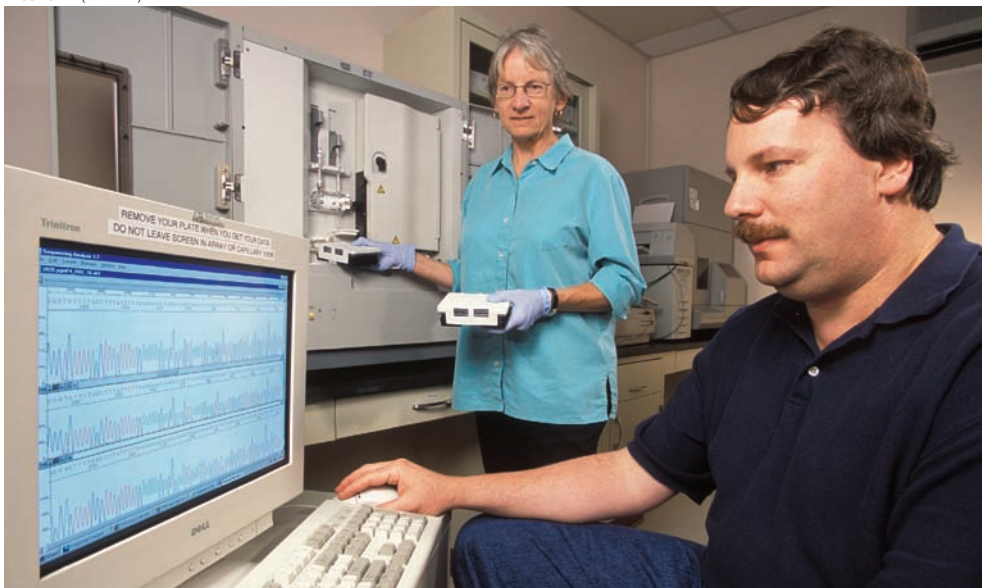


Arcobacter

Genome of Foodborne Pathogen Exposed



Technician Sharon Horn (retired) and microbiologist William Miller prepare samples of *Campylobacter* for automated analysis of DNA sequence. To better understand a little-known microbe called *Arcobacter butzleri*, Miller and colleagues are comparing it to related microbes such as *Campylobacter*. These comparisons may yield clues to *A. butzleri*'s survival strategies.

A little-known microbe called *Arcobacter butzleri* may make you sick if the water you drink or food you eat is contaminated with it.

But Agricultural Research Service microbiologist William Miller and colleagues have deciphered the sequence of the bacterium's genetic material. This scientific coup—a first for any of the world's *Arcobacters*—may speed discovery of innovative ways to control the microbial miscreant.

Many medical professionals regard *A. butzleri* as an emerging cause of foodborne disease, according to Miller. Based at the ARS Western Regional Research Center in Albany, California, near San Francisco, he did the genome-sequencing work with colleagues there and with others in the United States and abroad.

The target microbe has been implicated as a cause of outbreaks of food-related illnesses in Europe and Southeast Asia. It is associated with an array of unpleasant symptoms, including diarrhea, stomach cramps, nausea, vomiting, and fever—all of which can become chronic if left untreated.

Previously, the microbe was thought to be a species of *Campylobacter*, the world's leading cause of bacterial diarrhea. Later,

A. butzleri was reclassified to the *Arcobacter* genus.

Now, by comparing *A. butzleri*'s genetic makeup to that of other microbes, Miller and coinvestigators can learn more about its relatedness to them. Such comparisons are important: They may yield clues to *A. butzleri*'s survival strategies and—perhaps more importantly—to previously unknown vulnerabilities that scientists could exploit to keep food and water safe.

But *A. butzleri* hasn't made such comparisons easy.

The team's analysis has already revealed that many *A. butzleri* genes “don't seem to match up” with those from other microbes, Miller says. His observation is based on comparing *A. butzleri*'s genome sequence to other sequences posted on the World Wide Web.

“We don't know what these unique *A. butzleri* genes do,” says Miller. “That's one of the things that makes this pathogen so interesting.”

While research to discover the function of all of *A. butzleri*'s genes continues, Miller has already used the genomic data in developing what's known as a “typing method.” Medical professionals, public health agencies, and researchers can use it when they're tracking the source of foodborne-illness outbreaks.

Based on technology known as “multi-locus sequence typing,” the assay distinguishes *A. butzleri* from several cousins that could be outbreak culprits, namely *A. cibarius*, *A. cryaerophilus*, and *A. skirrowii*. And the typing method does more than just differentiate these species. It also “accurately and unambiguously fingerprints strains *within* each species,” Miller points out. “That makes it especially useful for investigating the source of outbreaks.”

Other scientists are already using the new assay, Miller says. He expects his scientific journal article on the test to be published this year. His article on sequencing the complete *A. butzleri* genome appeared in 2007 in the online journal *PLoS ONE*.—By **Marcia Wood**, ARS.

This research is part of Food Safety, an ARS national program (#108) described on the World Wide Web at www.nps.ars.usda.gov.

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