3.2)	2.4 (1.4–3.4)	2.0 (1.3–2.6)	1.8 (1.1–2.4)	1.6 (1.1–2.1)	0.9 (0.4–1.3)	1.2 (0.7–1.7)	1.7 (1.0–2.3)
Production	1.9 (1.4–2.5)	2.1 (1.5–2.6)	2.4 (1.6–3.1)	3.2 (2.4–4.0)	4.0 (3.2–4.8)¶	2.6 (2.0–3.2)	2.1 (1.5–2.8)	2.0 (1.4–2.6)	2.2 (1.7–2.7)	1.9 (1.3–2.5)	2.1 (1.5–2.7)	2.1 (1.4–2.8)
Transportation and material moving	1.7 (1.3–2.2)	1.7 (1.0–2.5)	2.7 (2.1–3.3)	3.1 (2.5–3.7)	3.6 (2.9–4.3)	2.3 (1.7–3.0)	2.3 (1.7–2.9)	1.8 (1.2–2.2)	2.2 (1.7–2.8)	1.5 (1.1–2.0)	2.0 (1.4–2.6)	1.9 (1.3–2.4)

Abbreviation: CI = confidence interval.

* Defined as working <35 hours during the reference week because of illness, injury, or other medical issue.

† Defined as employed persons who usually work ≥35 hours per week at all jobs combined.

§ HHS *Region 1:* Connecticut, Maine, Massachusetts, New Hampshire, Rhode Island, and Vermont; *Region 2:* New Jersey, New York, and the territories Puerto Rico and the Virgin Islands; *Region 3:* Delaware, District of Columbia, Maryland, Pennsylvania, Virginia, and West Virginia; *Region 4:* Alabama, Florida, Georgia, Kentucky, Mississippi, North Carolina, South Carolina, and Tennessee; *Region 5:* Illinois, Indiana, Michigan, Minnesota, Ohio, and Wisconsin; *Region 6:* Arkansas, Louisiana, New Mexico, Oklahoma, and Texas; *Region 7:* Iowa, Kansas, Missouri, and Nebraska; *Region 8:* Colorado, Montana, North Dakota, South Dakota, Utah, and Wyoming; *Region 9:* Arizona, California, Hawaii, Nevada and the territories American Samoa, Commonwealth of the Northern Mariana Islands, Federated States of Micronesia, Guam, Marshall Islands, and Republic of Palau; *Region 10:* Alaska, Idaho, Oregon, and Washington.

¶ Significantly exceeded the epidemic threshold.

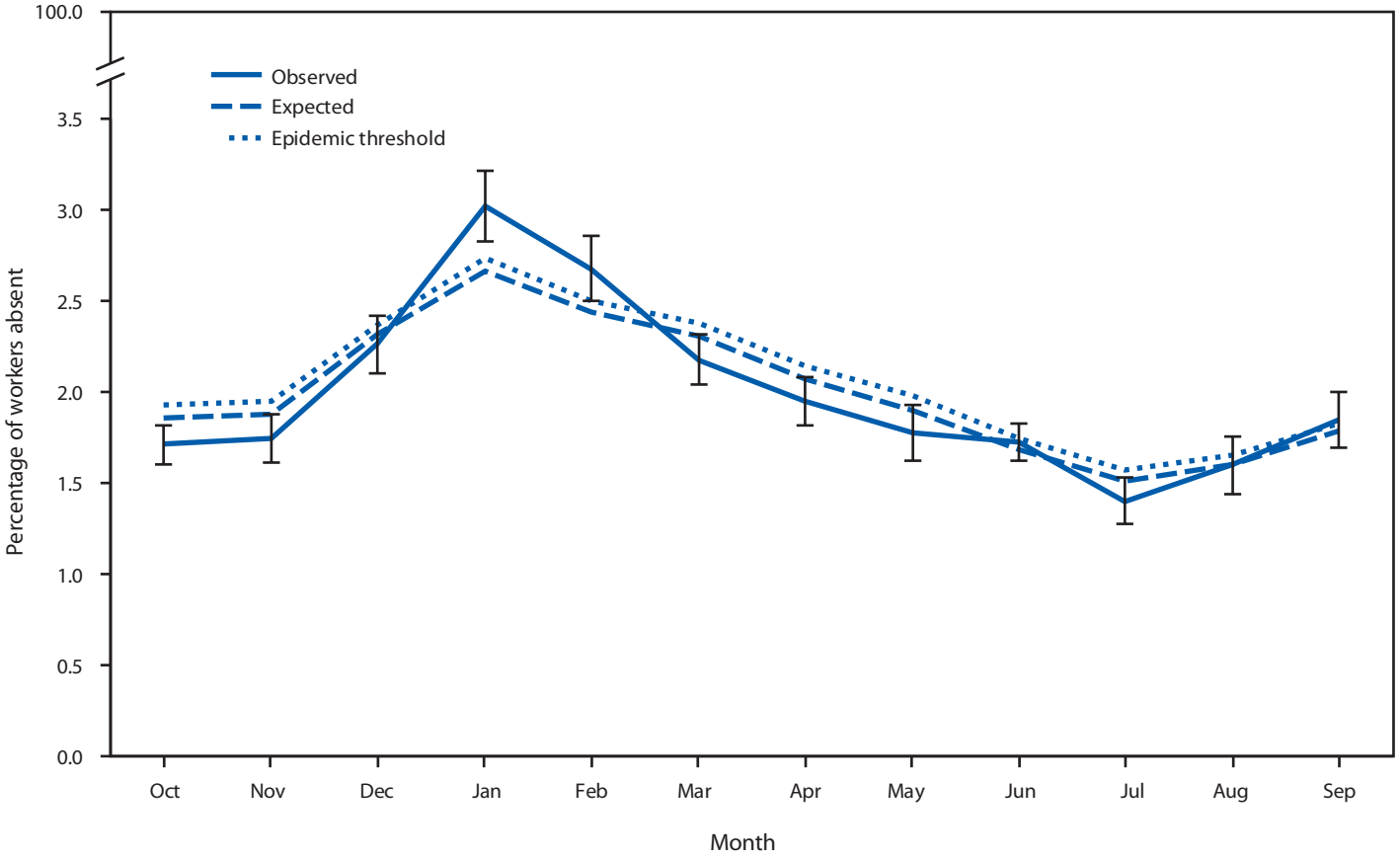
occupations in February (Table) Regional absenteeism peaks corresponded to concurrent peaks in influenza-like illness (ILI) activity in those regions.††

Discussion

These findings for 2017–18 are consistent with those of a study using conventional surveillance data, which characterized that season as a high severity influenza season that accelerated in November and peaked in late January and early February (*4*). For some time, it has been recognized that health-related workplace absenteeism correlates well with the prevalence of ILI and reaches seasonal peaks in conjunction with influenza activity as measured by other established methods during epidemics and pandemics (*7*). NIOSH's experience with workplace absenteeism surveillance during the 2009–10 influenza A(H1N1) pandemic indicated that peak workplace

†† https://gis.cdc.gov/grasp/fluview/fluportaldashboard.html.

FIGURE 1. Observed* versus expected† health-related workplace absenteeism§ among full-time workers¶ — Current Population Survey, United States, 2017–18 influenza season



* Error bars represent 95% confidence intervals (CIs) for point estimates.
† Expected values based on monthly averages for the previous five seasons. Epidemic threshold is the upper 95% CI for expected values.
§ Defined as working <35 hours during the reference week because of illness, injury, or other medical issue.
¶ Defined as employed persons who usually work ≥35 hours per week at all jobs combined.

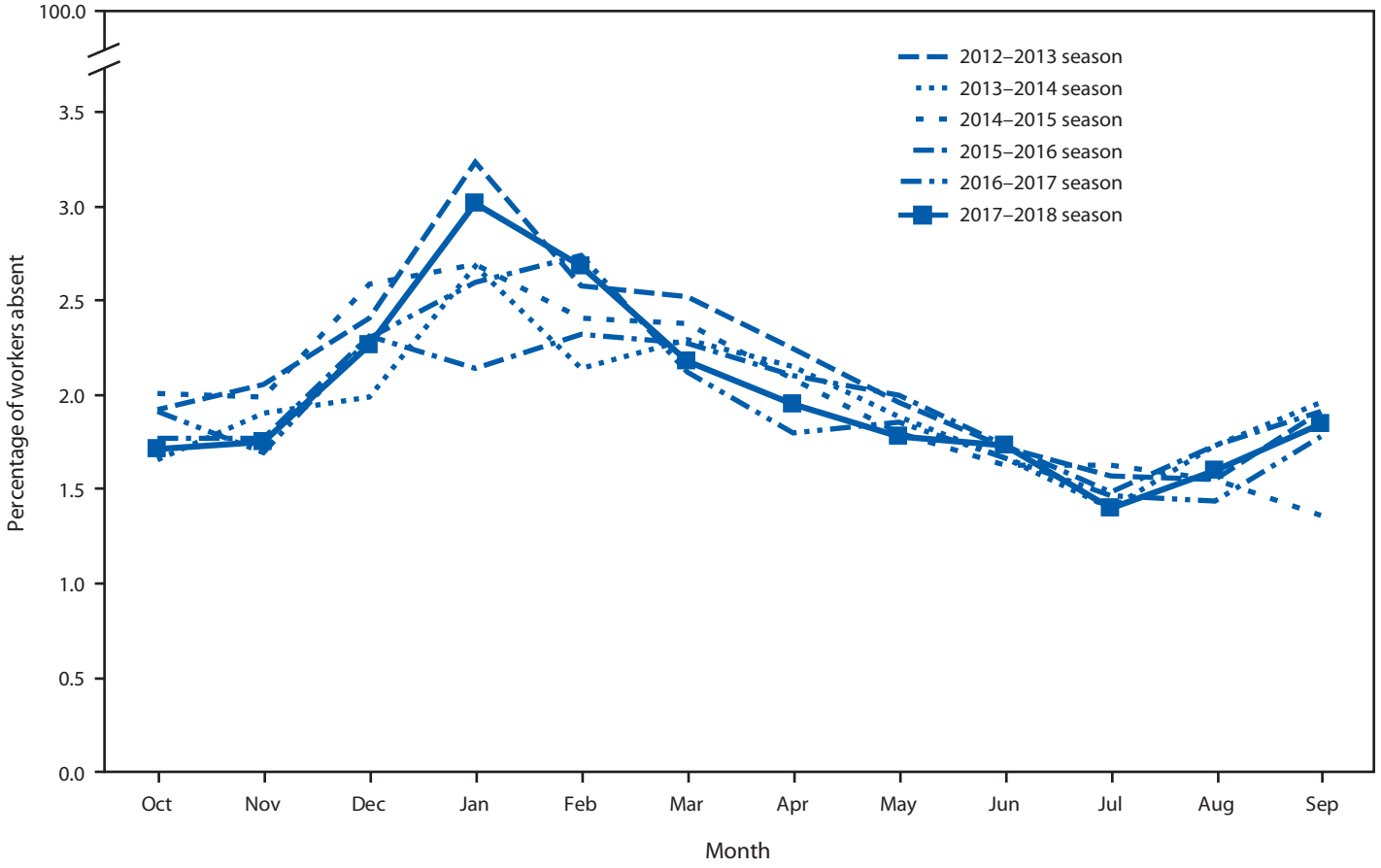
absenteeism was correlated with the highest occurrence of both ILI and influenza-positive laboratory tests (*2*). For this reason, data on workplace absenteeism have been used as a nonspecific or syndromic indicator of the occurrence of ILI in the community in various settings (*2*). Typically, these data have been collected in near real-time from individual or small, nonprobability samples of sentinel worksites, often as part of ad hoc surveillance efforts associated with particular events or outbreaks and intended to serve as epidemic early warning systems. Although timely, such systems are typically difficult to sustain and provide data that are generally less stable and reliable, of lower quality, and subject to increased bias (*2*). Samples from such systems also tend to be small and nonrepresentative and, therefore, less able to reflect variation in patterns of absenteeism across geographic, demographic, and occupational subgroups (*2*).

NIOSH's continuous population-based surveillance of absenteeism makes use of survey data that are valid, reliable, and nationally representative (*2*). Although the 1-month lag precludes CPS data from being sufficiently timely to be used as an early warning system, they are timely enough to provide a useful direct measure of a pandemic's impact on the working population and an indirect measure of a pandemic's economic impact (*8*). CPS data also provide information that can be used to maintain situational awareness during the interpandemic period, to evaluate the impact of control measures implemented during a pandemic (e.g., social distancing measures), and to inform future pandemic preparedness and response planning.

The associations of ILI and workplace absenteeism with occupation and other demographic characteristics are complex and mediated by factors such as vaccination coverage and access to paid sick leave (*9*). More study using additional data sources is needed to fully understand the reasons for increases in absenteeism related to sex, age, or specific occupations that are identified by these surveillance analyses.

The findings in this report are subject to at least five limitations. First, operationalized, health-related workplace

FIGURE 2. Health-related workplace absenteeism* among full-time workers† — Current Population Survey, United States, 2012–13 through 2017–18 influenza seasons



* Defined as working <35 hours during the reference week because of illness, injury, or other medical issue.
† Defined as employed persons who usually work ≥35 hours per week at all jobs combined.

absenteeism includes absences because of injuries, preventive care, and illnesses unrelated to influenza, which could attenuate or confound absenteeism's relation to influenza activity; however, the correlation between absenteeism and influenza activity has repeatedly been found to be strong in the U.S. population. Second, the survey data used for these analyses were self-reported or reported by a family member proxy respondent. Although the 1-week CPS recall period is very short, in principle, these data are subject to recall, social desirability, and other biases that affect self- and proxy-reported data. Third, monthly absenteeism estimates are based on 1-week measures and could have underestimated or overestimated the actual prevalence for any given month in a way not reflected in the 95% CIs. Fourth, the nature of CPS data only allows for calculation of health-related absenteeism among full-time workers; patterns of absenteeism and its relation to ILI might be different among part-time workers. Finally, the amount of overlap between absenteeism and conventional measures of medically attended illness is unknown and variable. Thus, some uncertainty exists regarding the extent to which absenteeism adds to conventional measures of influenza morbidity.

Because workers often share office space and equipment and have frequent face-to-face contact, the workplace can be an important setting for influenza transmission. Nearly two thirds of adults in the United States participate in the workforce, and estimates of influenza attack rates for working-aged adults (18–64 years) can be as high as 14.3% in a given influenza season (*10*). Surveillance of workplace absenteeism can provide an important supplementary measure of a pandemic's impact because conventional morbidity and mortality statistics might not fully reflect the disruption caused to the social and economic life of the community. Workplace absenteeism is also one component of the World Health Organization's Pandemic Influenza Severity Assessment impact indicator.[§§]

[§§] http://www.who.int/influenza/surveillance_monitoring/pisa/pisaindicators/en/.

Summary

What is already known about this topic?

Surveillance using mortality, health care encounters, and laboratory data does not reflect the full extent of influenza morbidity. CDC's National Institute for Occupational Safety and Health conducts monthly monitoring of health-related workplace absenteeism.

What is added by this report?

During the 2017–18 influenza season, absenteeism increased sharply in November and peaked in January, at a level significantly higher than the average during the previous five seasons. Workers who were male, aged 45–64 years, and working in certain U.S. Census regions and occupations were more affected than were other subgroups.

What are the implications for public health practice?

Workplace absenteeism is an important supplementary measure of influenza's impact on the working population that can inform prevention messaging and pandemic preparedness planning.

Vaccination and nonpharmaceutical interventions recommended for everyday use, such as staying home when sick, covering coughs and sneezes, practicing hand hygiene, and routinely cleaning frequently touched surfaces, are the most effective ways to prevent influenza transmission during seasonal epidemics, both in the community and in the workplace (*5*). During a pandemic, additional personal and community nonpharmaceutical interventions might be recommended, including social distancing measures in workplaces (*5*). NIOSH makes current and past seasons' absenteeism surveillance results available online (*6*). State and local health authorities, as well as employers, might wish to consult these results when developing and targeting prevention messages and use them to monitor long-term trends for their jurisdiction during interpandemic periods. Analysis of aggregated absenteeism data from multiple seasons might also help identify occupational groups at higher risk for influenza transmission.

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Bacterial and Fungal Infections in Persons Who Inject Drugs — Western New York, 2017

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During 2014–2017, CDC Emerging Infections Program surveillance data reported that the occurrence of invasive methicillin-resistant *Staphylococcus aureus* (MRSA) infections associated with injection drug use doubled among persons aged 18–49 years residing in Monroe County in western New York.* Unpublished surveillance data also indicate that an increasing proportion of all *Candida* spp. bloodstream infections in Monroe County and invasive group A *Streptococcus* (GAS) infections in 15 New York counties are also occurring among persons who inject drugs. In addition, across six surveillance sites nationwide, the proportion of invasive MRSA infections that occurred in persons who inject drugs increased from 4.1% of invasive MRSA cases in 2011 to 9.2% in 2016 (*1*). To better understand the types and frequency of these infections and identify prevention opportunities, CDC and public health partners conducted a rapid assessment of bacterial and fungal infections among persons who inject drugs in western New York. The goals were to assess which bacterial and fungal pathogens most often cause infections in persons who inject drugs, what proportion of persons who inject use opioids, and of these, how many were offered medication-assisted treatment for opioid use disorder. Medication-assisted treatment, which includes use of medications such as buprenorphine, methadone, and naltrexone, reduces cravings and has been reported to lower the risk for overdose death and all-cause mortality in persons who use opioids (*2*,*3*). In this assessment, nearly all persons with infections who injected drugs used opioids (97%), but half of inpatients (22 of 44) and 12 of 13 patients seen only in the emergency department (ED) were not offered medication-assisted treatment. The most commonly identified pathogen was *S. aureus* (80%), which is frequently found on skin. Health care visits for bacterial and fungal infections associated with injection opioid use are an opportunity to treat the underlying opioid use disorder with medication-assisted treatment. Routine care for patients who continue to inject should include advice on hand hygiene and not injecting into skin that has not been cleaned or to use any equipment contaminated by reuse, saliva, soil, or water (*4*,*5*).

* https://idsa.confex.com/idsa/2018/webprogram/Paper72151.html.

The team obtained and reviewed records for hospital admissions and ED visits during April 1–June 30, 2017, from a convenience sample of five hospitals in western New York. Patients of any age who had 1) positive cultures for *S. aureus* (excluding nasal specimens), *Candida* spp. in blood, or GAS from a normally sterile site or 2) diagnostic codes related to substance use and a bacterial or fungal pathogen or infection† were included. Injection drug use was defined as patient self-report of injection drug use; health care worker, relative, or friend report that the person injected drugs; or observation of injection equipment in the patient's room or belongings or skin lesions indicative of injection drug use (track marks). Demographic information, infection sites, bacterial and fungal pathogens, history of human immunodeficiency virus (HIV), hepatitis B and C, and clinical outcomes were abstracted from medical records for all patients with injection drug use. Information on substance use history and treatment was collected for a subset of persons whose infections were identified from *S. aureus*, *Candida* spp., or GAS culture. A chi-squared test was performed using SAS (version 9.4; SAS Institute) to compare the proportion of patients seen only in the ED to the proportion of hospitalized patients who were offered medication-assisted treatment. To assess the sensitivity of identifying patients with infections using diagnostic codes alone, the proportion of patients who injected drugs identified by positive cultures who also had diagnostic codes for both substance use and a bacterial or fungal pathogen or infection was calculated.

Among 1,002 patients who met either inclusion criterion, medical records for 111 (11%) documented injection drug use during the previous 12 months. The median age of these persons was 32 years (range = 18–68 years); 61% were women (Table). Skin and soft tissue infections accounted for 82 (74%) infections, and endocarditis accounted for 16 (14%). Among

† Infection and substance use related codes: A18.84, A31*, A32.82, A39*, A39.51, A41*–A44*, A46*, A48*, A49*, A54.83, B37* –B46*, B49, B95*–B96*, B99.8*, B99.9*, D73.3, E06.0, E32.1, G06*, H05*, I08, I33*, I38, I39, I40.0, I51.89, I72.9, I76, I80*, I96, J85*, J86*, K11.3, K12.2, K13.0, K61*, K65*, K68.1*, L01*–L04*, L08*, L97*, L98.4*, M00*, M01*, M27.2, M46.2*, M46.3*–M46.5, M65.0*, M71.0*, M72.6, M72.8, M86*, N15.1, R65.2*, R78.81, T79.8XXA, T80.2*, Z16, Z79.2. ICD-10 substance use related codes: F11*, F13*–F16*, F18*, F19*, T40*.

TABLE. Characteristics of persons who inject drugs and were evaluated in emergency departments or admitted to the hospital for bacterial or fungal infections (N = 111) — western New York, 2017*

Characteristic	No. (%)
Female sex	68 (61)
Median age (range), yrs	32 (18–68)
Microbiology	
Not cultured	15 (14)
No relevant cultures positive	26 (23)
Organism identified	70 (63)
Organism† (n = 70)	
Staphylococcus aureus§	56 (80)
Streptococcus spp.¶	11 (16)
Other bacteria**	22 (31)
Candida spp.	4 (6)
Fungal, not otherwise specified	1 (1)
Infection type††	
Skin and soft tissue§§	82 (74)
Endocarditis	16 (14)
Osteomyelitis	6 (5)
Pneumonia	5 (5)
Bacteremia without other infection type	3 (3)
Empyema	3 (3)
Septic arthritis	2 (2)
Other	4 (4)
Treatment outcome	
Died during hospital visit	4 (4)
Admitted to the hospital	79 (71)
Left against medical advice	33 (30)
Inpatients (% of 79 admissions)	20 (25)
ED only visits (% of 32 ED-only visits)	13 (41)
Length of stay	
All admitted patients: median (Q1–Q3) days	7 (4–29)
Admitted patients who did not leave against medical advice: median (Q1–Q3) days	9 (4–36)
All admitted patients: hospitalized >30 days	19 (24)
Drug used (n = 59)¶¶	
Opioids and cocaine	41 (69)
Opioids only	13 (22)
Opioids, cocaine, and methamphetamine	2 (3)
Opioids and methamphetamine	1 (2)
Cocaine only	1 (2)
Cocaine and methamphetamine	1 (2)
Offered medication-assisted treatment for opioid use disorder during visit (n = 57 using opioids)	23 (40)
Admitted patients (% of 44 admissions of persons with opioid use)	22 (50)
ED-only visits (% of 13 ED-only visits of persons with opioid use)	1 (8)
Bloodborne pathogens***	
Human immunodeficiency virus	7 (6)
Hepatitis B virus	4 (4)
Hepatitis C virus	41 (37)
Patients with diagnostic codes for both infection syndrome and substance use (n = 53 identified by culture)†††	39 (74)

Abbreviations: ED = emergency department; Q1 = quartile 1; Q3 = quartile 3.

* April 1–June 30, 2017, at five hospitals in western New York for patients of any age who injected drugs and had 1) positive cultures for *S. aureus* (excluding nasal specimens), *Candida* spp. in blood, or group A *Streptococcus* from a normally sterile site or 2) diagnostic codes including both substance use disorder and a bacterial or fungal pathogen or infection.

† Percentages are calculated among 70 patients with an organism identified and do not sum to 100 because 13 of 70 persons (19%) had an infection with more than one organism identified.

§ 30 methicillin-resistant *S. aureus* and 26 methicillin-sensitive *S. aureus*.

¶ Eight viridans group *Streptococcus*, two group A *Streptococcus*, and one group C *Streptococcus*.

** 12 gram-negative bacteria including *Enterobacter cloacae* (two), *Eikenella corrodens*, *Escherichia coli*, *Leclercia* spp., *Moraxella catarrhalis*, *Serratia marcescens*, *Sphingomonas paucimobilis*, unspecified gram-negative rods (three), unspecified anaerobic gram-negative cocci; 10 gram-positive bacteria including *Actinomyces* spp. (two), coagulase negative *Staphylococcus* (two [possible contaminants]), *Aerococcus viridans*, *Bacillus* spp., *Corynebacterium* spp., *Granulicatella* spp., unspecified gram-positive cocci chain, and unspecified gram-positive bacilli.

†† Infection types are not mutually exclusive, with the exception of bacteremia without other infection type, and other, which includes only patients without another infection type. Other includes intra-abdominal abscess, supraclavicular lymphadenitis, spontaneous bacterial peritonitis, and subacute fungal cerebritis with meningoencephalitis.

§§ Includes necrotizing fasciitis (two). Among 82 skin and soft tissue infections, 50 (61%) were documented in the medical record to be at a known injection site, 12 (15%) were not at an injection site, and for 20 (24%), it was unknown or not documented whether the infection was at an injection site.

¶¶ Patients for whom drug use data were collected.

*** Chronic infection with hepatitis B virus (HBV), hepatitis C virus (HCV), or human immunodeficiency virus (HIV) noted in the medical history, or the patient had 1) positive HBV surface antigen, 2) positive HCV antibody without RNA tested (could indicate resolved or cured infection) or detectable HCV viral load, or 3) positive HIV test in the record.

††† Excludes six patients without diagnostic codes available for review in the medical record.

skin and soft tissue infections, 50 (61%) were documented to be at an injection site, and 12 (15%) were not at an injection site. For 20 patients (24%), the medical record did not document whether the infection was at a site where the person injected drugs. Overall, 79 persons (71%) were hospitalized, of whom 19 (24%) were hospitalized for ≥30 days. Four (4%) patients died before leaving the hospital. Thirty-three (30%) patients left the hospital against medical advice, including 13 (41%) of 32 persons seen only in the ED and 20 (25%) of 79 persons admitted to the hospital.

Of 70 patients with at least one pathogen identified from a clinical culture, 13 (19%) had a polymicrobial infection. The most common bacterial and fungal pathogens were *S. aureus* (56; 80%); streptococci (11; 16%), including eight viridans group and two GAS; and *Candida* spp. (4; 6%). The most common bloodborne pathogen identified§ was hepatitis C

§ Hepatitis B virus (HBV), hepatitis C virus (HCV), HIV chronic or acute infection noted in the medical history, or the patient had 1) positive HBV surface antigen, 2) positive HCV antibody without RNA tested (could indicate resolved or cured infection) or detectable HCV viral load, or 3) positive HIV test in the record.

virus; 41 (37%) patients had a current or previous hepatitis C virus infection documented in the medical record; seven (6%) had a history of HIV infection, and four (4%) had hepatitis B virus infection.

Among a subset of 59 (53%) patients with *S. aureus*, *Candida* spp., or GAS infections from whom drug use data were collected, 57 (97%) used opioids, including 50 who injected opioids and seven with an unknown route of opioid administration. Among 44 inpatients, 22 (50%) were offered medication-assisted treatment for opioid use disorder, whereas one of 13 (8%) persons seen only in the ED was offered medication-assisted treatment (p-value = 0.01). Most patients with an infection identified by culture (74%) also had diagnostic codes for both substance use and an infection or pathogen.

Discussion

On average, at least one person with a bacterial or fungal infection who also injects drugs visited one of the five assessed hospitals every day during the analysis period. This investigation highlights the importance of preventing opioid misuse, treating opioid use disorder, and emphasizing the risks of bacterial and fungal infections as well as bloodborne pathogens during care of persons who inject drugs. In this assessment, infections related to injection drug use most often occurred at the site of injection and were predominantly caused by common skin and mouth flora that are introduced during injection. Infections related to injection also included invasive infections, such as endocarditis. Many of the infections required prolonged hospital stays, with 24% of patients hospitalized for at least 30 days. Although nearly all patients injected opioids, many were not offered medication-assisted treatment for opioid use disorder. Those seen only in the ED were less likely to be offered medication-assisted treatment than inpatients.

This assessment was limited to western New York; however, bacterial and fungal infections might also occur frequently in other communities in the United States. Although the prevalence of injection drug use is unknown, the age-adjusted rate of overdose deaths involving any drug in Monroe County, New York, where four of the five hospitals were located, was 24.5 per 100,000 residents in 2016,[¶] compared with 19.8 drug overdose deaths per 100,000 residents for the United States as a whole (*6*).

The findings in this report are subject to at least three limitations. First, the number of bacterial and fungal infections among persons who inject drugs was likely underestimated because the data did not include outpatient visits or infections in persons who did not seek health care. Second, medical records do not always specify the route of drug administration; records indicating that the patient used drugs but did not document injection were excluded, which also might underestimate the number of persons injecting. Finally, the method of identifying infections could bias the distribution of pathogens or infection types. *S. aureus*, *Candida* spp. and GAS infections were identified by both culture and diagnostic codes. Infections with other pathogens or without a pathogen identified were identified by diagnostic codes only, and therefore were more likely to be missed. However, evidence suggests that most infections were identified through diagnostic codes. Among *S. aureus*, *Candida* spp., and GAS infections identified by culture, 74% had codes for both an infection syndrome and substance use.

Routine care for patients who continue to inject should include advice on hand hygiene and not injecting into skin that has not been cleaned or to use any equipment contaminated by reuse, saliva, soil, or water (*4*,*5*). Risk factors for bacterial and fungal infections found in other recent assessments include skin breakdown and limited access to clean running water and showers (*7*). Where legal, syringe service programs can provide referrals to treatment for substance use disorder, clean equipment, and education about safer injection practices. Other services, such as prompt wound care, laundry, and showers could also help prevent serious bacterial and fungal infections (*8*). Because some persons who misuse prescription opioids transition to injecting opioids, primary prevention strategies that can reduce the risk for opioid misuse and potential subsequent infection from unsafe injection practices include appropriate opioid prescribing practices and efforts to ensure access to nonopioid treatments for pain (*9*).

Summary

What is already known about this topic?

Bacterial and fungal infections among persons who inject drugs are increasing.

What is added by this report?

Among a sample of persons in western New York who inject drugs and were hospitalized or treated in the emergency department for a bacterial and fungal infection, *Staphylococcus aureus* was the most common pathogen. Nearly all persons with such infections injected opioids; most were not offered medication-assisted treatment to reduce injection drug use.

What are the implications for public health practice?

Health care visits for bacterial and fungal infections represent an opportunity to treat the underlying opioid use disorder with medication-assisted treatment. Because many infections are caused by skin flora such as *S. aureus*, injecting without first cleaning the injection site and washing hands increases the risk for bacterial and fungal infections.

[¶] New York State Opioid Dashboard. https://www.health.ny.gov/statistics/opioid.

Medication-assisted treatment addresses the underlying opioid use disorder through decreased cravings and prevents infections by reducing injection drug use. Initiating medication-assisted treatment when persons who inject opioids are found to have a bacterial or fungal infection might also improve retention of these patients in treatment for both the infection and substance abuse (*10*). Hospitalizations and ED visits for these infections are opportunities to link patients to treatment for opioid use disorder and prevent recurrent infections.

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Genetic Characterization of Measles and Rubella Viruses Detected Through Global Measles and Rubella Elimination Surveillance, 2016–2018

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All six World Health Organization (WHO) regions have established measles elimination goals, and three regions have a rubella elimination goal. Each region has established a regional verification commission to monitor progress toward measles elimination, rubella elimination, or both, and to provide verification of elimination* (*1*,*2*). To verify elimination, high-quality case-based surveillance is essential, including laboratory confirmation of suspected cases and genotyping of viruses from confirmed cases to track transmission pathways. In 2000, WHO established the Global Measles and Rubella Laboratory Network (GMRLN) to provide high-quality laboratory support for surveillance for measles, rubella, and congenital rubella syndrome (*3*). GMRLN is the largest globally coordinated laboratory network, with 704 laboratories supporting surveillance in 191 countries (*4*). This report updates a previous report and describes the genetic characterization of measles and rubella viruses during 2016–2018 (*5*). The genetic diversity of measles viruses (MeVs) and rubella viruses (RuVs) has decreased globally following implementation of measles and rubella elimination strategies. Among 10,857 MeV sequences reported to the global Measles Nucleotide Surveillance (MeaNS) database during 2016–2018, the number of MeV genotypes detected in ongoing transmission decreased from six in 2016 to four in 2018. Among the 1,296 RuV sequences submitted to the global Rubella Nucleotide Surveillance (RubeNS) database during the same period, the number of RuV genotypes detected decreased from five in 2016 to two in 2018. To strengthen laboratory surveillance for measles and rubella elimination, specimens should be collected from all confirmed cases for genotyping, and sequences from all wild-type measles and rubella viruses should be submitted to MeaNS and RubeNS in a timely manner.

Laboratory Surveillance for Measles and Rubella Viruses

Countries report data from measles and rubella cases identified through laboratory-supported case-based surveillance systems to WHO. Laboratory testing includes both serologic and molecular confirmation of suspected cases and genetic characterization of viruses from confirmed cases. Participating GMRLN laboratories report MeV and RuV sequence data† from confirmed cases to MeaNS and RubeNS databases, which were initiated in 2005 as a joint project between Public Health England and WHO.§ In addition to the reported sequence data from GMRLN, sequences also are downloaded from GenBank, the genetic database maintained by the National Institutes of Health.¶ To ensure the quality of sequence information, GMRLN has established a molecular proficiency testing program and has accredited 86 laboratories within the six WHO regions for MeV and RuV detection and genotyping (*6*).

According to the monthly reports of 184 countries that reported measles and rubella case-based surveillance data in 2018, a total of 317,445 serum specimens were received by the participating GMRLN laboratories from patients with suspected cases, an increase of 101% compared with the number of specimens received in 2016. Among 275,020 (87%) specimens tested for measles immunoglobulin M, 78,950 (29%) were positive; 203,898 (64%) also were tested for rubella immunoglobulin M, and 11,874 (6%) were positive. By the end of 2018, MeaNS contained 47,521 MeV sequences, a 93% increase from the 24,571 sequences reported as of July 1, 2015 (*5*). During this time, the number of RuV sequences in RubeNS increased 73%, from 1,820 to 3,149.

Characterization of Measles and Rubella Viruses

In addition to monitoring the occurrence and distribution of MeV and RuV genotypes, the characterization of individual circulating wild-type MeVs is critical for monitoring progress toward regional elimination goals. One element of the evidence required for the verification of measles elimination is documentation of ≥12 months with no circulation of an endemic lineage of MeV in the presence of a well-performing surveillance system; verification of measles elimination is achieved after ≥36 months of interrupted measles transmission (*7*). To

* Verification of elimination is defined as the absence of endemic virus transmission for a continuous period of ≥36 months in the presence of a high-quality surveillance system and confirmed by the regional verification commission.

† The standard sequence window for measles virus is the 450-nucleotide carboxy-terminal of the nucleocapsid gene in the MeV genome; the standard sequence window for rubella virus is a 739-nucleotide fragment (nucleotides 8,731–9,469) in the E1 gene in the RuV genome.

§ http://www.who-measles.org/Public/Web_Front/main.php.

¶ https://www.ncbi.nlm.nih.gov/genbank/.

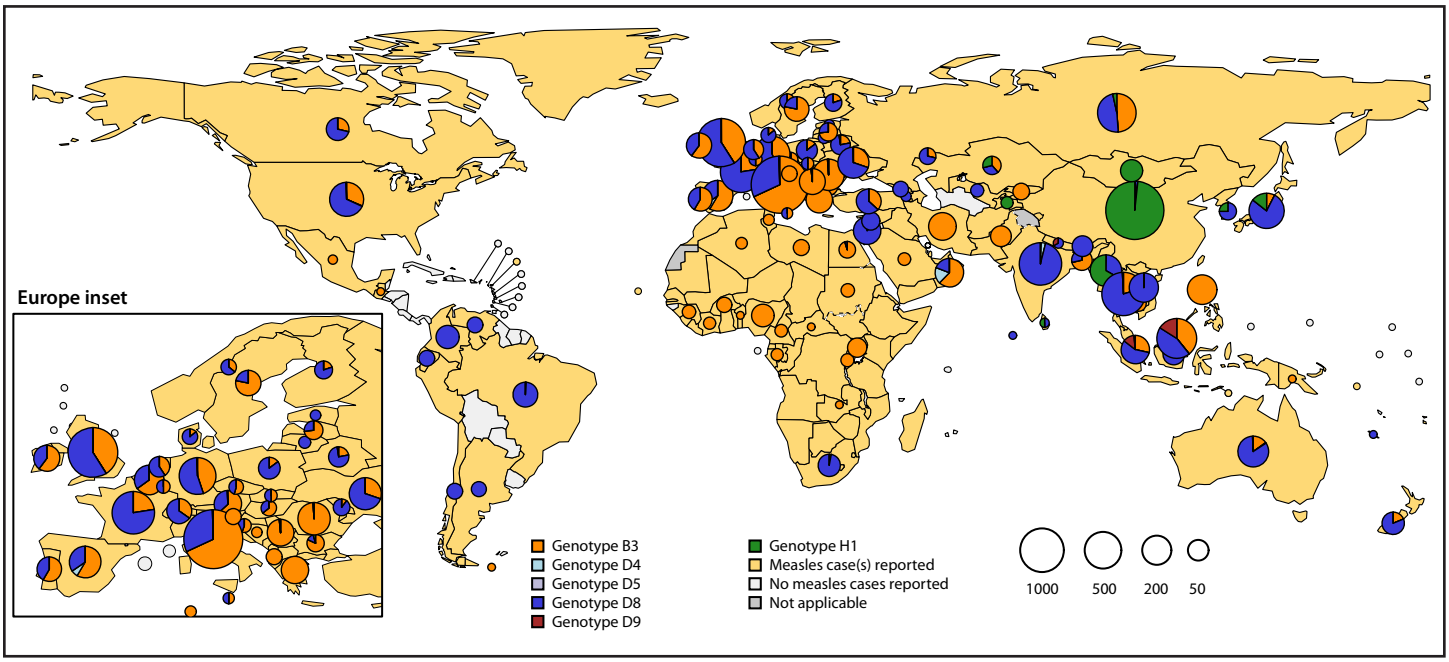
describe transmission patterns of defined lineages of MeV, GMRLN established standard methods for naming the genetic characteristics of wild-type MeVs derived from the 450 nucleotides sequence encoding the 150 carboxy-terminal amino acids of the N protein (N450), a highly variable region of the genome, including a convention for nominating specific N450 sequences as "named strains" (5). Each N450 sequence submitted to MeaNS is assigned a distinct sequence identifier (DSId), allowing viruses with identical N450 sequences to be identified. An index for the diversity of each MeV genotype reported to MeaNS, defined as the number of distinct sequences divided by the total number of records in the database, is calculated. If multiple MeV cases (generally ≥50) with the same DSId are associated with extensive transmission in multiple countries, and if the sequence has been made publicly available by submission to GenBank, then members of GMRLN can request that the N450 sequence be nominated as a named strain. Generally, the name assigned is the WHO name of the earliest example of the strain within MeaNS and does not imply any epidemiologic significance regarding the source of infection.

During 2016–2018, six of the 24 recognized MeV genotypes were detected (Figure). The number of MeV genotypes detected decreased from six (B3, D4, D5, D8, D9, and H1) in 2016 to four (B3, D4, D8, and H1) in 2018 (Table 1). The number of reported cases of MeV genotype H1, which is endemic in China, declined 87%, from 2,625 in 2016 to 333; in 2018, genotypes B3 and D8 accounted for 95% of reported sequences.

Also, during 2016–2018, the diversity index decreased for each detected genotype, except for genotype H1, as the number of circulating genotype H1 viruses decreased by 87%. During 2016–2018, 32 named strains were identified (five for genotype B3, 11 for genotype D4, eight for genotype D8, two for genotype D9, and six for genotype H1). Among the 10 most commonly reported named strains, two appeared in all six regions (Table 2).

During 2016–2018, five of the 13 recognized RuV genotypes were detected, and the number of detected RuV genotypes decreased from five in 2016 (58% of the sequences belonged to genotype 1E and 40% to genotype 2B) to two (1E and 2B) in 2018 (Table 1). However, global virologic surveillance for rubella is incomplete. With the exception of the Region of the Americas, which has eliminated rubella, the virus remains endemic in all regions. Among 866 sequences reported to RubeNS in 2018, 837 (96.6%) came from the Western Pacific Region (primarily from China and Japan); the African and Eastern Mediterranean regions, two regions with large numbers of reported confirmed rubella cases, were not represented in the RubeNS database in 2018.

FIGURE. Global distribution of measles virus genotypes,* 2016–2018



Source: World Health Organization.
* The size of the circles reflects the numbers of replicates reported for each genotype.

Discussion

GMRLN continues to provide high-quality laboratory support to surveillance for measles and rubella virus transmission and critical evidence needed for the verification of elimination. The increase in serologic testing and the number of sequences reported to the databases reflect an expansion of the capacity of GMRLN as well as the resurgence of measles in many countries during 2018. With support of the molecular surveillance data provided by GMRLN, measles elimination has been verified by 81 (42%) of the 194 WHO member countries and rubella by 76 (39%) of the 194 countries.** Moreover, the decreasing diversity indices for the most frequently detected MeV genotypes suggest that the number of chains of transmission is decreasing globally because of increasing population immunity. However, many countries reporting laboratory-confirmed measles and rubella cases have failed to collect specimens for genetic characterization, particularly during outbreaks. With only four remaining MeV genotypes detected in circulation and a decrease in sequence variability within MeV genotypes, increases in specimen collection and reporting of sequences to MeaNS from countries with confirmed measles cases are needed to better track MeV transmission patterns. In addition, most countries still have not submitted sufficient sequence information to provide adequate baseline genetic characterization of RuVs.

The MeaNS database recognizes distinct N450 sequences and assigns DSIds to enable the identification of related MeVs in different countries and regions. In addition, a convention of

** WHO Immunization, Vaccines and Biologicals database.

TABLE 1. Measles virus genotypes, distinct N450* sequences, diversity index,† and rubella virus genotypes reported globally — Measles Nucleotide Surveillance (MeaNS) database and Rubella Nucleotide Surveillance database, 2016–2018

	2016			2017			2018		
Genotype	No. of records (%)	No. of DSIds	Diversity index	No. of records (%)	No. of DSIds	Diversity index	No. of records (%)	No. of DSIds	Diversity index
Measles virus									
B3	705 (14)	96	0.136	2,665 (45)	170	0.064	2,923 (44)	219	0.075
D4	51 (1)	7	0.137	15 (<1)	6	0.400	19 (<1)	2	0.105
D5	1 (<1)	1	1.000	N/D	N/D	N/D	N/D	N/D	N/D
D8	1,541 (31)	166	0.108	2,561 (44)	208	0.081	3,396 (51)	281	0.083
D9	96 (2)	11	0.115	46 (<1)	5	0.109	N/D	N/D	N/D
H1	2,625 (52)	204	0.078	544 (9)	70	0.129	333 (5)	40	0.120
Total	**5,019 (100)**	**485**	**N/A**	**5,831 (100)**	**459**	**N/A**	**6,671 (100)**	**542**	**N/A**
Rubella virus									
1E	10 (4)	N/A	N/A	13 (7)	N/A	N/A	933 (88)	N/A	N/A
1G	6 (3)	N/A	N/A	2 (1)	N/A	N/A	N/D	N/A	N/A
1H	1 (<1)	N/A	N/A	1 (<1)	N/A	N/A	N/D	N/A	N/A
1J	1 (<1)	N/A	N/A	N/D	N/A	N/A	N/D	N/A	N/A
2B	221 (92)	N/A	N/A	172 (91)	N/A	N/A	130 (12)	N/A	N/A
Total	**239 (100)**	**N/A**	**N/A**	**188 (100)**	**N/A**	**N/A**	**1,063 (100)**	**N/A**	**N/A**

Abbreviations: DSIds = distinct sequence identifiers; N/A = not applicable; N/D = genotype not detected.
* N450: Sequences for the 450-nucleotide carboxy-terminal of the nucleocapsid gene in the measles virus genome. Data from the MeaNS database is available at http://www.who-measles.org/Public/Web_Front/main.php.
† The diversity index for each measles virus genotype reported to MeaNs is defined as the number of distinct sequence identifiers divided by the total number of records.

TABLE 2. The 10 most common distinct N450* measles virus (MeV) sequences (named strains) reported globally — Measles Nucleotide Surveillance (MeaNS) database, 2016–2018

DSId*	MeV genotype	MeV strain name	No. of records	No. of countries	No. of WHO regions
4,299	B3	MVs/Dublin.IRL/8.16/	2,719	43	4
4,221	D8	MVs/Osaka.JPN/29.15/	1,235	32	6
2,668	H1	MVs/Hong Kong.CHN/49.12/	1,149	9	4
4,807	D8	MVs/Herborn.DEU/05.17/	900	15	3
4,683	D8	MVs/Gir Somnath.IND/42.16/	814	36	4
5,096	B3	MVs/Saint Denis.FRA/36.17	567	18	3
4,283	D8	MVs/Cambridge.GBR/5.16/	561	20	3
2,283	D8	MVi/Hulu Langat.MYS/26.11/	494	30	6
2,728	H1	MVs/Aichi.JPN/9.13/	388	3	2
4,742	D8	MVs/Samut Sakhon.THA/49.16	355	20	4

Abbreviations: DSIds = distinct sequence identifiers; WHO = World Health Organization.
* N450: Sequences for the 450-nucleotide carboxy-terminal of the nucleocapsid gene in the MeV genome. Data from the MeaNS database is available at http://www.who-measles.org/Public/Web_Front/main.php.

Summary

What is already known about this topic?

Monitoring progress toward measles and rubella elimination requires high-quality case-based surveillance, including genetic characterization of measles viruses and rubella viruses.

What is added by this report?

During 2016–2018, the number of reported measles virus genotypes declined from six to four; two (B3 and D8) accounted for 95% of reported sequences. Of 13 rubella virus genotypes, reported genotypes declined from five to two.

What are the implications for public health practice?

Diversity of measles and rubella viruses has decreased globally, consistent with progress toward elimination. Continued collection of specimens from all confirmed cases for genotyping and submission of wild-type virus sequences to global databases will strengthen case-based surveillance.

naming the MeV strains with the same DSId is used. However, when defining endemic circulation of a specific MeV strain, caution should be exercised in interpreting the significance of MeV N450 sequences with different DSIds, named strains, or both. Given the conserved nature of the MeV genome, even within the highly variable N450 coding region, identical N450 sequences can be detected over multiple years and thus might not be linked or in the same direct line of transmission within a country or region. Conversely, sequences with a single nucleotide difference within an identified short chain of MeV transmission will be given different DSIds, with different names, even though they might be epidemiologically linked.

The current naming convention does not describe MeV lineages derived from sequence analysis of regions of the MeV genome other than N450. To further differentiate viral transmission chains, additional sequence information from other regions of the genome is needed. Using an expanded sequence window in addition to the N450 sequence has been proposed for countries and regions where measles has been eliminated or is nearing elimination (*8*). To improve the utility of these expanded sequence windows, Public Health England is developing updated versions of the MeaNS and RubeNS databases, along with analysis tools that should be available by the end of 2019. Distinct lineages within RuV genotypes have been described (*9*); however, WHO has not yet recommended a nomenclature for describing these lineages.

The findings in this report are subject to at least two limitations. First, sequences representing chains of transmission in countries with inadequate virologic surveillance are not represented in the global databases. Second, the geographical distribution of sequences reported to the global databases does not align with the distribution of reported measles and rubella cases.

To provide a more comprehensive overview of circulating viruses and their temporal and geographic distribution, strengthening of case-based surveillance by national programs is essential. WHO's Manual for the Laboratory-based Surveillance of Measles, Rubella, and Congenital Rubella Syndrome provides guidance for increasing specimen collection for virus detection and sequencing (*6*). Countries moving toward elimination are recommended to obtain genotype information from ≥80% of all chains of transmission (i.e., outbreaks or case clusters) (*6*). Once identified by national or regional GMRLN laboratories, all sequences from wild-type MeVs should be submitted to MeaNS and RuVs to RubeNS within 2 months of specimen receipt in the laboratory. Sequences reported in countries should be linked to named strains if possible. When feasible, supplementary information (e.g., travel history, source of infection, and location) should be submitted with sequence information. With increased sequence reporting and use of new sequencing approaches, GMRLN will provide enhanced support for monitoring progress toward and verifying achievement of measles and rubella elimination.

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All authors have completed and submitted the ICMJE form for disclosure of potential conflicts of interest. No potential conflicts of interest were disclosed.

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Erratum

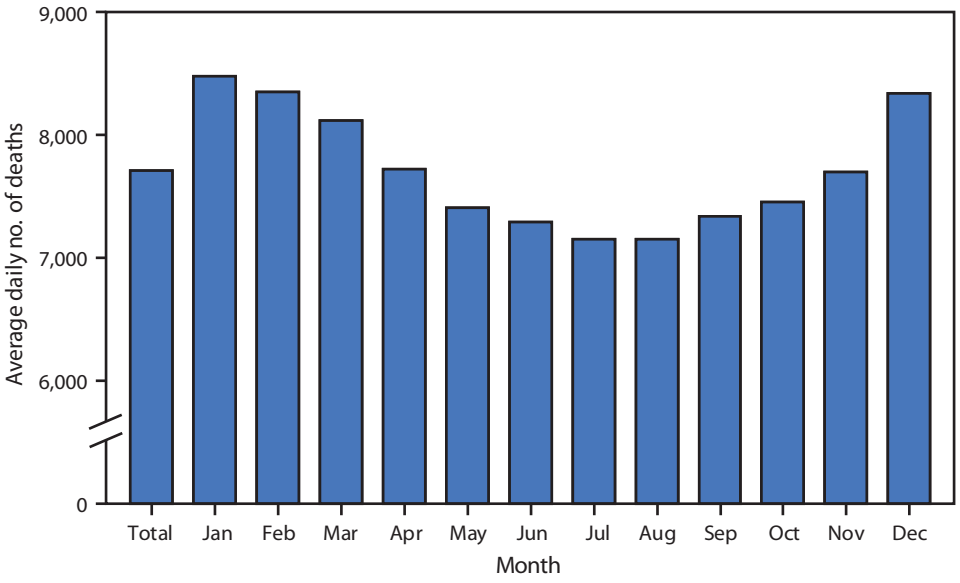
Vol. 68, No. 22

In the report "Community Assessments for Mosquito Prevention and Control Experiences, Attitudes, and Practices — U.S. Virgin Islands, 2017 and 2018," on page 500, the author order should have been "Krystal R. Seger, MSPH[1]; Joseph Roth Jr., MPH[2]; Amy H. Schnall, MPH[3]; **Esther M. Ellis, PhD[1]; Brett R. Ellis, PhD[1]**." On page 504, the corresponding author should have been "**Brett R. Ellis, brett.ellis@doh.vi.gov, 340-626-2801**."

QuickStats

FROM THE NATIONAL CENTER FOR HEALTH STATISTICS

Average Daily Number of Deaths,* by Month — United States, 2017



* Deaths include U.S. residents only.

In 2017, an average of 7,708 deaths occurred each day. January, February, and December were the months with the highest average daily number of deaths (8,478, 8,351, and 8,344, respectively). June, July, and August were the months with the lowest average daily number of deaths (7,298, 7,157, and 7,158, respectively).

Source: National Vital Statistics System. Underlying cause of death data, 1999–2017. https://wonder.cdc.gov/ucd-icd10.html.

Reported by: Jiaquan Xu, MD, jiaquanxu@cdc.gov, 301-458-4086.

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