Arizona Department of Health Services

Lab-Based Surveillance of *Shigella* in Arizona, 2008

Shigella is the third most common cause of bacterial gastroenteritis in the United States, after *Campylobacter* and *Salmonella* infection. Unlike *Campylobacter*, *Salmonella* and *E. coli* O157 infections, for which foodborne outbreaks are the most common source of transmission, *Shigella* is mainly transmitted from person to person.[1] Day care centers are ideal settings that can propagate the person to person spread of shigellosis and its secondary spread within the community. Improper handwashing, diapering practices, and fecal contamination of water-play areas (e.g., kiddie pools), have been associated with *Shigella sonnei* infections in day-care centers.[3] *Shigella* infection is easily transmitted from person to person by the fecal-oral route, and a small infectious dose of 10-100 organisms is needed to cause infection.[4]

Reporting positive laboratory tests for *Shigella* to ADHS is required under Arizona Administrative Code R9-6-204. All commercial, diagnostic and hospital laboratories must submit reports of positive tests to the ADHS Office of Infectious Disease Services and send the isolate to the Arizona State Public Health Laboratory (ASL) for further confirmation and serotyping. In 2008, 598 laboratory confirmed cases of *Shigella* were reported to ADHS.

Basic information about the patient's sex, age, and address is included in the laboratory reports. State and local public health departments in Arizona collect additional information about clinical illness and risk factor exposures using a standardized questionnaire. These epidemiological data, along with laboratory information from the testing performed at ASL, provide the basis for identifying clusters of *Shigella*.

The state laboratory provides subgrouping and serotyping of all *Shigella* isolates submitted. There are four major subgroups of *Shigella*: *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri* and *Shigella sonnei*, and these can be further distinguished by serotypes. Additionally, all *Shigella* isolates received are genetically fingerprinted by using pulsed-field gel electrophoresis (PFGE), using the *Xba* I restriction enzyme. The fingerprints generated are processed using Bionumerics software. PFGE matches provide further evidence that organisms from separate cases are similar. Many clinical laboratories are able to identify the presence of *Shigella* species, and some are able to identify the group, but routine identification of groups and serotypes, as well as PFGE analysis, is performed only at the state laboratory. This specific testing is unique to public health laboratories and can provide information important to public health investigations.

Of the 598 cases of *Shigella* reported to ADHS, isolates were received at ASL for 584 (97%). The majority of the submissions were from hospital laboratories (412, 70%); 172 (29%) were from commercial and diagnostic laboratories. Fourteen positive tests were reported to ADHS without a corresponding isolate being submitted to ASL for serotyping.

Of the 584 isolates identified and serotyped in 2008, 70% (140) were *Shigella sonnei*, with *S. flexneri* accounting for another 27%. The distribution of the four *Shigella*

subgroups is shown in Figure 1 and the serotype distribution is shown in Table 1. *Shigella sonnei* is commonly associated with outbreaks in daycare centers. In the community, these outbreaks can last for weeks and are very difficult to control. Other subgroups of *Shigella* such as *Shigella flexneri* are not commonly transmitted in daycare centers but have appeared in foodborne outbreaks involving produce. All *Shigella* subgroups can cause dysentery; however, *S. sonnei* generally causes milder disease than *S. dysenteriae* and *S. flexneri*.

Figure 1: Distribution of* Shigella *isolates reported in Arizona, by the four subgroups, 2008

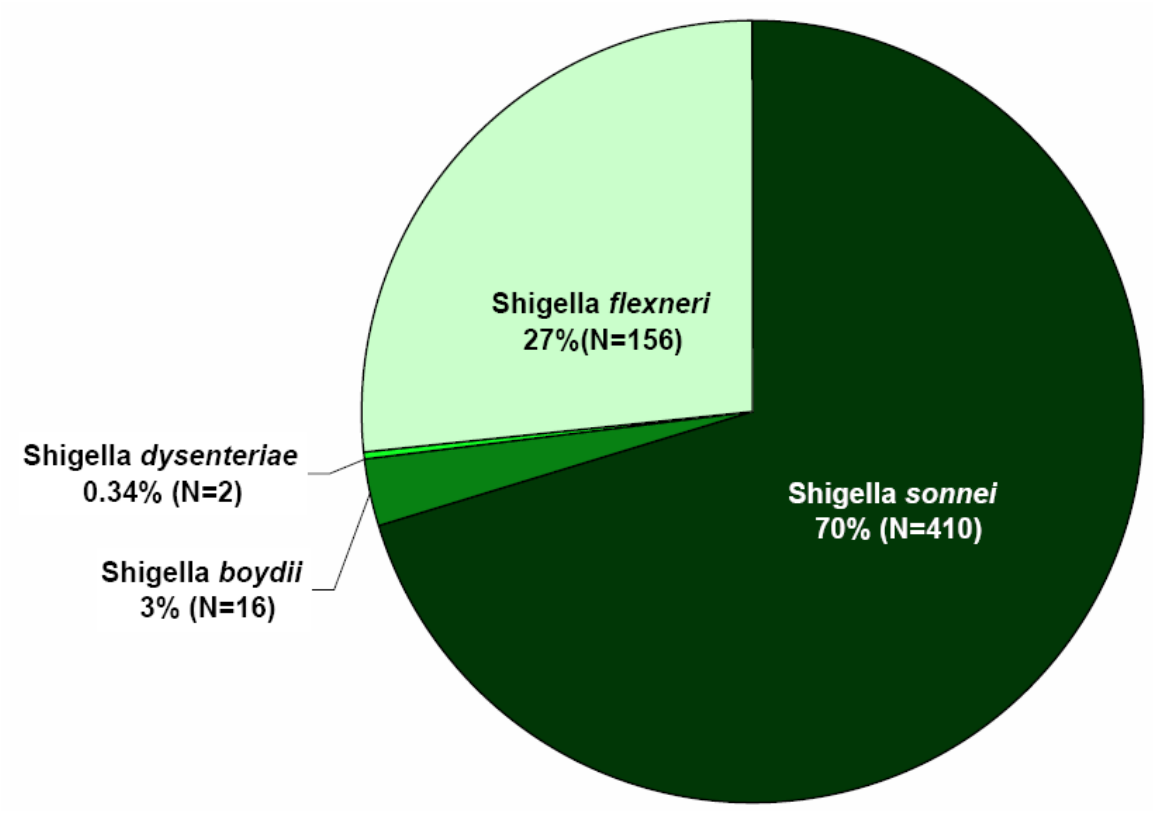

Table 1:* Shigella *isolates serotyped at ASL, 2008

Serotype	Number of isolates	Percent of total (%)
***Shigella sonnei*- TOTAL**	**410**	**70.2**
***Shigella flexneri*- TOTAL**	**156**	**26.7**
Shigella flexneri 1	36	
Shigella flexneri 2	54	
Shigella flexneri 3	28	
Shigella flexneri 4	12	
Shigella flexneri 6	9	
Shigella flexneri variant y	3	
Shigella flexneri 88-893 (Provisional)	3	
Shigella flexneri serotype unknown	11	
***Shigella boydii*- TOTAL**	**16**	**2.7**
Shigella boydii 2	7	
Shigella boydii 4	6	
Shigella boydii 18	1	
Shigella boydii serotype unknown	2	
***Shigella dysenteriae*- TOTAL**	**2**	**0.4**
Shigella dysenteriae 3	1	
Shigella dysenteriae serotype unknown	1	
Total	**584**	**100%**

In 2008, 572 *Shigella* isolates were tested with PFGE; 478 of these isolates were assigned a banding pattern. There were 10 clusters of *Shigella sonnei* with more than 10 cases each, with onset dates of infection distributed over a span of three to four months. These patterns are: J16X01.1166 (N=28), J16X01.2200(N=27), J16X01.1280(N=18), J16X01.1067(N=17), J16X01.0283(N=15), J16X01.0172(N=14), J16X01.1111(N=14), J16X01.0199(N=13), J16X01.0408(N=13), J16X01.2453(N=13). From these clusters, J16X01.1166 is the only pattern that matched a nationwide *Shigella* cluster. The first isolate from this cluster was identified in July 2008 and the most recent isolate was identified in early March 2009. (An additional 41 cases have been identified in 2009, beyond the 28 listed above for 2008). CDC identified that this cluster accounts for 2.5% of all *S. sonnei* in the CDC PulseNet database and the majority of the matching isolates were identified from Pennsylvania, Virginia, and several other northeastern and western states. Most of these cases appear to have been associated with cases attending or working at daycare centers or contacts of these individuals. It is important to note that while PFGE can be used to assess the relatedness of bacterial isolates, *Shigella sonnei* isolates can be clonal in nature and therefore some clusters may not indicate true outbreaks.

Of the 598 confirmed *Shigella* cases reported in 2008, 53% are female, with a median age of 7 years. Forty-six percent (n=271) of all *Shigella* isolates were recovered from children aged < 5 years, and 65% of cases occurred in children between 1 and 14 years of age. Among the children under 5 years of age, 69% of cases were found to be *S. sonnei* and the median age of cases of *S. sonnei*, *S. boydii*, *S. flexneri*, and *S. dysenteriae* infections were 6,9, 8, and 2 years respectively. It is common to see a larger number of cases in young children, who are unable to practice food or personal hygiene and have not yet acquired immunity to *Shigella*.

Standardized questionnaires were completed for 374 (62%) of the 598 confirmed cases of reported *Shigella*. Of these 374 cases, diarrhea was present in 98% of cases, with 55% of the cases reporting having bloody stools (dysentery). Thirty percent (113/374) were hospitalized, 17% responded to having attended daycare or worked at a daycare and 1% responded to being employed as a food handler.

The laboratory-based surveillance of *Shigella* is important to identify trends in populations particularly at risk from infection. Many approaches to develop a *Shigella* vaccine have been attempted; however, the immunity offered by vaccines is serotype specific. For now, interventions aimed at targeting daycare centers, such as appropriate hand washing practices, separation of food preparation and diaper-changing responsibilities, and caring for children in smaller groups are the primary way to prevent disease transmission.[2]

References:

1. Gupta A, Polyak C. *Laboratory-Confirmed Shigellosis in the United States, 1989-2002: Epidemiologic Trends and Patterns*. CID 2004; 38:1372-1377.

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4. Shiferaw B, Shallow S. Trends in Population-Based Active Surveillance for Shigellosis and Demographic Variability in FoodNet Sites, 1996-1999. CID 2004; 38:S175-S180