NHGRI-NIAID Workshop on Eukaryotic Pathogens and Disease Vectors Sequencing

Hyatt Regency Bethesda
Bethesda, MD 20814
November 21, 2006

Chairs: William Gelbart and Claire Fraser-Liggett

Goals: The NHGRI and NIAID jointly sponsored a workshop to help identify the most significant human eukaryotic pathogens and invertebrate vectors of infectious diseases for potential sequencing in a collaborative, coordinated effort between NHGRI and NIAID, and to evaluate the usefulness and limitations of pathogen and vector genomic data.

Participants: Researchers in the fields of pathogens, disease vectors, genomics, bioinformatics, and infectious diseases as well as representatives from U.S. federal and international funding agencies.

Anticipated outcomes:

- Identification of the most significant human eukaryotic pathogens and invertebrate vectors of infectious diseases for potential sequencing
- Determination of criteria for prioritization
- Determination of the usefulness of sequence data and sequence data resources

Summary:

The workshop consisted of eight presentations that provided background information on 1) eukaryotic pathogens and disease vectors responsible for human infectious diseases; and 2) the usefulness and limitations of genomic sequence information for understanding the biology of pathogens and vectors, as well as for leading to candidate targets for vaccines, therapeutics, and medical diagnostics. Participants were asked to recommend a prioritized list of eukaryotic pathogens and disease vectors to sequence. They were also asked to discuss the usefulness and limitations of pathogen and vector genomic data.

The main conclusions drawn by the participants are as follows:

- Pathogen and vector sequencing projects have already provided genomic data sets that are a valuable research resource to the scientific community. These data sets have already begun to deliver significant benefits, not only in terms of basic biological knowledge, but also in terms of discovering drug, vaccine, and diagnostic targets for human infectious diseases. There is no reason to believe that the utility of this approach has been exhausted.

- There is a need for collaboration and coordinated efforts between NHGRI and NIAID. These efforts should draw on combined strengths in sequencing capacity and experience, as well as expertise in microbial genomics and infectious diseases.

Summarized below are specific recommendations from participants regarding future sequencing of eukaryotic pathogen and vector genomes:

1. Assign highest priority to sequencing the genomes of *Anopheles*, *Plasmodium*, and *Trypanosoma*, given the magnitude of global health problems resulting from infectious diseases caused by these organisms.
2. Support sequencing of additional genomes of eukaryotic pathogens and disease vectors, including additional isolates where a reference genome is available. Examples include, but are not limited to, *Giardia*, *Crytosporidium*, *Entamoeba*, *Cyclospora*, and *Toxoplasma gondii*.
3. Encourage well-designed genomic sequencing projects that may help to elucidate the biology and pathogenesis of eukaryotic pathogen and disease vectors and lead to new and improved therapeutic interventions and medical diagnostics.
4. Support sequencing projects that do not focus solely on individual strains, but rather on multiple, related strains and species. These projects should enable comparative studies of pathogen and vector genomics, and studies of microbial population genomics.
5. Facilitate genomic research on pathogens and vectors by:
    - Supporting the concept of funding a genomic resource for sequencing pathogens and vectors that will be available to the scientific community and can include Expressed Sequence Tags (ESTs), cDNAs, and other resources for assembly, annotation, and more.
    - Providing reagents as well as genomics platforms that are complementary to sequencing platforms.
    - Supporting small-scale genome projects that can be informative for developing and committing to large scale genome sequencing projects.
    - Supporting the unrestricted, rapid release of genomic data into international databases, such as GenBank, that are accessible to the scientific community and the public via the Internet.
    - Supporting resources that enable the use of genomic data generated in large scale sequencing projects. Examples include databases, bioinformatic and computational tools, and continued and sustained support for annotation and curation.
6. Establish an external scientific group representing the pathogen and vector research community as well as infectious diseases and genomics communities for the purpose of providing scientific guidance to the two Institutes in pathogen and vector genomics and sequencing projects.

Agenda:

TIME	TOPIC	SPEAKERS
8:00	Welcome Meeting objective: The identification and prioritization of those human pathogens and human disease vectors most in need of sequencing as well as a discussion on the usefulness and limitations of pathogen and vector genomic data	 Francis Collins Anthony Fauci
8:15	Charge to Group Meeting goal: To prepare a list of pathogens and disease vectors whose public sequence information is considered critical, and to categorize these organisms in priority bins	Claire Fraser-Liggett
8:30	The Landscape Arthropod Disease Vectors, Genomics, and Public Health Comparative and Functional Genomics of Trypanosomatid Parasites	Ben Beard Steve Beverley
9:10	The Use of Genomics in Vaccine Development	Rino Rappuoli
9:30	Break	
9:50	The Usefulness and Limitation of Genomic Data Genomic Revolution or Genomic Revelation: Francis Bacon or Maimonides? Opportunities in intra/inter-species comparative genomics and getting genomic-scale datasets into the hands of end users	 Jose Ribeiro David Roos
10:30	The Power of Comparative Genomics for Annotating Vector/Pathogen Genomes	Manolis Kellis
10:50	Case Studies for Sequencing Eukaryotic Genomes and Invertebrate Vectors of Diseases After the TriTryp Genomes *Aedes aegypti* Post-Genome	 Najeeb El-Sayed Dave Severson

11:30	Strawman Proposal for Criteria of Selecting What Eukaryotic Pathogens and Disease Vectors to Sequence	William Gelbart
11:45	Lunch and Free Discussions	
13:00	Breakout Groups Selection of critical eukaryotic pathogens and disease vectors to sequence; Assignment of selected sequencing targets in priority bins	Christos Louis David Roos
15:00	Break	
15:20	Breakout Group Reports Proposed eukaryotic pathogens and disease vectors for sequencing in priority bins	Christos Louis David Roos
15:50	Discussion and Summary Discussion of how proposed pathogens and vectors fit the selection criteria Meeting summary	William Gelbart Claire Fraser-Liggett
17:00	Adjournment	

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