**Impact of 13-Valent Pneumococcal Conjugate Vaccine on Invasive Pneumococcal Disease Among Adults with HIV — United States, 2008–2018**

**Supplemental Digital Content**

**Methods**

*Surveillance methods*

IPD cases were identified through the Active Bacterial Core surveillance (ABCs), an active, laboratory- and population-based surveillance platform for invasive bacterial diseases in select counties of 10 states across the United States (California: 3 county Bay area; Colorado: 5 county Denver area; Georgia: 20 county Atlanta area; Maryland: 6 county Baltimore area; New York: 7 county Rochester area and 8 county Albany area; Oregon: 3 county Portland area; Tennessee: 20 urban counties; Connecticut, Minnesota, New Mexico: the entire state)1. Since the surveillance areas changed over time1, we included cases reported among adults aged ≥19 years old residing in areas that were part of the surveillance catchment area during 2008–2018 and report HIV status of the cases (California: 1 county; Colorado: 5 county Denver area; Georgia: 20 county Atlanta area; Maryland: 6 county Baltimore area; Oregon: 3 county Portland area; Tennessee: 11 counties; Connecticut, Minnesota, New Mexico: the entire state).

*Statistical methods*

Information on persons with diagnosed HIV infection is reported by health departments to the National HIV Surveillance System of the CDC from all 50 states, the District of Columbia, and 6 U.S. dependent areas (American Samoa, Guam, the Northern Mariana Islands, Puerto Rico, the Republic of Palau, and the U.S. Virgin Islands). After removal of personally identifiable information, data are submitted to CDC. The number of PWH in the ABCs catchment area for a particular year was based on the place of residence at the time of HIV diagnosis.

Race and ethnicity groups were assigned by first identifying those with Hispanic ethnicity. Those who were not Hispanic (including those with unknown or missing ethnicity) were categorized by their race. For analyses involving serotype, we assumed that cases without serotype information had the same distribution of PCV13-type, PPSV23 unique type, or NVT as cases with serotype information. For analyses involving race and ethnicity, we assumed that the distribution among patients missing these data was the same as among patients with known race and ethnicity. For both assumptions, simple proportions were used to fill in missing data, imputing missing serotype first, followed by race and ethnicity.

1. Centers for Disease Control and Prevention. Surveillance Population. Accessed August 25, 2020. <https://www.cdc.gov/abcs/methodology/surv-pop.html>