Shigella

Annual Summary

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Foodborne and Diarrheal Diseases Branch
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Laboratory-Confirmed *Shigella* Surveillance Annual Summary, 2002

The Annual Summary contains surveillance data on reported laboratory-confirmed *Shigella* isolates in the United States. The National *Shigella* Surveillance System collects reports of isolates of *Shigella* from every state in the United States. This information is reported electronically through the Public Health Laboratory Information System (PHLIS) by the State Public Health Laboratory Directors and State and Territorial Epidemiologists to the Foodborne and Diarrheal Diseases Branch (FDDB) and the Biostatistics and Information Management Branch (BIMB) of the Division of Bacterial and Mycotic Diseases in the National Center for Infectious Diseases.

The National *Shigella* Surveillance System is based on data collected by state and territorial public health laboratories. *Shigella* isolates are submitted to the state public health laboratory by clinical diagnostic laboratories. The state and territorial laboratories confirm the isolates as *Shigella,* perform subtyping, and submit the data for reporting through PHLIS. Unusual or untypable isolates are forwarded to the National *Shigella* Reference Laboratory at the Centers for Disease Control and Prevention for further characterization or confirmation. These results are reported back to the state laboratory, where they are reported to CDC through PHLIS.

The capture of isolates in the National *Shigella* Surveillance System is considered to be consistent. However, some *Shigella* isolates may not be forwarded or reported to state public health laboratories and therefore are not captured. In addition, irrespective of the surveillance system, many cases of *Shigella* illness are not reported because the ill person does not seek medical care, the health-care provider does not obtain a specimen for diagnosis or the laboratory does not perform culture for *Shigella*. The results of surveillance reported herein are therefore substantial underestimates of the true number of infections.

The number of isolates reported by state represents the state where laboratory confirmation and subtyping were performed. In some instances, the reporting state is not the same as the state of residence of the person from whom the isolate was obtained. For the Annual Summaries, duplicate records are deleted.

There are 4 major subgroups and 43 recognized serotypes of *Shigella,* shown in Table A below.

Table A. Subgroups, Serotypes and Subtypes of *Shigella*

Subgroups	**Serotypes and Subtypes**
Group A: *Shigella dysenteriae*	15 serotypes (type 1 produces Shiga toxin)
Group B: *Shigella flexneri*	8 serotypes and 9 subtypes
Group C: *Shigella boydii*	19 serotypes
Group D: *Shigella sonnei*	1 serotype

These subgroups and serotypes are differentiated from one another by their biochemical traits (such as ability to ferment mannitol) and antigenic properties (Table B).

Table B. Classification of *Shigella* subgroups.

			Carbohydrate fermentation		
Species	**Group**	**Serotypes**	**Glucose**	**Mannitol**	**Lactose**
S. dysenteriae	A	15	+	-	-
S. flexneri	B	8	+	+	-
S. boydii	C	19	+	+	-
S. sonnei	D	1	+	+	Late

Subgroups A, B, C and D represent serologically and biochemically defined groups of shigellae that historically have been treated as species: subgroup A for *S. dysenteriae*; subgroup B for *S. flexneri*; subgroup C for *S. boydii* and subgroup D for *S. sonnei*. Since there are no recognized environmental or animal reservoirs for *Shigella*, except higher primates, the isolates reported herein are all from infected humans.

The Statistical Outbreak Detection Algorithm (SODA), developed by BIMB and FDDB, is a statistical algorithm based on the National Surveillance Data. It is designed to detect unusual clusters of *Salmonella* and *Shigella* infection. SODA compares current *Salmonella* and *Shigella* isolates reported through PHLIS by subgroup or serotype with a 5 year historical baseline for that subgroup or serotype for the specified time period to detect unusual increases from the baseline. Analyses can be conducted at state, regional, or national levels. Since 1996, SODA has been implemented at CDC and selected state health departments. If you would like more information on SODA, please call the PHLIS Helpdesk (404) 639-3365.

Annual Highlights for 2002

A total of 12,992 *Shigella* isolates were reported from public health laboratories in 50 states in 2002 (Table 1). This represents a 13% decrease compared with 1992 and a 22% increase from 2001. The national rate of reported *Shigella* isolates in 2002 was 4.5 per 100,000 population based on 2002 census population estimate figures for the United States.

Similar to previous years, *Shigella* was isolated frequently from children under 5 years of age, who accounted for 29.7% of all isolates. About 32.3% of all isolates came from persons aged 5-19 years, and 30.7% from persons aged 20-59, with declining numbers thereafter. The median age of patients by subgroup is shown in Table 4. The distribution of *Shigella* isolates between the sexes was similar, with females accounting for 51.7% of persons from whom *Shigella* was isolated. Gender differences were most notable for a preponderance of females in three age groups, 20-29 (65.2%), 70-79 (60.8%), and 60-69 (57.1%) and for a relative paucity of females in three age groups 40-49 (43.9%), 30-39 (47.5%), and 80+ (47.9%). These gender differences reflect similar findings among reported isolates of *Shigella sonnei*. Among reported isolates of *Shigella flexneri*, a male predominance is seen, particularly in the age groups 30-39 (68.9%), 40-49 (67.1%) and 20-29 (55.3%). These estimates, however, are not complete since Illinois does not report age of persons from whom *Shigella* isolates are

obtained.

The frequency of reported subgroups, and the frequency of reported serotypes within these groups for all *Shigella* isolates are shown in Tables 1 and 2. Of the 12,992 isolates, 12,517 (96.3%) were subgrouped. Trends of subgroups remained constant, with subgroup D (*S. sonne*i) accounting for the largest percentage of isolates (83.5%), followed by subgroup B (*S.flexneri,* 12.2%), *subgroup C (S. boydii,* 0.8%) and subgroup A (*S. dysenteriae*,0.3%). *Shigella* isolate serotype trends by year are shown in Table 5 and in Figure 2. Over the past decade, the numbers of reported *Shigella* isolates in subgroups A, B and C, and the proportions of all reported *Shigella* isolates due to these three subgroups have enjoyed a steady decline. The decrease over time in reported isolates of *Shigella* subgroup D (*S. sonnei*) has been less smooth, and subgroup D now accounts for a greater proportion of all reported *Shigella* isolates (83.5%) than in any year since 1968, when National Shigella Surveillance began. The number (475) and the proportion (3.7%)of all reported *Shigella* isolates that were not identified as belonging to a specific subgroup have also declined to new historic lows. The highest numbers and proportions of all reported Shigella isolates that were not identified as belonging to a specific subgroup were reported by California (396, 14.4%), Colorado (21, 10.0%), and Tennessee (14, 7.4%).

Shigella transmission occurs via the fecal-oral route. The majority of subgroup D (*S. sonnei)* infections in the United States occur in young children and are associated with crowding and poor personal hygiene. Daycare centers have been implicated in many large *S. sonne*i outbreaks that can last many months and affect many persons (1,2). In 2002, a prolonged multi-state daycare-associated outbreak of *S. sonnei* infections in the South and Mid-Atlantic regions contributed significantly to the national burden of culture-confirmed shigellosis (3). *S. sonne*i has also been transmitted through unchlorinated wading pools (4), interactive water fountains (5), food items such as parsley (6) and bean dip (7), and men who have sex with men (MSM) (8). Until recently, the dominant subgroup causing illness among MSM was subgroup B (*S. flexneri)* (9). However, in a large outbreak among MSM in San Francisco, the dominant serotype was subgroup D (*S. sonnei)* (8).

Geographic trends by region for subgroup D (*S. sonnei)* isolates from 1988 to 2002 are illustrated in Figure 3. All regions except the West North Central, East North Central, and East South Central regions exhibited increases in subgroup D *(S. sonnei)* isolates from 2001 to 2002.

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