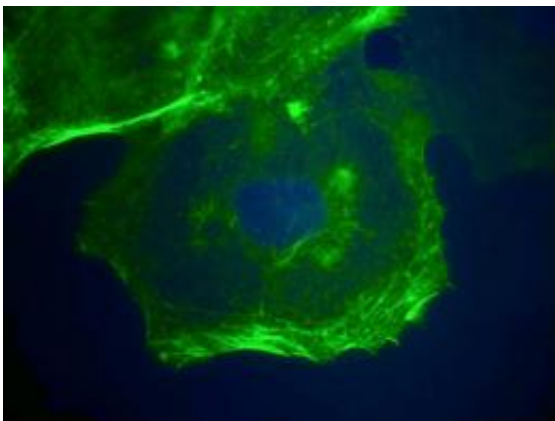


Research traces bacteria in salmonella outbreaks

August 31 2011, By Krishna Ramanujan



The photo shows human cells poisoned with salmonella toxins. The blue in the center of the cells shows the nucleus, while the green color represents "actin stress fibers" that formed as a result of toxins. Lorraine Rodriguez-Rivera (Wiedmann lab) and Rasika Jinadasa (Duhamel lab)

(Medical Xpress) -- During such mass food-poisoning outbreaks as the recent contamination of ground turkey, speedy identification of the bacteria involved can save lives and reduce illness. New research co-authored by a Cornell food scientist will accelerate the process of identifying strains of salmonella bacteria behind food poisonings -- and reduce the time it takes to track the culprit from farm to fork.

The paper, published in the Aug. 24 issue of the journal [BMC Genomics](#), offers a comparative study of the [genome](#) sequences of 47 different

[salmonella strains](#), including 16 that were sequenced for the first time. One of the genomes analyzed was for salmonella Heidelberg, the strain that was recently involved in the ground turkey outbreak in more than 30 states.

Also, four of the serovars (a group of closely related microorganisms distinguished by a characteristic set of antigens) sequenced have been implicated in outbreaks in the last four years: Serovar Wandsworth caused an outbreak with 65 reported cases in 20 states in 2007; serovar Montevideo caused an outbreak with 272 reported cases in 2009-10 in 44 states; serovar Hvittingfoss caused an outbreak with 90 reported cases in Illinois in 2010; and serovar Baildon was involved in an outbreak with 80 reported cases in 15 states, also in 2010.

"The data generated by this paper can be used to rapidly identify [salmonella outbreak](#) strains by their [genome sequence](#)," said Martin Wiedmann, professor and director of graduate studies in food science and technology at Cornell and the paper's senior author.

The research by Wiedmann and his co-authors may also help health officials predict strain-specific characteristics, such as risk groups and the diseases caused by such strains.

The [genomic analysis](#) found that the salmonella pathogen can be divided into two main groups, called clade A and clade B, with each clade differing in genes that potentially affect the way these pathogens disperse and the kind of infection they cause, according to the study.

The two groups differ in the carbon resources they use, which can make them more adapted to certain hosts. Preliminary data show that while both strains can cause disease in humans, clade A is more abundant in mammals, and clade B is more common in reptiles.

In the United States, an estimated 11 percent of the food-borne illnesses are caused by salmonella, making it the most prevalent non-viral foodborne pathogen.

The work was done in collaboration with Life Technologies, a global biotechnology tools company. Lead authors include postdoctoral associate Henk den Bakker and graduate student Andrea Morena Switt, both in Wiedmann's lab.

Provided by Cornell University

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