

***Shigella sonnei* Infections**

[Announcer] This program is presented by the Centers for Disease Control and Prevention.

[Kathy Harben] Hi, I'm Kathy Harben and today I'm talking with Dr. Nancy Strockbine, Chief of the *Escherichia* and *Shigella* Reference Unit at CDC. Our conversation is based on a paper about *Shigella sonnei* infections, which appears in CDC's journal, Emerging Infectious Diseases. Welcome, Dr. Strockbine.

[Nancy Strockbine] Thank you. It's nice to be with you.

[Kathy Harben] Dr. Strockbine, what is *Shigella sonnei*?

[Nancy Strockbine] *Shigella sonnei* is one of four species of *Shigella* that are recognized for historical and medical reasons and are classified on the basis of biochemical and antigenic differences. *Shigella sonnei* only has one antigenic variant we call a serotype, while the other *Shigella* species each have many serotypes which helps distinguish one strain from another within a species. Because about 75 percent of *Shigella* infections in developing countries are caused by *Shigella sonnei*, the lack of antigenic variation within this species makes it difficult to discriminate between strains. This is especially a challenge during outbreak investigations. Bacteriologists have tried many methods over the years to tell one strain of *Shigella sonnei* from another, without a great deal of success.

Shigella lives nearly exclusively in people's intestinal tracts where it can invade the cells lining the large intestine and cause serious disease. People usually become infected by ingesting contaminated food or water or putting their contaminated hands or other objects in their mouths. *Shigella* can survive on inanimate objects up to five months. Most people who become infected with *Shigella* develop diarrhea, which is often bloody; fever; and stomach cramps starting a day or two after ingesting the organism. *Shigella* can cause large outbreaks, particularly in places where good hygiene practices are difficult to follow.

[Kathy Harben] Why was this study done?

[Nancy Strockbine] Understanding the diversity that exists within a species is very important for epidemiologic investigations and evolutionary studies. To learn about the diversity within *Shigella sonnei* and the evolution of its members, the authors tested a large collection of isolates from different times and places with a sensitive typing method to detect repeated sequences throughout the genome. They were particularly interested to see how many groups they could identify and if there was any clustering of strains by time or location. Understanding the amount of genetic variation and the relatedness of strains helps us appreciate the way the organism is changing and interpret our laboratory findings to track and control the spread of infections.

[Kathy Harben] What regions and years were analyzed?

[Nancy Strockbine] A total of 1,672 strains isolated between 1943 and 2008 from over 50 countries in Africa, Asia, Europe, North America, South America, and the Pacific region were looked at. Sixty-six percent of the isolates were from patients who got their infections in Taiwan.

[Kathy Harben] What was discovered?

[Nancy Strockbine] A simple family lineage showing the descent of *Shigella sonnei* strains from a common group of strains was identified. They defined three major groups among the strains in the collection, with two of these comprised of strains distributed widely across the world, and one containing strains from only Africa, Asia, and Europe. The sub-typing method used allowed improved discrimination between strains, but more than 80 percent of the strains tested concentrated within one group.

[Kathy Harben] What is the public health importance of this discovery?

[Nancy Strockbine] The structure of the family lineage discovered for *Shigella sonnei* increases our understanding of the evolution of this organism and provides a framework to study the emergence of new strains. Should a particularly virulent strain arise, it will be helpful to fit it into the lineage presented to determine from what major group it evolved. This knowledge could provide clues about factors affecting its emergence and possible ways to intervene to control the spread of infection.

[Kathy Harben] Thanks, Dr. Strockbine. I've been talking with Dr. Nancy Strockbine about a paper, *Global Distribution of Shigella sonnei Clones*, which appears in the October 2011 issue of CDC's journal, Emerging Infectious Diseases. You can see the entire article online at www.cdc.gov/eid.

If you'd like to comment on this podcast, send an email to eideditor@cdc.gov. That's e-i-d-editor - one word - at c-d-c-dot-gov. I'm Kathy Harben, for Emerging Infectious Diseases.

[Announcer] For the most accurate health information, visit www.cdc.gov or call 1-800-CDC-INFO.