BioHealthBase: BioDefense Public Health Database

Richard Scheuermann*[1], Burke Squires[1], Shubhada Godbole[1], Kevin Biersack, Carey Gire, Zuoming Deng, Aihui Wang, Jianjun Wang, Tammie Ajayi, Sanjeev Kumar, Jason Lucas, Soumya Sengupta, Surabhi Sharma, Paul Shrabstein, Sharmila Vattikuti, Bryan Walters, Chris Larsen[2], Al Ramsey[2], James Wolowicz[2], Xianying Wei[3]

Northrop Grumman Life Sciences, *Principal Investigator, [1]University of Texas Southwestern Medical Center, [2]Vecna Technologies, and [3]Amar International

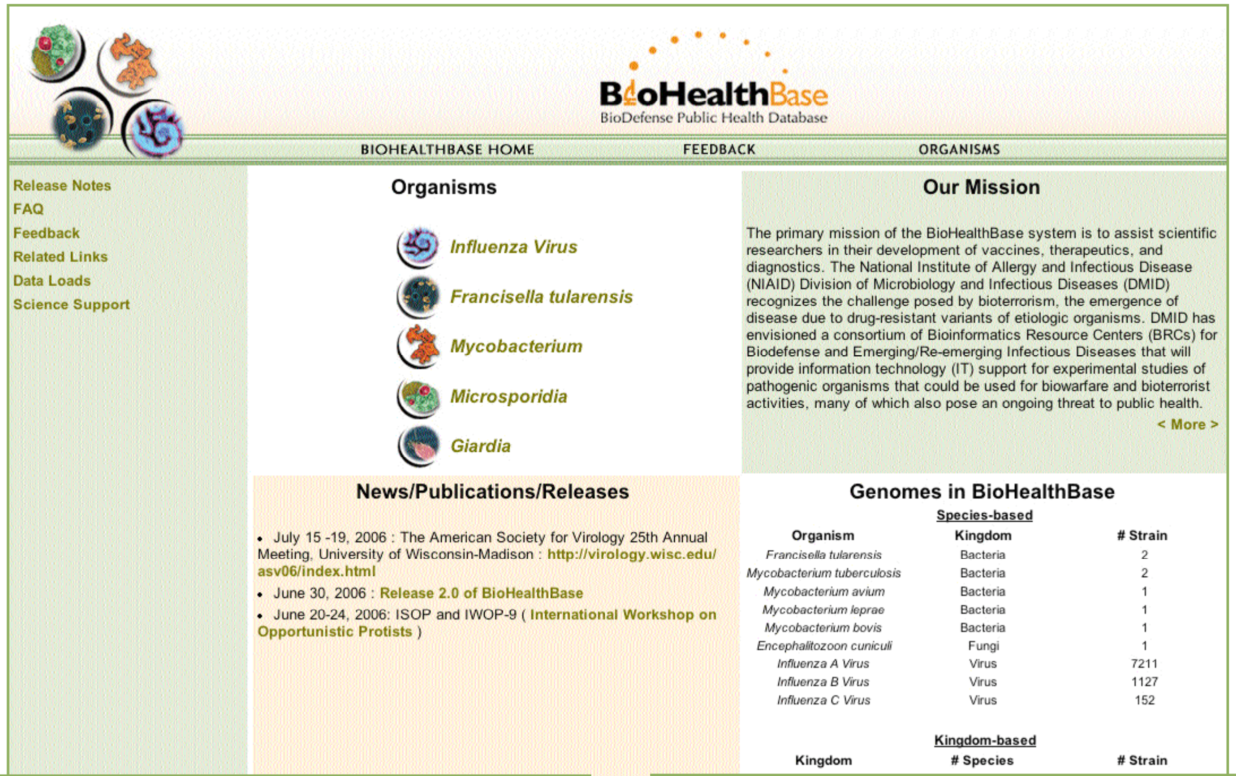
www.biohealthbase.org

INTRODUCTION

The Biodefense/Public Health DataBase (BioHealthBase) BRC focuses on six priority pathogens to help fill in gaps in genomic and other data critical to scientific researchers. The six pathogens are *Francisella tularensis* bacteria; *Influenza* (flu) virus; *Mycobacterium tuberculosis* (TB) bacteria; *Microsporidia* parasites; *Giardia lamblia* (giardiasis) parasite; *and Ricinus communis* (castor bean) plant (toxin).

BIOHEALTHBASE OFFERS

- Integrated data sets from NCBI, UniProt, Pfam, BioCyc, IEDB, and other sources
- Web-based data-mining and visualization tools
- Structural features and functional annotations for gene and protein sequences
- Metabolic and signaling pathway annotation
- Host-pathogen interaction models
- Protein localization and operon predictions (bacteria)
- Epitope predictions and validated epitopes from the IEDB (influenza)
- Influenza seqence alignments and polymorphism frequencies



BioHealthBase
BioDefense Public Health Database

BIOHEALTHBASE HOME | FEEDBACK | ORGANISMS

Release Notes
FAQ
Feedback
Related Links
Data Loads
Science Support

Organisms

Influenza Virus
Francisella tularensis
Mycobacterium
Microsporidia
Giardia

Our Mission

The primary mission of the BioHealthBase system is to assist scientific researchers in their development of vaccines, therapeutics, and diagnostics. The National Institute of Allergy and Infectious Disease (NIAID) Division of Microbiology and Infectious Diseases (DMID) recognizes the challenge posed by bioterrorism, the emergence of disease due to drug-resistant variants of etiologic organisms. DMID has envisioned a consortium of Bioinformatics Resource Centers (BRCs) for Biodefense and Emerging/Re-emerging Infectious Diseases that will provide information technology (IT) support for experimental studies of pathogenic organisms that could be used for biowarfare and bioterrorist activities, many of which also pose an ongoing threat to public health.

< More >

News/Publications/Releases

- July 15 -19, 2006 : The American Society for Virology 25th Annual Meeting, University of Wisconsin-Madison : http://virology.wisc.edu/asv06/index.html
- June 30, 2006 : Release 2.0 of BioHealthBase
- June 20-24, 2006: ISOP and IWOP-9 (International Workshop on Opportunistic Protists)

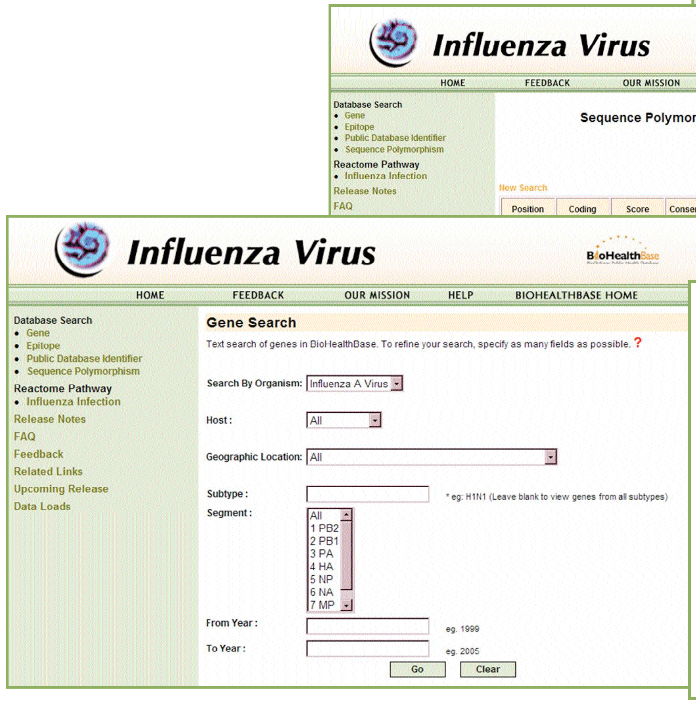
Genomes in BioHealthBase

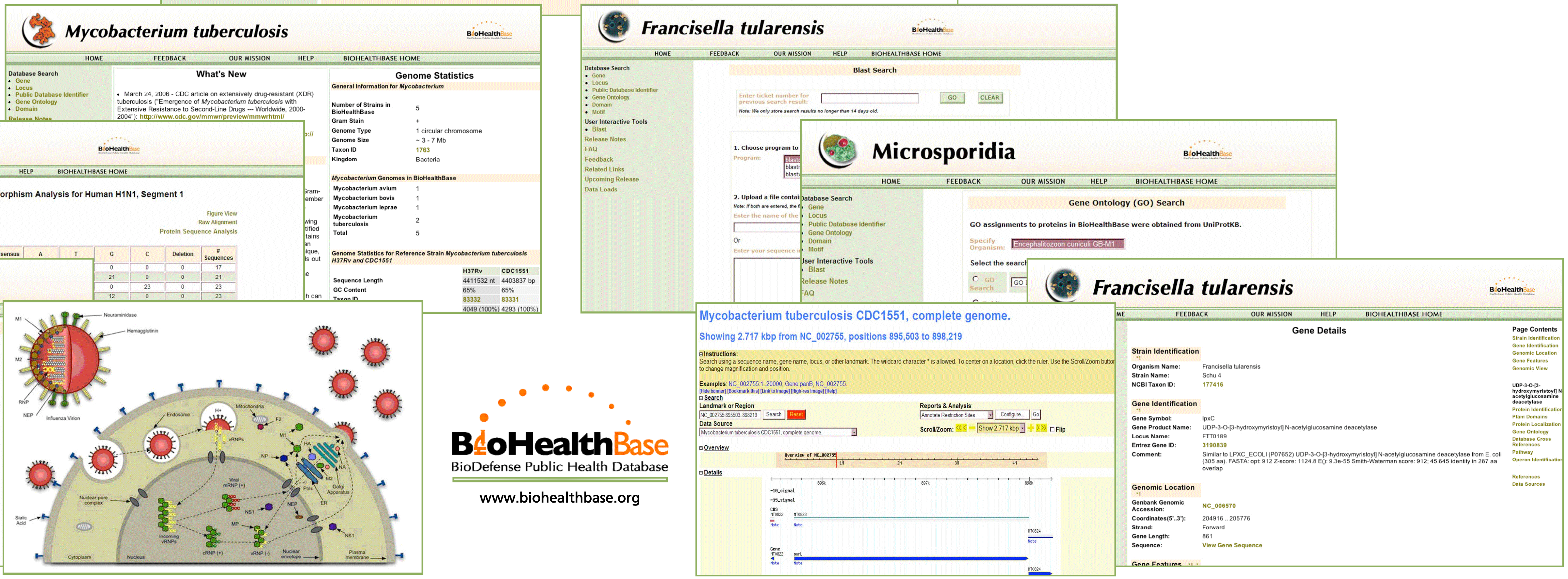
Species-based

Organism	Kingdom	# Strain
Francisella tularensis	Bacteria	2
Mycobacterium tuberculosis	Bacteria	2
Mycobacterium avium	Bacteria	1
Mycobacterium leprae	Bacteria	1
Mycobacterium bovis	Bacteria	1
Encephalitozoon cuniculi	Fungi	1
Influenza A Virus	Virus	7211
Influenza B Virus	Virus	1127
Influenza C Virus	Virus	152

Kingdom-based

Kingdom	# Species	# Strain





Mycobacterium tuberculosis

HOME | FEEDBACK | OUR MISSION | HELP | BIOHEALTHBASE HOME

What's New

Genome Statistics

Francisella tularensis

Blast Search

Influenza Virus

Sequence Polymorphism Analysis for Human H1N1, Segment 1

Microsporidia

Gene Ontology (GO) Search

GO assignments to proteins in BioHealthBase were obtained from UniProtKB.

Influenza Virus

Gene Search

Francisella tularensis

Gene Details

Mycobacterium tuberculosis CDC1551, complete genome.

Showing 2.717 kbp from NC_002755, positions 895,503 to 898,219

BioHealthBase
BioDefense Public Health Database
www.biohealthbase.org

FUTURE DIRECTIONS

Future releases of BioHealthBase are planned to include an automated genomic annotation pipeline, comparative genomics analysis, proteomics data tools, enhanced visualization tools for 3D protein structures, and molecular interactions and cellular networks with a user-friendly interface for data retrieval and analysis.

ACKNOWLEDGEMENTS

This project is funded in whole or in part with federal funds:
Contract No.: HHSN266200400041C
ADB Contract Number: N01-AI-40041

National Institute of Allergy and Infectious Diseases
National Institutes of Health
Department of Health and Human Services