

**Topic**


- Cases and Deaths
- Case Rates
- Death Rates
- Syndromes
- Serotypes
- Surveillance Report

**Year**

2019

**Dataset version:** Mar 2021  
**Final run:** Jun 16, 2021

**Note:** Click [here](#) to access Surveillance Reports prior to 2019.

 [Data Download](#)

Group A *Streptococcus* (GAS) | Group B *Streptococcus* (GBS) | ***Haemophilus influenzae* (HFlu)** | *Neisseria meningitidis* (NMen) | *Streptococcus pneumoniae* (SPN) | [Bact Facts](#)

**Active Bacterial Core Surveillance (ABCs) Report  
Emerging Infections Program Network  
*Haemophilus influenzae*, 2019**

**ABCs Areas:** California (3 county San Francisco Bay area); Colorado (5 county Denver area); Connecticut; Georgia; Maryland; Minnesota; New Mexico; New York (15 county Rochester and Albany areas); Oregon; Tennessee (20 urban counties)

**ABCs Population:** The surveillance areas represent 45,041,453 persons. Source: National Center for Health Statistics bridged-race vintage 2019 postcensal file.

**ABCs Case Definition:** For routine ABCs surveillance, a case of invasive bacterial disease is defined as isolation of *H. influenzae* (Hi) from a normally sterile site or detection of ABCs pathogen-specific nucleic acid in a specimen obtained from a normally sterile body site, using a validated molecular test in a resident of one of the surveillance areas.

**ABCs Methodology:** ABCs personnel routinely contacted all microbiology laboratories serving acute care hospitals in their area to identify cases. Standardized case report forms that include information on demographic characteristics, clinical syndrome, and outcome of illness were completed for each identified case. Serotyping was done on Hi isolates at CDC and state laboratories. Regular laboratory audits assessed completeness of active surveillance and detected additional cases.

All rates of invasive Hi disease were calculated using population estimates from the bridged-race vintage postcensal file. For national estimates, race- and age-specific rates of disease were applied from the aggregate surveillance areas to the race- and age-specific distribution of the U.S. population. Cases with missing data, excluding ethnicity, were multiply imputed using sequential regression imputation methods.<sup>†</sup>

**ABCs Profiles**

Race	No.	Rate*
Black	200	2.4
White	729	2.2
Other	42	1.1
Total	972	2.2

**National Estimates of Invasive Disease**

Total Cases: 7,130 (2.17/100,000 population)  
Deaths: 1,050 (0.32/100,000 population)

Serotype	B		Non-B		Non-Type <sup>†</sup>		Unknown	
	No.	Rate*	No.	Rate*	No.	Rate*	No.	Rate*
<1	2	0.39	17	3.33	25	4.90	2	0.39
1	1	0.19	7	1.35	6	1.16	2	0.39
2-4	1	0.06	7	0.44	12	0.75	1	0.06
5-17	0	0.00	8	0.11	10	0.14	3	0.04
18-34	1	0.01	12	0.11	49	0.47	12	0.11
35-49	4	0.05	14	0.16	52	0.59	14	0.16
50-64	4	0.04	73	0.84	102	1.17	24	0.28
65-74	4	0.09	57	1.34	122	2.88	22	0.52
75-84	0	0.00	25	1.21	129	6.26	26	1.27
≥85	0	0.00	13	1.53	98	11.52	9	1.06
Total	17	0.04	233	0.52	605	1.34	116	0.26

\*Per 100,000 population for ABCs areas      †Non-typeable isolates

**Syndromes**

Syndrome	Cases		Deaths	
	No.	%*	No.	%*
Meningitis	66	6.8	5	8.0
Bacteremia Without Focus	223	23.0	26	13.8
Pneumonia With Bacteremia	557	57.3	89	16.3

\*Percent of cases  
<sup>†</sup>Deaths per 100 cases with known outcome

**† Surveillance Note**

Missing race (n=89) data were multiply imputed using sequential regression imputation methods.

**Citation**

Centers for Disease Control and Prevention. 2019. Active Bacterial Core Surveillance Report, Emerging Infections Program Network, *Haemophilus influenzae*, 2019. [www.cdc.gov/abcs/downloads/HFLU\\_Surveillance\\_Report\\_2019.pdf](http://www.cdc.gov/abcs/downloads/HFLU_Surveillance_Report_2019.pdf)