

CDC Antimicrobial Resistance Threats Report

Drug-resistant Nontyphoidal *Salmonella* Data Methods

Estimates of the annual number of infections, hospitalizations, and deaths from nontyphoidal *Salmonella* that were resistant to at least one recommended antibiotic in 2022 and 2023 were reported.

To measure resistance, nontyphoidal *Salmonella* isolates (pure samples of nontyphoidal *Salmonella*) obtained from patient specimens that underwent whole genome sequencing (WGS) at public health laboratories participating in PulseNet [2] or at CDC were analyzed for the presence of antimicrobial resistance determinants (acquired genes or mutations known to confer resistance) and assigned a predicted resistance pattern by the CDC National Antimicrobial Resistance Monitoring System (NARMS) [3]. Sequencing followed PulseNet standard operating procedures for the Illumina Miseq platform [4]. Reads with a base call quality score ≥ 30 , and coverage $\geq 30\times$ were assembled using SPAdes v3.7 (or later), in line with PulseNet protocols [5]; contigs with coverage below 10% average genome coverage were excluded from final assemblies. Resistance determinants were detected using either the ResFinder database (downloaded July 30, 2020, or later) (90% identity, 50% gene coverage) and the *Salmonella* spp. PointFinder scheme (downloaded August 30, 2019, or later) or AMRFinderPlus v3.12.8 (or later) implemented in PulseNet 2.0.

Isolates were defined as resistant to at least one recommended antibiotic if they had at least one resistance determinant for ampicillin, ceftriaxone, ciprofloxacin (nonsusceptible, intermediate or resistant), azithromycin, or trimethoprim-sulfamethoxazole. Prevalence of resistance was calculated by dividing the number of isolates with at least one determinant known to confer resistance to specific antibiotics by the total number of isolates sequenced and screened for resistance determinants [6]. The Clopper-Pearson exact method was used to calculate 95% confidence intervals (range of values likely to include the true value).

Annual estimates of illnesses, hospitalizations, and deaths were generated using multiplicative models consistent with methods described in Scallan et al. [7]. Successive factors are applied by multiplication to obtain proportional increases or decreases in the count. Briefly, laboratory-confirmed illnesses reported to FoodNet [8-11] were scaled up to the U.S. population. Number of illnesses was estimated by applying year- and pathogen-specific underdiagnosis multipliers to the national laboratory-confirmed illnesses. The underdiagnosis multipliers accounted for ill people not seeking medical care, not submitting specimens for testing, and laboratories not reporting a pathogen.

Numbers of hospitalizations and deaths were estimated by applying incidences of hospitalization and death and year-specific underdiagnosis multipliers for hospitalizations to the national laboratory-confirmed illnesses. The underdiagnosis multipliers for hospitalizations accounted for hospitalized people not submitting specimens for testing and laboratories not reporting a pathogen. In contrast to Scallan et al. foodborne-focused analyses [7], these models estimated all infections occurring in the United States regardless of transmission route (i.e., not restricted to foodborne or domestically acquired infections).

To estimate the burden attributable to infections caused by drug-resistant nontyphoidal *Salmonella*, annual resistance proportions from NARMS were incorporated into the model.

Resistance prevalence, with associated binomial uncertainty, was used to probabilistically partition total estimated illnesses, hospitalizations, and deaths into resistant components. Means and 95% credible intervals (range of values likely to include the true value) were calculated.

References

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