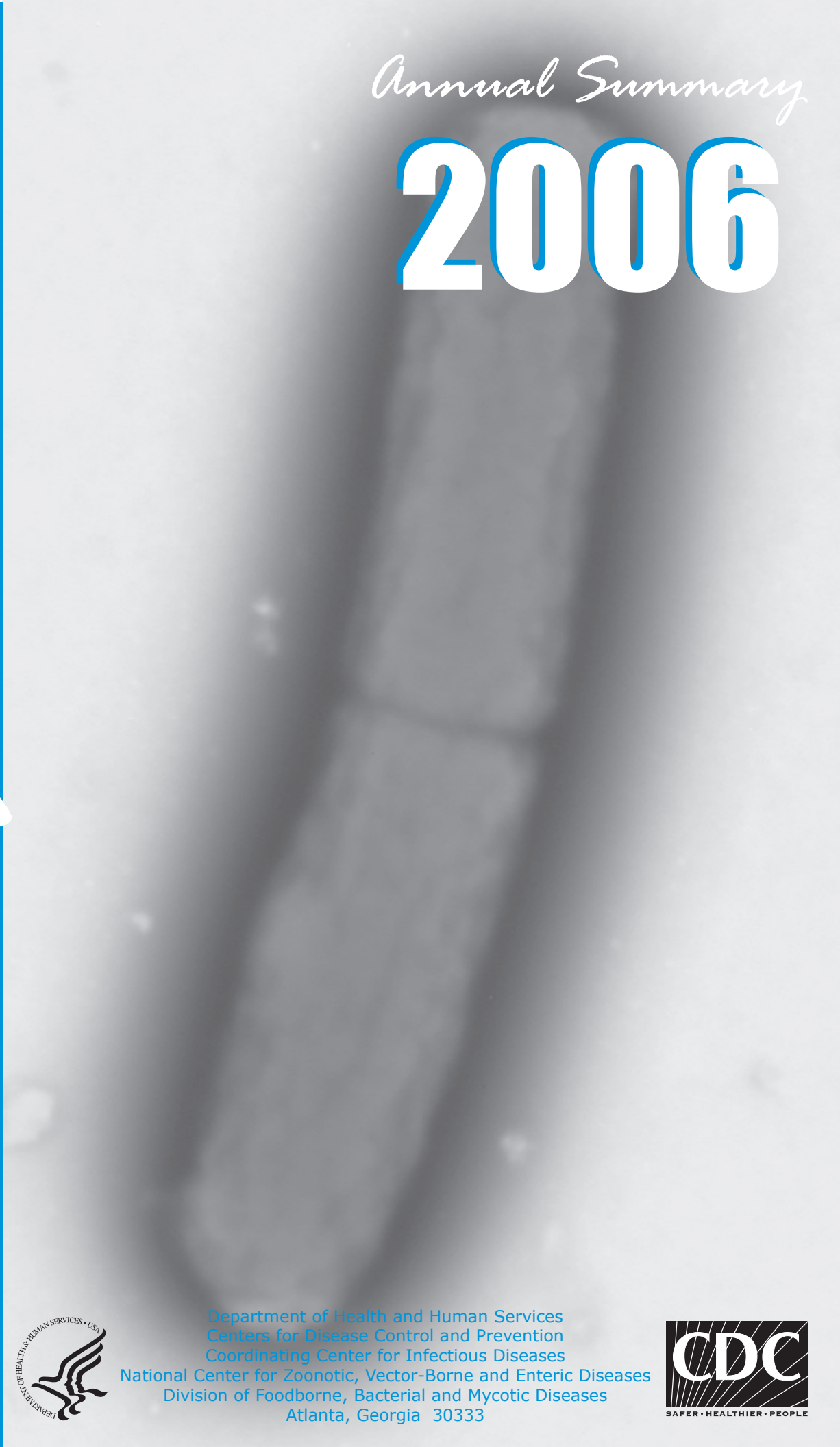
Shigella

Annual Summary 2006



Department of Health and Human Services
Centers for Disease Control and Prevention
Coordinating Center for Infectious Diseases
National Center for Zoonotic, Vector-Borne and Enteric Diseases
Division of Foodborne, Bacterial and Mycotic Diseases
Atlanta, Georgia 30333

CDC
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Richard Bishop
Biostatistician, Northrop Grumman Contractor
Biostatistics Office

Nancy Strockbine, Ph.D.
Chief, National Reference Lab for *E*. coli and *Shigella*
Enteric Disease Laboratory Preparedness Branch

Benjamin Nygren
Surveillance Epidemiologist
Enteric Diseases Epidemiology Branch

Eric Mintz, M.D., M.P.H.
Chief, Diarrheal Diseases Epidemiology Section
Enteric Diseases Epidemiology Branch

Division of Foodborne, Bacterial and Mycotic Diseases

National Center for Zoonotic, Vector-Borne and Enteric Diseases

Coordinating Center for Infectious Diseases

Centers for Disease Control and Prevention

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Centers for Disease Control and Prevention
Division of Foodborne, Bacterial and Mycotic Diseases
Enteric Diseases Epidemiology Branch
Mail Stop: A38
1600 Clifton Road
Atlanta, Georgia 30333
Telephone: 404-639-2206
http://www.cdc.gov/ncidod/dbmd/foodborne/index.htm

The Adobe Acrobat (PDF) version of this document can be viewed on the world-wide web at http://www.cdc.gov/ncidod/dbmd/phlisdata/shigella.htm. Further information concerning data described in this report can be obtained by contacting the Foodborne and Diarrheal Diseases Branch at telephone number (404) 639-2206. For further information concerning PHLIS please contact the Biostatistics Office at telephone number (404) 639-1364.

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Laboratory-Confirmed *Shigella* Surveillance
Annual Summary, 2006

The Annual Summary of the National *Shigella* Surveillance System contains surveillance data on reported laboratory-confirmed *Shigella* infections in the United States. The National *Shigella* Surveillance System collects reports of isolates of *Shigella* from every state in the United States. This information was reported electronically through the Public Health Laboratory Information System (PHLIS) by the State Public Health Laboratory Directors and State and Territorial Epidemiologists to the Enteric Diseases Epidemiology Branch (EDEB) and the Biostatistics Office of the Division of Foodborne, Bacterial and Mycotic Diseases in the National Center for Zoonotic, Vectorborne and Enteric Diseases at the Centers for Disease Control and Prevention (CDC).

The National *Shigella* Surveillance System is based on data reported 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 to CDC. Unusual or untypable isolates may be forwarded to the National *Shigella* Reference Laboratory at the Enterics Diseases Laboratory Branch (EDLB) at CDC for further characterization or confirmation. These results are then reported back to the state laboratory by CDC.

The capture of the data concerning isolates in the National *Shigella* Surveillance System is considered to be fairly consistent. However, data on some *Shigella* isolates may not be forwarded or reported to state public health laboratories and therefore are not ascertained. 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 *Shigella* infections.

The National *Shigella* Surveillance System database is dynamic; the number of isolates reported for previous years may change according to the addition or correction of isolate reports.

The number of isolates reported by geographical area (e.g. 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 were deleted. All isolates reported herein were from infected humans.

There are 4 major subgroups of *Shigella*, designated A, B, C and D, and 43 recognized serotypes (Table A). Subgroups A, B, C and D have historically been treated as species: subgroup A for *Shigella* dysenteriae; subgroup B for *Shigella* flexneri; subgroup C for *Shigella* boydii and subgroup D for *Shigella* sonnei. These subgroups and serotypes are differentiated from one another by their biochemical traits (ability to ferment D-mannitol) and antigenic properties. The most recently recognized serotype belongs to subgroup C (S. boydii) (1).

Table A. Classification of *Shigella* Subgroups

Subgroup	Species	Number of serotypes	Fermentation of D-mannitol	Subgroup B group antigens
A	*S. dysenteriae*	15	-	-
B	*S. flexneri*	8[a]	+	+
C	*S. boydii*	19[b]	+	-
D	*S. sonnei*	1	+	-

[a] = Serotypes 1-5 are subdivided into 11 subserotypes.

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

The Statistical Outbreak Detection Algorithm (SODA), developed by BSO and EDEB, is a statistical algorithm performed on the National Surveillance Data to detect unusual clusters of Shigella infection. SODA compares current *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 at (404) 639-3365.

Challenges for the Public Health Laboratory Information System (PHLIS)

Integrated surveillance system software development in several states and at the CDC has interrupted the normal use of the Public Health Laboratory Information System (PHLIS) system such that some *Shigella* surveillance reports are delayed and obtained in a variety of formats outside of the PHLIS system.

PHLIS is the public health laboratory-based, national surveillance system for infectious diseases. Reports of *Salmonella*, *Shigella*, Campylobacter, and Shiga toxin-producing E. coli isolates are transmitted electronically through PHLIS to CDC, with accompanying basic epidemiologic data, and serotype data where appropriate. PHLIS is the only national source of critically useful serotype information for these pathogens. PHLIS has been experiencing challenges during the past several years. Since 1998, PHLIS software has not been updated, and it remains a legacy DOS-based system that is increasingly difficult to use. The number of participating states has dramatically decreased over the last 3 years and will continue to decline as states seek alternatives to PHLIS.

A replacement for the current system has been developed by CDC and is currently being implemented. The new system will transfer the same surveillance data currently collected in PHLIS via the Public Health Information Network Messaging System (PHIN MS), which is a secure internet pipeline for data transmission to CDC. Each reporting site will be responsible for exporting current disease data to a delimited ascii file then transmitting the data to CDC using the PHINMS administrative tool. We hope that all reporting sites will transmit their data using this simplified system over the next several months.

We encourage reporting partners to use the PHLIS reporting system if serotype specific *Shigella* reports cannot be transmitted to CDC through new integrated surveillance systems. If PHLIS reporting is impossible, please contact the PHLIS Help Desk (404-639-3365) to arrange alternative data submission pathways.

Annual Highlights for 2006

A total of 10,336 *Shigella* isolates were reported from public health laboratories in 50 states in 2006 (Table 1). This represents a stabilization in the incidence of laboratory- confirmed *Shigella* from the sharp decreases that occurred in 2004. The national incidence of laboratory-confirmed *Shigella* in 2006 was 3.5 per 100,000 population. Similar to previous years, *Shigella* was isolated frequently from children < 5 years of age, who accounted for 32% of all isolates. About 32% of all isolates came from persons aged 5-19 years, and 27% from persons aged 20-59, with smaller percentages in older age groups. The median age of patients by species is shown in Table 4. Among patients for whom gender was reported, 53% were female. Females accounted for more cases than males in all age groups except < 5 years (49% female) and 40-49 years (45% female). Among patients 20-29 years of age, a female predominance was particularly evident at 68% of isolates. These gender differences were most striking among patients infected with *Shigella* sonnei, where females accounted for 72% of patients 20-29 years of age, 64% of patients 30-39 years of age, 54% of patients 40-49 years of age, and 62% of patients 50-59 years of age. Among patients infected with *Shigella* flexneri, a male predominance was seen, particularly in the age groups 30-39 (67%), 40-49 (76%), and 50-59 (60%) years of age. Patient gender was not reported for 9.1% of all isolates and patient age was not reported for 6.1% of isolates.

The frequency of subgroups and the frequency of serotypes within these subgroups for all *Shigella* isolates are shown in Tables 1 and 2. Of the 10,336 isolates, 9,108 (88%) were subgrouped. The proportion of *Shigella* isolates that were subgroup D (S. sonnei) was 72%, followed by subgroup B (S. flexneri) 14%, subgroup C (S. boydii) 1.1%, and subgroup A (S. dysenteriae) 0.5%. *Shigella* isolate subgroup and serotype trends by year are shown in Table 5 and in Figure 2. Over the past decade, the numbers of *Shigella* isolates in subgroups A, B, and C, and the proportions of all *Shigella* isolates due to these three subgroups have declined. The number (1,228) and the proportion (12%) of *Shigella* isolates that were not identified as belonging to a specific subgroup increased slightly. The highest numbers of reported *Shigella* isolates that were not identified as belonging to a specific subgroup were reported by Texas (520), Illinois (289), and California (231). The highest proportions of reported *Shigella* isolates that were not identified as belonging to a specific subgroup within each state where 5 or more total isolates were submitted were Ohio (28/30, 93%), Illinois (289/370, 78%) and Texas (520/1,591, 33%).

Incidence by region for subgroup D (S. sonnei) isolates from 1991 to 2006 are illustrated in Figure 3. Several regions showed increases in subgroup D (S. sonnei) isolates from 2005 to 2006: the South Atlantic region, Mountain, and West North Central. *Shigella* transmission occurs via the fecal-oral route. Most subgroup D (S. sonnei) infections in the United States occur in young children and in association with crowding and poor personal hygiene. Daycare centers have been implicated in many large S. sonnei outbreaks, that can last many months and affect many persons (2,3,4). In 2005, a strain of S. sonnei resistant to ampicillin and trimethoprim-sulfamethoxazole emerged as a cause of prolonged, community-wide outbreaks of shigellosis associated with child care centers in three States (2). Antimicrobial treatment options for children infected with this strain are few, and include oral azithromycin, “off-label” use of fluoroquinolones, or intramuscular agents such as ceftriaxone (2, 14). S. sonnei has also been transmitted through unchlorinated wading pools (6), interactive water fountains (7), food items such as parsley (8) and bean dip (9), and men who have sex with men (MSM) (10). Until recently, the dominant subgroup causing illness among MSM was subgroup B (S. flexneri) (11, 12). However, in large outbreaks

among MSM in San Francisco, the dominant serotype was subgroup D (S. sonnei) (10).

Recent trends in shigellosis in the United States are reviewed in publications by Amita Gupta, Sumathi Sivapalasingam and their co-authors (13,14).

Note about removal of S. boydii 13 from the *Shigella* scheme for *Shigella* Surveillance Summary:

Bacterial isolates initially identified by traditional biochemical and serologic methods as *Shigella* boydii serotype 13 are no longer included within the *Shigella* scheme. Isolates of this serotype were added to the *Shigella* scheme in 1958 (15), but subsequent findings from DNA-DNA reassociation studies reported by Brenner et al. in 1973 raised questions about their inclusion within the genus *Shigella* (16). In these studies, Brenner and colleagues observed that S. boydii 13 strains showed a high level of interrelatedness (92 to 98%) but only averaged 65% relatedness to strains of the other *Shigella* species, E. coli and other Escherichieae. Recent findings from 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 (17, 18).

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