

100K Genome Project takes aim at foodborne diseases

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An ambitious effort to sequence the genomes of 100,000 infectious microorganisms and speed diagnosis of foodborne illnesses has been launched by the University of California, Davis, Agilent Technologies and the U.S. Food and Drug Administration.

Professor Bart Weimer of the UC Davis School of Veterinary Medicine serves as director of the 100K Genome Project and co-director of the recently established BGI@UC Davis facility, where the sequencing will be done. Other collaborators include the U.S. [Centers for Disease Control and Prevention](#) and the U.S. [Department of Agriculture](#).

The new five-year microbial pathogen project focuses on making the [food](#) supply safer for consumers. The group will build a free, [public database](#) including sequence information for each pathogen's genome -- the complete collection of its hereditary information. The database will contain the genomes of important foodborne pathogens including Salmonella, Listeria, and E. coli, as well as the most common foodborne and waterborne viruses that sicken people and animals.

The project will provide a roadmap for developing tests to identify pathogens and help trace their origins more quickly. The new genome database also will enable scientists to make discoveries that can be used to develop new methods for controlling disease-causing bacteria in the food chain.

“This landmark project harnesses UC Davis’ partnership with BGI, a

world leader in genomics, to mine information about the most deadly foodborne pathogens,” said Harris Lewin, vice chancellor for research at UC Davis. “It will revolutionize our basic understanding of these disease-causing microorganisms.”

The sequencing project is critically important for tackling the continuing outbreaks of often-deadly foodborne diseases around the world. In the United States alone, foodborne diseases annually sicken 48 million people and kill 3,000, according to the CDC.

“It’s becoming more and more apparent that the persistence and pervasiveness of these organisms in the food supply stem from their genetic flexibility, which enables specific strains of bacteria to adapt in food, the environment and animals,” Weimer said.

“The lack of information about food-related bacterial genomes is hindering the research community’s ability to improve the safety and security of the world [food supply](#),” he said. “The data provided by the 100K Genome Project will make diagnostic tests quicker, more reliable, more accurate and more cost-effective.”

The FDA is providing more than 500 already completed Salmonella whole-genome draft sequences, thousands of additional important food pathogen strains for sequencing, and bioinformatic support. FDA scientists also will participate in guiding the project and providing technical assistance when needed.

The CDC will provide its foodborne disease expertise, strains to be sequenced and other information for use in the project. CDC experts will also serve on the steering committee for the project.

The U.S. Department of Agriculture’s Food Safety and Inspection Service will also collaborate on the project and intends to submit

important bacterial strains to UC Davis for sequencing.

UC Davis, in addition to coordinating the sequencing at its newly formed BGI@UC Davis sequencing facility, is providing access to the university's collection of bacterial samples along with bioinformatic analysis capabilities.

Agilent Technologies is contributing scientific expertise, instrumentation and funding to support a portion of UC Davis activities.

“A problem of this magnitude demands an equally large countermeasure,” said Mike McMullen, president of Agilent’s Chemical Analysis Group. “We see this project as a way to improve quality of life for a great many people, while minimizing a major business risk for food producers and distributors.”

At the new BGI@UC Davis facility, high-throughput technologies -- also known as next-generation sequencing -- will be used to rapidly examine the genomes of the targeted microorganisms. A small number of entire genomes will be completely sequenced for use as reference genomes, while the vast majority of bacterial strains will be sequenced and assembled as draft genomes that will eventually be released to the public. This strategy is intended to help the researchers identify sets of biomarker genes that are associated with certain important pathogen traits.

As sequences are completed, they will be stored in the National Institutes of Health’s National Center for Biotechnology Information’s public database. The U.S. Department of Agriculture’s Food Safety and Inspection Service as well as the food safety and zoonotic disease unit of the U.S. Centers for Disease Control and Prevention will also collaborate on the project.

UC Davis is forming a consortium including additional partners to support The 100K [Genome Project](#).

“This is a dynamic, collaborative effort, and there are a number of ways that potential partners from industry, government agencies, academia and research institutes can join us to expand the knowledge base for foodborne disease bacteria,” Weimer said.

More information: The FDA’s press release, “FDA, UC Davis, Agilent Technologies and CDC to create publicly available food pathogen genome database,” is available at: www.fda.gov/NewsEvents/Newsroom/PressAnnouncements .

Provided by UC Davis

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