100K Pathogen Genome Project maps first genomes

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(Phys.org) — Striking a blow at foodborne diseases, the 100K Pathogen Genome Project at the University of California, Davis, today announced that it has sequenced the genomes of its first 10 infectious microorganisms, including strains of Salmonella and Listeria.

"We are creating a free, online encyclopedia or reference database of genomes so that during a foodborne disease outbreak, scientists and public health professionals can quickly identify the responsible microorganism and track its source in the food supply using automated information-handling methods," said professor Bart Weimer, director of the 100K Genome Project and co-director of BGI@UC Davis, the Sacramento facility where the sequencing is carried out.

Weimer estimates that the availability of this genomic information will cut in half the time necessary to diagnose and treat foodborne illnesses, and will enable scientists to make discoveries that can be used to develop new methods for controlling disease-causing microorganisms in the food chain.

The project is dedicated to sequencing the genomes of 100,000 bacteria and viruses that cause serious foodborne illnesses in people around the world.

In the United States alone, foodborne diseases annually sicken 48 million people and kill 3,000, according to the Centers for Disease Control and Prevention.
The initial 10 genome sequences mark the first in a series that the project will enter into a publicly available database at the National Center for Biotechnology Information of the National Institutes of Health.

"This initial release validates the entire process, from start to finish, of acquiring the bacterium, producing the **genome sequence**, and making automated public releases," Weimer said.

A genome is the complete collection of an organism's hereditary information.

Weimer said that the 100K Genome Project currently is sequencing a second set of 1,500 **microbial genomes**, with an anticipated release in the fall of 2013.

Provided by UC Davis


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