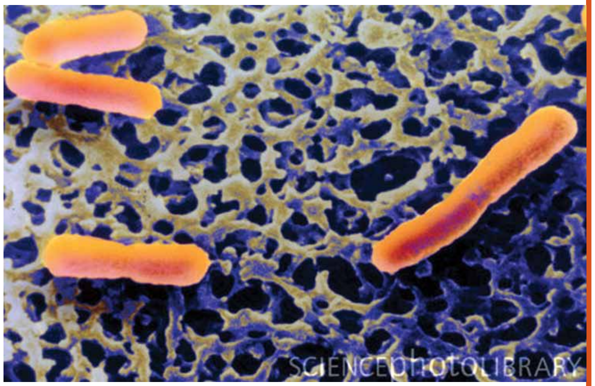
National Enteric Disease Surveillance: *Shigella* Surveillance Overview

Surveillance System Overview: National *Shigella* Surveillance

Shigella is estimated to cause nearly half a million illnesses each year in the United States, with more than 5,400 hospitalizations and 38 deaths (1). *Shigella* infections most often cause gastroenteritis, manifested by diarrhea, fever, and stomach cramps starting a day or two after exposure to the bacteria. The diarrhea is often bloody. The primary mode of transmission is from one person to another. *Shigella* infections may also be acquired from eating contaminated food or drinking, swimming in, or playing with contaminated water.

National *Shigella* surveillance data are collected through passive surveillance of laboratory-confirmed human *Shigella* infections. Clinical diagnostic laboratories submit *Shigella* isolates to state and territorial public health laboratories, where they are confirmed, speciated, and subtyped. Unusual or untypable isolates are forwarded to the National *Shigella* Reference Laboratory in the Enteric Diseases Laboratory Branch (EDLB) at the Centers for Disease Control and Prevention (CDC); results are reported back to public health laboratories.



Colored scanning electron micrograph (SEM) of *Shigella flexneri* bacteria.

State and territorial public health laboratories report *Shigella* infections electronically to CDC through a variety of mechanisms. Data are collected into the Laboratory-based Enteric Disease Surveillance (LEDS) system. The Division of Foodborne, Waterborne, and Environmental Diseases (DFWED) in the National Center for Emerging and Zoonotic Infectious Diseases maintains national *Shigella* surveillance in LEDS. The annual summaries of these data are the national source of species and subtype information for *Shigella*.

Isolates are reported by state and represent the state where laboratory confirmation and subtyping occurred; the reporting state may not be the same as the state of residence of the ill person. Reports include basic demographic information on the patient, and the species, subtype, and specimen source for the isolate. Duplicate records are deleted. Reporting rates vary by state and year. Not all isolates are forwarded or reported to state public health laboratories and are therefore not all are reported to national-level surveillance. The national *Shigella* surveillance data are dynamic; data from previous years may change as isolate reports are added or corrected.

Although all *Shigella* infections are nationally notifiable, for several reasons many cases are likely not recognized (2). Not all persons ill with *Shigella* infection seek medical care, healthcare providers may not obtain a specimen for laboratory diagnosis, or the clinical diagnostic laboratory may not perform the necessary diagnostic tests. The numbers of isolates with incomplete and unknown species and subtype data vary by state and year.

Other sources of national-level *Shigella* surveillance data

Several other systems at CDC conduct surveillance for *Shigella*. The National Notifiable Diseases System (NNDSS) collects and compiles reports of nationally notifiable infectious diseases, including shigellosis (3). NNDSS collects data from states on both laboratory-confirmed and probable cases of infection (probable cases are defined as illnesses in persons with an epidemiological link to a confirmed case). NNDSS data is collected from states in a number of mechanisms, including the National Electronic Diseases Surveillance System (NEDSS) which is under development; currently, laboratory information is not available from NNDSS. The National Antimicrobial Resistance Monitoring System (NARMS) monitors antimicrobial resistance among enteric bacteria including Shigella from humans (4). The National Outbreak Reporting System (NORS) collects reports of foodborne, waterborne, enteric person-to-person and animal contact-associated disease outbreaks from state and territorial public health agencies (5).

Overview of *Shigella* Subgroups

The genus *Shigella* has 4 species or subgroups (A, B, C, and D) and 43 serotypes (Table A). Subgroups A, B, C, and D have historically been treated as species: subgroup A is referred to as *S. dysenteriae*; subgroup B as *S. flexneri*; subgroup C as *S. boydii*, and subgroup D as *S. sonnei*. Subgroups and serotypes are differentiated from each other by their biochemical characteristics (e.g., ability to ferment D-mannitol) and antigenic properties. The most recently recognized serotype belongs to subgroup C (*boydii*) (6).

Isolates of *S. boydii* serotype 13 were added to the *Shigella* scheme in 1958, but subsequent findings from DNA-DNA reassociation studies reported in 1973 raised questions about their inclusion within the genus *Shigella* (7). In these studies, Brenner et. al. observed that *S. boydii* 13 strains showed a high level of interrelatedness (92-98%) but only averaged 65% relatedness to strains of other *Shigella* species, *Escherichia coli*, and other *Escherichieae*. Findings from recent phylogenetic studies support those from the DNA relatedness studies and show that organisms formerly classified as *S. boydii* serotype 13, some of which can produce gas from glucose, are more appropriately regarded as *Escherichia albertii* (8, 9). Therefore, as of 2006, CDC no longer includes isolates identified by traditional biochemical and serologic methods as *S. boydii* serotype 13 within the *Shigella* scheme.

Table A. Classification of Shigella subgroups

Subgroup	Species	Number of Serotypes	Fermentation of D-mannitol
A	dysenteriae	15	-
B	flexneri	8[a]	+
C	boydii	19[b]	+
D	sonnei	1	+

[a] Group B serotypes 1–5 are subdivided into 11 subserotypes

[b] Although the numbering scheme for Group C serotypes extends to serotype 20, there are only 19 serotypes because *S. boydii* 13 is now reclassified as *Escherichia albertii*, and has been removed from the scheme

References

1. Scallan, E, Hoekstra RM, Angulo FJ, Tauxe RV, Widdowson MA, Roy SL, et al. Foodborne illness acquired in the United States---major pathogens. Emerg Infect Dis 2011; 17(1): 7-15.
2. Scallan E, Jones TF, Cronquist A, Thomas S, Frenzen P, Hoefer D, et al. Factors associated with seeking medical care and submitting a stool sample in estimating the burden of foodborne illness. Foodborne Pathog Dis. 2006 Winter;3(4):432-438.
3. National Notifiable Diseases Surveillance System (NNDSS), shigellosis: http://www.cdc.gov/osels/ph_surveillance/nndss/casedef/shigellosis_current.htm
4. National Antimicrobial Resistance Monitoring System (NARMS): http://www.cdc.gov/narms/
5. National Outbreak Reporting System (NORS): http://www.cdc.gov/outbreaknet/nors/ .
6. Ewing WH, Reavis RW, Davis BR. Provisional *Shigella* serotypes. Can J Microbiol 1958; 4: 89-107.
7. Brenner DJ, Fanning GR, Miklos GV, Steigerwalt, AG. Polynucleotide sequence relatedness among *Shigella* species. Int J Syst Bacteriol 1973; 23:1-7.
8. Brenner DJ, Steigerwalt AG, Wathen HG, Gross RJ, Rowe B. Confirmation of aerogenic strains of *Shigella boydii* 13 and further study of *Shigella* serotypes by DNA relatedness. J Clin Microbiol 1982; 16: 432-436.
9. Hyma KE, Lacher DW, Nelson AM, Bumbaugh AC, Janda JM, Strockbine NA, Young VB, Whittam TS. Evolutionary genetics of a new pathogenic *Escherichia* species: *Escherichia albertii* and related *Shigella boydii* strains. J Bacteriol 2005; 187: 619-28.

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Recommended citation:
Centers for Disease Control and Prevention (CDC).
National *Shigella* Surveillance Overview. Atlanta, Georgia:
US Department of Health and Human Services, CDC, 2011.