On March 1st and 2nd, one-hundred thirty scientific experts in bacterial genomics and molecular epidemiology, representing 57 institutions around the world, gathered for a workshop in Arlington, VA, entitled, *Disease Outbreak Detection in the Genomics Era: A Global Road Map Forward*. The meeting was hosted by researchers from the U.S. Food and Drug Administration's Center for Food Safety and Applied Nutrition (CFSAN) and jointly coordinated by public health scientists on both sides of the Atlantic including FDA and The Danish Food Institute at the Technical University of Denmark. The majority of those in attendance were experts in the areas of global public health, animal health, infectious disease genomics, bioinformatics, and computational sciences and represented 24 different government agencies across 12 countries including The United States, Canada, Denmark, Germany, The United Kingdom, Sweden, New Zealand, France, Portugal, Japan, Mexico, and China. The primary purpose of this meeting was to define and develop solutions to questions and challenges surrounding the deployment of next-generation DNA sequencing tools for public health and disease outbreak detection on a global scale.

Whole-genome sequencing (WGS) technology is contributing long anticipated solutions to what were once viewed as insurmountable challenges in the genetic analysis of bacterial pathogens. Complete genome sequences from multiple bacterial strains can now be collected and analyzed in just a few days, underscoring the potential of this technology as a molecular epidemiological tool to assist in disease outbreak investigations. Recent examples in the literature illustrate the ability of WGS to discern high-resolution genetic relatedness of otherwise indistinguishable isolates based on the genetic changes that accrue within individual bacterial strains. Proof-of-principle studies have been undertaken successfully using the technology at the U.S. FDA, the CDC, Northern Arizona University (Dr. Paul Keim's laboratory), Public Health Canada, Harvard and Cornell Universities, The Sanger-Wellcome Trust in the United Kingdom, The Danish Technical University and Danish Food Institute, The University of Muenster in Germany, and various industry colleagues engaged in WGS technology development.

The first meeting responsible for organizing a coordinated and global direction for the use of WGS in the public health arena was hosted by the Danish Food Institute/Danish Technical University and occurred in September 2011 in Brussels where a select group of 30 experts from around the world assembled for two days to adopt and endorse the concept of a single global pathogen identification and tracking system based on WGS technology. In full, eleven articles were adopted by the committee that *in toto* provided a conceptual framework for a movement forward using WGS as the basis for a global pathogen identification network. (http://www.genomeweb.com/sequencing/next-gen-sequencing-shows-promise-public-health-faces-technical-political-social). The meeting was framed in the following summation:

> *"The rapid advancement of genome technologies holds great promise for improving the quality and speed of clinical and public health laboratory investigations, and for decreasing their cost. The latest generation of genome DNA sequencers is now capable of providing highly detailed and robust information on disease-causing microbes, and in the near future these technologies will be suitable for routine use in national, regional and*

global public health laboratories. With additional improvements in instrumentation, these next- or third-generation sequencers are likely to replace conventional culturing and typing methods to provide point-of-care clinical diagnosis, providing essential information for quicker and better treatment of patients. Provided there is free-sharing of information by all clinical and public health laboratories, the comprehensive understanding these genomic tools provide on infectious disease agents could spawn a global database or a system of linked databases of pathogen genomes that would ensure more efficient detection, prevention, and control of endemic, emerging and other outbreak occurrences world-wide."

The follow-up meeting in Arlington, earlier this month, shared the Brussels accords with the larger global public and clinical health and health policy community and provided a more detailed plan forward for countries capable of deploying this technology. Specific objectives that were addressed included an expanded follow-up to the 2011 Brussels meeting and a detailed debate concerning the short and long term obstacles and solutions for a global system for identification of microbial pathogens based on genomic information. The meeting also provided an overview of ongoing initiatives in this area and discussed how worldwide collaboration can be achieved to establish a globally distributed WGS system.

During the meeting, a draft road map forward for establishing a global disease outbreak detection system using shared genomic information for bacterial, viral, and parasitic microorganisms was developed. Workshop participants provided insight and perspective to a number of obstacles facing the successful development of such a system. Several important issues addressed at the meeting included: (1) where and how WGS data will be stored and curated for the world health science community; (2) the appropriate metadata to be attached to genome sequence submissions for disease detection and identification; (3) the specific computer resources required to implement a global genome-based disease detection network; (4) recommendations for data analysis pipeline design and determination of data types and categories to be included in such a database; (5) pinpointing potential political and legal restrictions for the sharing of genomic data on a global level; and (6) identifying essential steps for formatting of data necessary for point-of-care clinical utility and rapid detection for all aspects of public health.

To facilitate discussion on these important issues, an international cadre of subject matter experts addressed several topics related to the event including applications of WGS to solving foodborne and clinical disease outbreaks and other aspects of genomic epidemiology; available web-based tools and data management systems for desktop analysis of WGS data; health policy perspectives and the importance of global data sharing; and US and world regulatory perspectives on WGS technology.

Other highlights disclosed at the meeting included (1) a leading role for The National Center for Biotechnology Information (NCBI) at the National Institutes of Health to develop a portal to

upload short read archives (SRA) of draft genomes and provide a rapid pipeline for identification and clustering to other draft genomes in the database.

This also will include rapid annotation and a brief report of important features relating to multidrug resistance and virulence in these pathogens. NCBI would work with global partners (EBI and DDBJ) to create a global network to upload data from local international laboratories. Agilent reported a collaborative effort with UC Davis, BGI, FDA and NCBI to sequence 100,000 genomes of human pathogens at the new genomic facilities at the UC Davis veterinary school. This genomic sequencing collaboration requested isolates from the attendees for draft sequences to help produce a large reference database to be housed at NCBI SRA with critical and informative metadata attached to produce a valuable publicly available genomic resource.