

Genome of Bad-Boy *Campylobacter* Sequenced

Inquisitive ARS scientists have laid bare the genetic makeup of a little-known food-poisoning microbe called *Campylobacter lari*. This bad-guy bacterium is a close relative of the better known *C. jejuni*, the culprit in millions of cases of diarrhea in humans every year.

Microbiologist William G. Miller did the genome work in his laboratory at the ARS Western Regional Research Center in Albany, California. *C. lari* has attracted the California team's attention because it is "what we consider an emerging pathogen," Miller says. "It's beginning to show up in other countries, so we need to keep it on our radar here."

Knowing the genetic makeup of a foodborne pathogen such as *C. lari* is a strong first step toward understanding and controlling it. For example, the research opens the door to creating an accurate, affordable, gene-based test to quickly detect the pathogen in samples from people or foods. Such a test would help public health officials track a food-poisoning outbreak to its source.

What's more, the genome is a treasure trove of information for scientists—like Miller—who want to compare and contrast it to other troublesome *Campylobacter* species, such as *C. jejuni* or *C. coli*. Similarities and differences among these genomes will provide important clues to how *Campylobacter* successfully infects us, which may lead to new tactics to outmaneuver the genes that orchestrate infection.

Miller began his genome journey by working forward from a rough draft prepared for ARS by the Institute for Genomic Research, Rockville, Maryland. Digging deeper, Miller filled in gaps and polished rough spots. He now plans to post this important first draft on the World Wide Web early in 2007. Insights that emerge from scientists' scrutiny of this genome will further ensure the safety of the foods we eat.—By **Marcia Wood, ARS.**

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PEGGY GREB (K11472-1)



Technician Sharon Horn and microbiologist William Miller prepare samples of *Campylobacter* for automated analysis of DNA sequence. The monitor shows the sequence of a DNA sample run earlier.

Unraveling the *Listeria* Genome

If knowledge is power, Agricultural Research Service scientists are gaining the upper hand on *Listeria monocytogenes*.

Researchers at the ARS Eastern Regional Research Center (ERRC) in Wyndmoor, Pennsylvania, and the Institute for Genomic Research in Rockville, Maryland, sequenced four strains of *Listeria* related to foodborne listeriosis outbreaks—an important step toward developing a management strategy for this deadly bacterium.

"Researchers in the ERRC Microbial Food Safety Research Unit have completed whole genome sequencing and comparison of four genomes, which allowed us to significantly improve our understanding of *Listeria*," says research leader John B. Luchansky. In addition to finding serotype-specific and strain-specific genome sequences, they found that these four *Listeria* strains have largely similar genetic content and organization.

The team believes a few unique regions could account for epidemiological and antigenic differences among strains. Understanding these differences will improve scientists' ability to assess the risk posed by contamination of food by this bacterium.

They also confirmed that *Listeria* bacteria have 15 genes in a regulatory protein family known as "Crp/Fnr," considerably more than most bacteria have. Luchansky and molecular biologists Darrell Bayles and Gaylen Uhlich are investigating whether these sequences influence the bacterium's virulence or persistence in the food supply.

The scientists have estimated the percentage of the genome for which there is no known function and identified specific genes that warrant further investigation. They've also started to pursue proteomics and genomics studies, Luchansky says. This involves comparing different strains of bacteria—or the same strain growing under different environmental conditions—to determine whether there are differences in the level of gene or protein expression under the conditions tested.

Knowing more about the bacterium will enable regulatory agencies and the food industry to make better informed decisions about safety standards and control strategies, Uhlich says. And uncovering the genetic information that defines *Listeria's* survival, growth, persistence, and ability to cause disease will help scientists better understand the bacterium's virulence, its presence in the environment, and its persistence in the food chain.

"Ultimately, we hope to learn enough about *Listeria* to prevent contamination, decrease prevalence, and reduce disease," Bayles says. "This research puts us in a better position to make scientifically sound decisions about managing the threat of foodborne listeriosis."—By **Laura McGinnis, ARS.**

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