

Genetic sequencing of little bug holds big potential

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As bacteria go, *Bacillus megaterium* doesn't exactly get a lot of press. Most people have never heard of it. Yet the common little bug with the grandiose name is yielding important information about subjects that are vital to public interest: AIDS, bioterrorism and environmental cleanup.

For the past three decades, Patricia Vary, a Distinguished Research Professor Emeritus at Northern Illinois University and former chair of biological sciences, has been working to develop a better understanding of the genetic makeup of *B. megaterium*, or *B. meg*, as she calls it.

In the process, Vary and her colleagues developed a strain of *B. meg* that acts as an ideal host for the cloning of foreign DNA. For the past several years, this patented strain has been used by Abbott Laboratories for the production of a viral protein used in diagnostic tests for AIDS.

Most recently, the National Science Foundation provided a grant of \$630,000 to The Institute for Genomic Research (TIGR), which is working with Vary and her research group at NIU to sequence the *B. meg* genome. Vary is among the three principal investigators on the research project, and NIU is receiving about \$40,000 of the grant money.

Bacillus megaterium is a harmless bacterium, found across the globe in a variety of habitats, including soil. Yet *B. meg* also is a closely related cousin of the deadly pathogen that causes anthrax, which is often associated with bioterrorism. Comparisons of the two genomes could

help detect genes that are specific to anthrax, clarify the role of those genes in disease and enhance diagnostics and treatment.

“The genomes of all known bacterial pathogens have been sequenced,” says Vary, who retired from the classroom in 2004 but has continued her research efforts, often working with students.

“However, we don’t know much about non-pathogenic bacteria, which make up 99.9 percent of all bacteria. By sequencing *B. meg*, we’ll be able to compare it with the anthrax bacterium and hopefully find out what makes a pathogen a pathogen. Ultimately, this will help us learn how to better detect harmful bacteria in the environment.”

What makes *B. meg* unique in the world of bacteria is its cell structure. Bacterial cells often contain plasmids—circular units of DNA that replicate within a cell independently of the chromosomal DNA and give the bacterium some advantage in nature. Plasmids are also used as a basic component in cloning.

“Many bacteria have one or two plasmids; the strain of *B. meg* that I work with has seven,” Vary explains. “I developed a strain for cloning, used by Abbot for AIDS diagnostics. Also my students and I have been sequencing all of the *B. meg* plasmids and studying their interactions.”

Because common types of bacteria play significant roles in all major earth cycles, a better understanding of their genetics could also lead to major technological innovations in other areas. For example, the so-called “oil-eating bacteria,” used to clean up oil spills, also contain multiple plasmids.

“We want to find out if *B. meg* plasmids harbor genes of potential use in the cleanup of toxic compounds,” Vary says. “I think we’re going to be discovering some genes that could be interesting.”

While Vary has made major strides in the understanding of *B. meg* over the decades, The Institute for Genomics Research (TIGR) brings substantial expertise and resources to the genome sequencing project.

Located in Rockville, Md., TIGR is a not-for-profit center dedicated to deciphering and analyzing genomes—the complex molecular chains that constitute each organism’s unique genetic heritage. Since it was founded in 1992, TIGR has been at the forefront of the genomics revolution, deepening the understanding of life and producing results with wide-ranging applications in medicine, agriculture, energy, the environment and biodefense.

In 1995, TIGR helped launch the genome era with its landmark publication of the first full DNA sequence of a free-living organism, the bacterium *Haemophilus influenzae*. Over the next decade, the institute and its collaborators sequenced the complete genomes of more than 50 organisms or microbial strains—more than any other research center. In 1998, it published a sequence of the human genome.

The *B. meg* sequencing project also has outreach and education components that will benefit the NIU community. This past May, 10 NIU students and faculty, including Vary, attended a workshop at TIGR, where they learned how to use powerful new software for the annotation of gene sequences. Annotation is the analysis of the sequence to determine the genes and their function.

This coming fall, a workshop will be held to teach NIU biology students how to use the software. Vary and her research group also will debut a Web site, following the progress of the *B. meg* sequencing. In the spring of 2007, Vary will lead a workshop for high school and community college students on the basics of cloning and sequencing.

“We not only want to learn as much as possible about *B. meg*,” Vary

adds, “but we also want students at NIU and beyond to benefit from this project.”

Source: Northern Illinois University

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