

Linking the Scientific and Regulatory Environments for PHEMCE

> Robert W. Fisher 07 January 2016





U.S. Food and Drug Administration Medical Countermeasures Initiative



FDA and PHEMCE¹

- PHEMCE: protecting the U.S. from threats
 - Chemical, biological, radiological, nuclear (CBRN)
 - Emerging infectious diseases
- FDA: ensuring that medical countermeasures (MCMs) to counter these threats are safe, effective, and secure
 - Drugs, vaccines, diagnostic tests, personal protective equipment (PPE)

¹Public Health Emergency Medical Countermeasures Enterprise





Medical Countermeasures Initiative (MCMi)

Promote development and availability of safe, effective medical countermeasures





FDA MCMi

- Launched August 2010 in response to PHEMCE review of the U.S.'s readiness for public health emergencies
- FDA-wide initiative to coordinate medical countermeasure development, preparedness, and response
- FDA's MCMi:
 - Establishes clear regulatory pathways for MCMs
 - Supports regulatory decision-making through the development of tools, standards, and approaches to assess MCM safety, efficacy, and quality
 - Establishes effective policies and mechanisms to safeguard and facilitate rapid access to MCMs
 - Is managed by FDA's Office of Counterterrorism and Emerging Threats



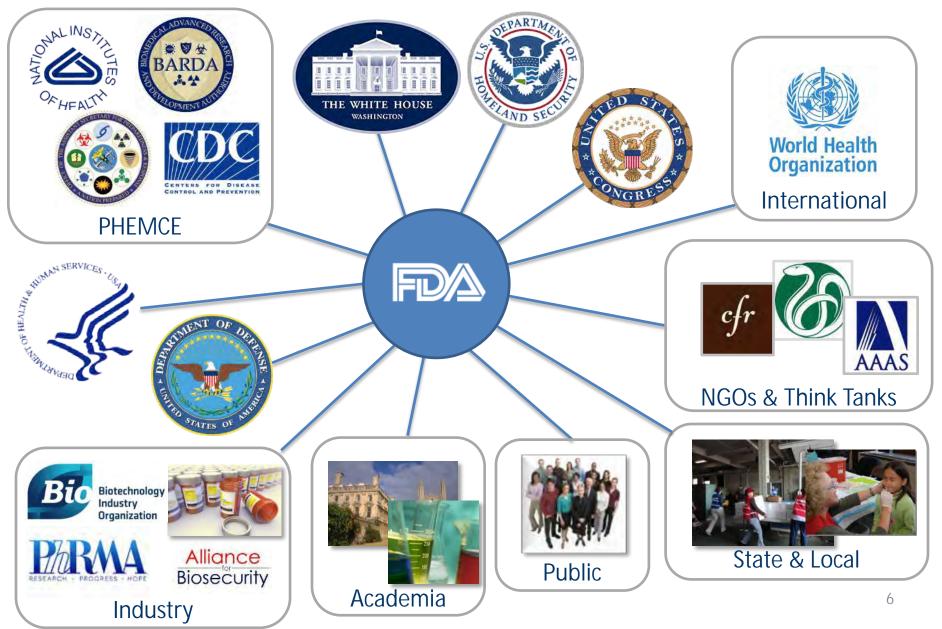


OCET Responsibilities

- Coordinates MCMi
- FDA point of entry on policy, planning for:
 - Global health security
 - Counterterrorism
 - Emerging threats
- Identify and resolve complex scientific and regulatory challenges for MCMs
- Lead emergency use activities
- Develop and implement preparedness plans & programs



External Stakeholders







Building on Success

- Established agreements between FDA and its international counterparts that enabled information-sharing and effective collaboration
- Extended the expiry dating of certain lots of oral doxycycline for the prevention of anthrax disease held by state and local public health preparedness stakeholders
- Funded the establishment a centralized repository of bacterial pathogens with well-characterized antimicrobial resistance profiles (in collaboration with CDC) representing more than 160 pathogens





Regulatory science case studies

- Anthrax vaccine stability: Drusilla Burns
- MCM dosing in special populations: Kevin Krudys
- Infectious disease diagnostics & FDA: Heike Sichtig



Thank you!

Robert W. Fisher Robert.Fisher@fda.hhs.gov 202-329-3957

http://www.fda.gov/medicalcountermeasures

AskMCMi@fda.hhs.gov











Resources

- MCMi Regulatory Science program
 - <u>http://www.fda.gov/EmergencyPreparedness/Counterterrorism/</u> <u>MedicalCountermeasures/MCMRegulatoryScience/default.htm</u>
- Extramural research funding and current projects
 - <u>http://www.fda.gov/EmergencyPreparedness/Counterterrorism/</u> <u>MedicalCountermeasures/MCMRegulatoryScience/ucm391617.htm</u>
- Animal Rule information and guidance
 - <u>http://www.fda.gov/EmergencyPreparedness/Counterterrorism/</u> <u>MedicalCountermeasures/MCMRegulatoryScience/ucm391604.htm</u>
- MCMi news and events (workshops, etc.)
 - <u>http://www.fda.gov/EmergencyPreparedness/Counterterrorism/</u> <u>MedicalCountermeasures/AboutMCMi/ucm262925.htm</u>

CBER MCM Research and a Case Study: Prolonging Anthrax Vaccine Shelf Life

Scope of CBER's MCM-Related Regulatory Science Program

Agents/Diseases

- Anthrax
- Botulism
- Tularemia
- Smallpox
- Viral hemorrhagic fevers
- Pandemic Influenza
- Emerging Infectious Disease

Chemical/Radiological/Nuclear Threats

Cell therapies

Scope of CBER's MCM-Related Regulatory Science Program

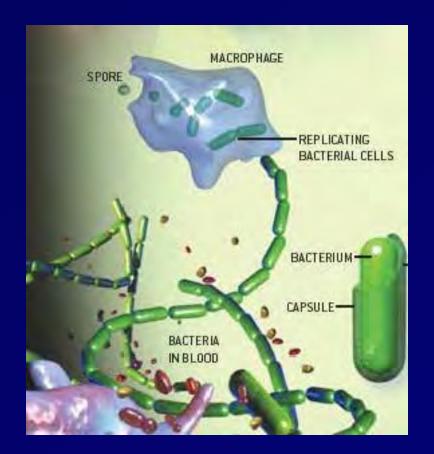
Issues addressed

- Manufacturing
- Product quality
- Assay development, especially potency and other lot release assays
- Animal models
- Biomarkers/correlates of protection
- Clinical trial design
- Post-marketing safety

Case study: Prolonging anthrax vaccine shelf life

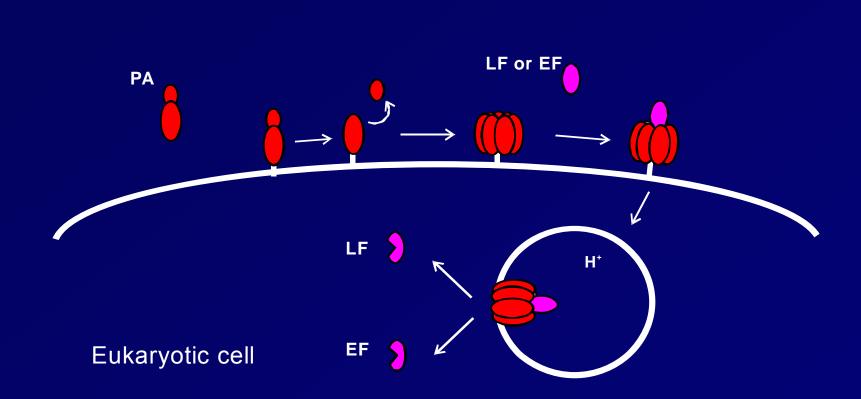
- Anthrax is one of the most feared bioweapons
- Efforts are underway to develop new generation anthrax vaccines
- Not expected to be used for routine immunization of the general population
- Stockpiled for use in an emergency, so stability is key

Anthrax

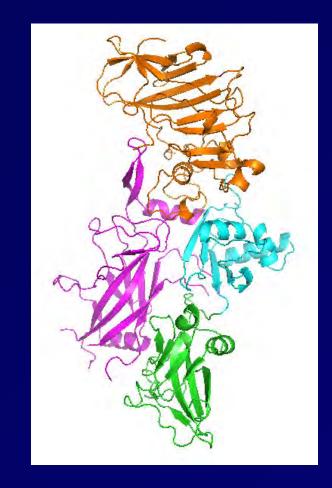


From Collier and Young, Sci. Am. March 2002

Mechanism of action of anthrax toxin

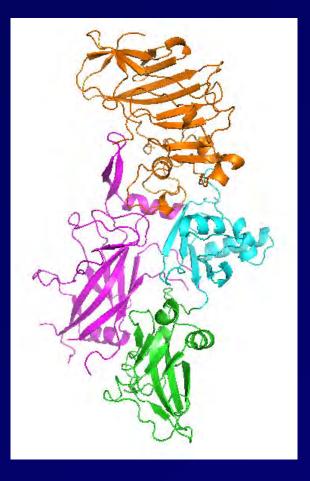


New generation anthrax vaccine design



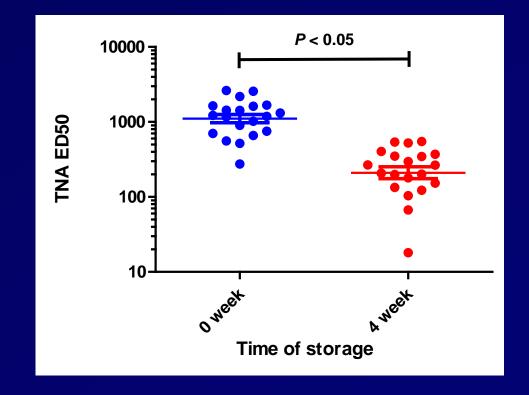
- Based on PA (usually a recombinant form, rPA)
- Elicits toxin neutralizing antibodies
- Toxin neutralizing antibodies correlate with protection
- Neutralizing antibodies will be used as a measure of protection to assess the efficacy of new rPA vaccines

rPA vaccines



- Development is simple in concept but difficult in execution
- Development has stalled because of lack of stability

Toxin neutralizing titers of mice immunized with adjuvanted rPA vaccine



Understanding the molecular basis for rPA vaccine instability

- What changes in rPA occur upon storage?
 - Structural changes
 - Compositional changes

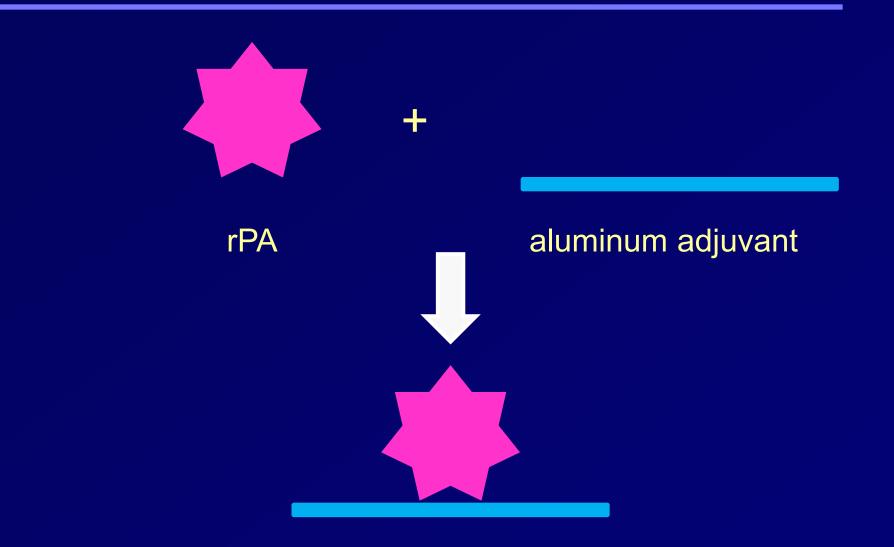
Do changes occur long-term that affect immunogenicity?

Understanding the molecular basis for rPA vaccine instability

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 - Compositional changes

Do changes occur long-term that affect immunogenicity?

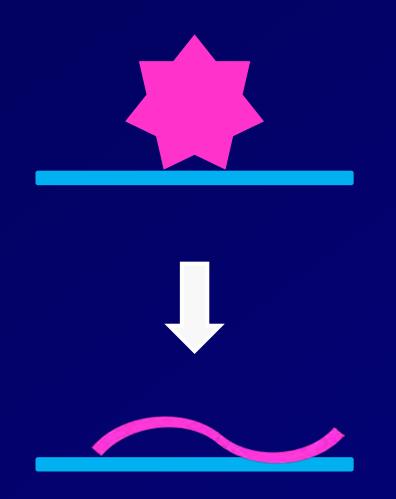
Formulation of rPA vaccine



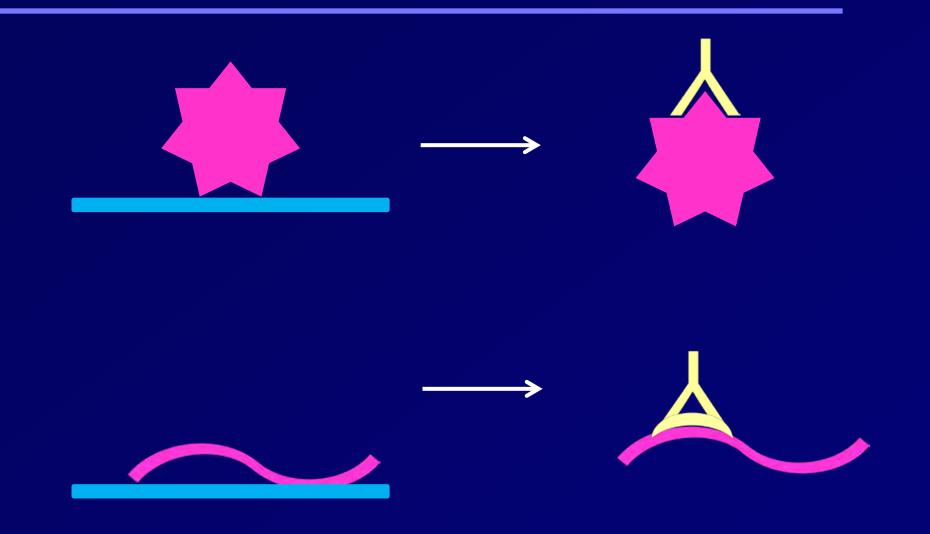
Structural changes during storage detected by:

- Melting point analysis
- Intrinsic protein fluorescence
- Immunogenicity of specific regions of the protein

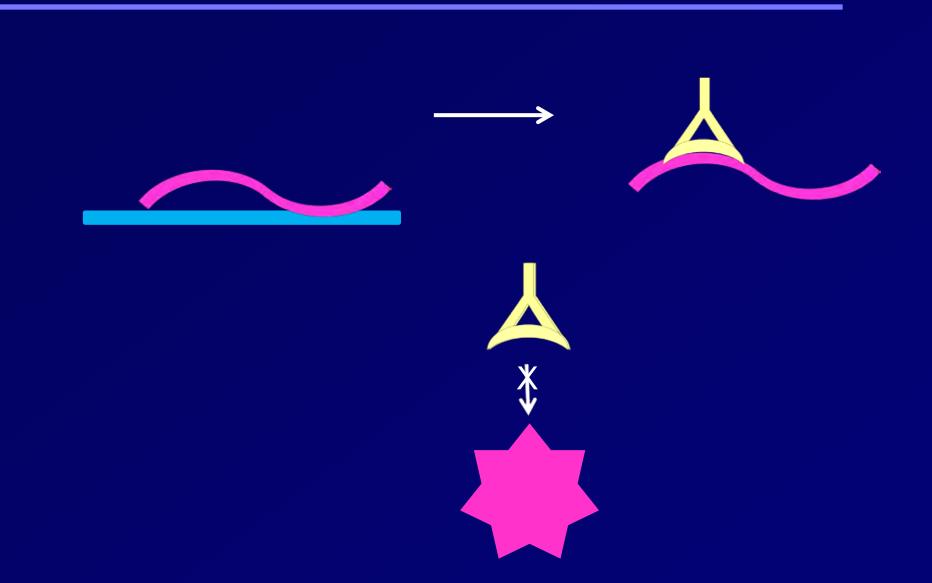
Over time rPA denatures on aluminum hydroxide adjuvant



Antibody population induced depends on antigen conformation



Antibody to buried epitopes may not recognize native antigen



Effect of adsorption onto aluminum adjuvant

 Dynamic structural changes in the protein occur upon storage on aluminum hydroxide adjuvant leading to loss of folded structure

 Conformational epitopes that may represent important neutralizing epitopes are lost Understanding the molecular basis for rPA vaccine instability

- What changes in rPA occur upon storage?
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 - Compositional changes

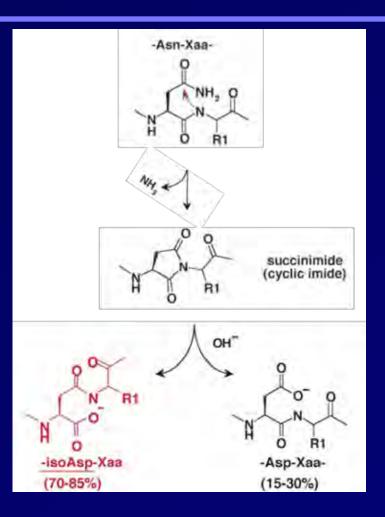
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Understanding the molecular basis for rPA vaccine instability

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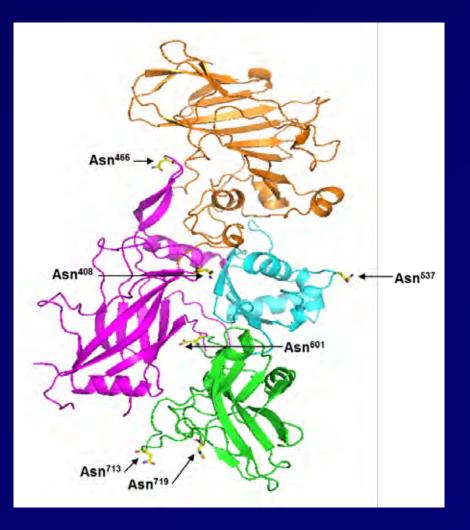
Do changes occur long-term that affect immunogenicity?

Deamidation of Asn residues in proteins



Adapted from Reissner, K.J. and Aswad, D.W., Cell. Mol. Life Sci. 60:1281-1295 (2003)

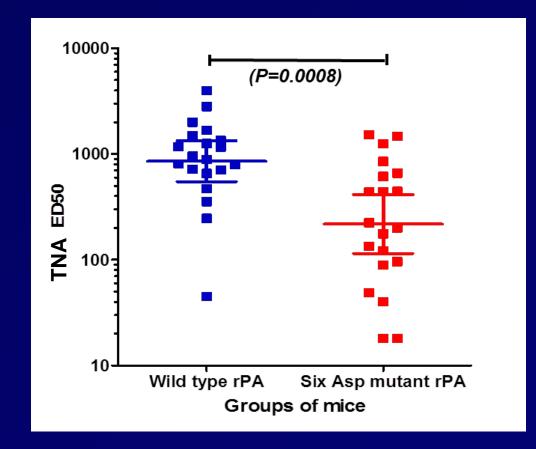
Deamidation-prone Asn residues of PA



Does spontaneous demidation of Asn residues play a role in the instability of rPA vaccines?

- Use site-specific mutagenesis to change six
 deamidation-prone Asn residues of rPA to Asp
- Purify the "genetically deamidated" mutant protein
- Examine its immunogenicity

Immunogenicity of rPA and six-Asp rPA



Possible causes of low immunogenicity

- Conformational differences between WT and six-Asp rPA mutant
- Loss of immunodominant B-cell epitopes
- Differences in eliciting T-cell help

Conclusions

- Multiple factors may play a role in rPA vaccine instability
 - Significant structural changes that affect immunogenicity can occur when proteins are bound to aluminum adjuvant
 - Non-enzymatic protein modifications occur slowly over time that affect immunogenicity
- Use of adjuvants that allow retention of structure and use of conditions that slow deamidation might prolong vaccine lifetime

Acknowledgements

Anita Verma Leslie Wagner Miriam Ngundi Scott Stibitz, CBER Beth McNichol, CBER

Juan Arciniega, CBER Rocio Dominguez-Castillo, CBER Juan Amador-Molina, CBER Bruce Meade, Meade Biologics



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Determining the Dose of MCM Products in Special Populations

Kevin M. Krudys Team Leader, Division of Pharmacometrics Office of Clinical Pharmacology Center for Drug Evaluation and Research January 7, 2016



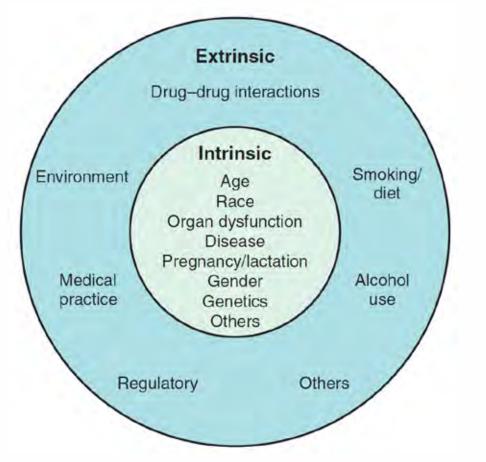
Selection of an Effective Dose in Humans

- Under the Animal Rule, a thorough understanding of the PK and PD data for the investigational drug or biologic is essential in selection of a dose regimen expected to be effective in humans.
- Clinical trials in healthy humans should evaluate safety and PK data over a range of doses
- Multiple approaches to human dose selection are possible, with varying levels of uncertainty



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But Is This The Right Dose for <u>YOU</u>?



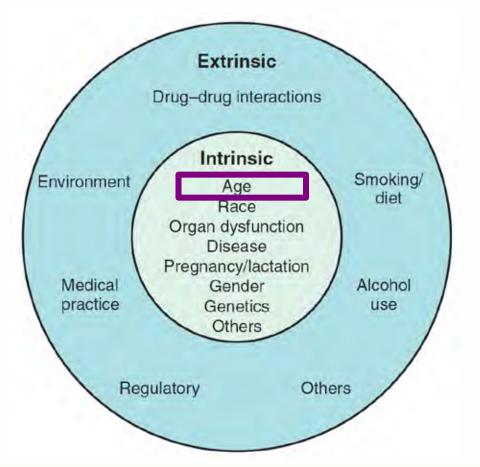
Huang et. al., Clinical Pharmacology and Therapeutics 2008

- Differences in response to medical products can be attributed to intrinsic and extrinsic factors
- For example, PK interactions with medical products concomitantly used in the clinical scenario
- Quantitative methods, such as PK modeling can be used to derive dosing of MCM products in special populations



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Case Study #1: Pediatric Dosing of Raxibacumab for Inhalation Anthrax



Slides adapted from Dr. Jerry Yu's presentation, November 2, 2012 Anti-Infective Drugs Advisory Committee Meeting



www.fda.gov

Starting Assumptions and Question

- 40 mg/kg dosing regimen may provide an acceptable benefit/risk profile for adult patients
- Adult and pediatric patients are similar in terms of:
 - Disease progression
 - Response to the treatment
 - Exposure-response (E-R) relationship

What pediatric dose of Raxibacumab is predicted to match adult exposure at 40 mg/kg?



Workflow to Determine the Pediatric Dose

<u>Learn</u> from adult population PK analysis

- **§** The relationship between PK parameters *vs* body weight
- § Inter-subject variability

Simulate pediatric PK profiles using different dosing regimens

§ Various combinations of dose and body weight band

Select a pediatric dosing regimen

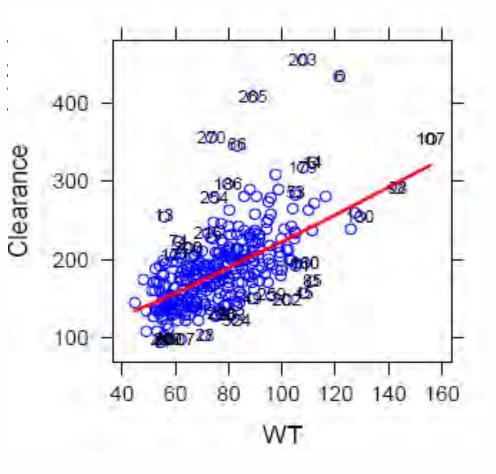
- S Match the exposure (e.g., AUC^{*}) observed in adults at 40 mg/Kg
- **§** Simple to implement

* AUC: Area under the concentration curve



Raxibacumab Clearance vs. Body Weight in Adults

Healthy adult PK @ 40 mg/Kg

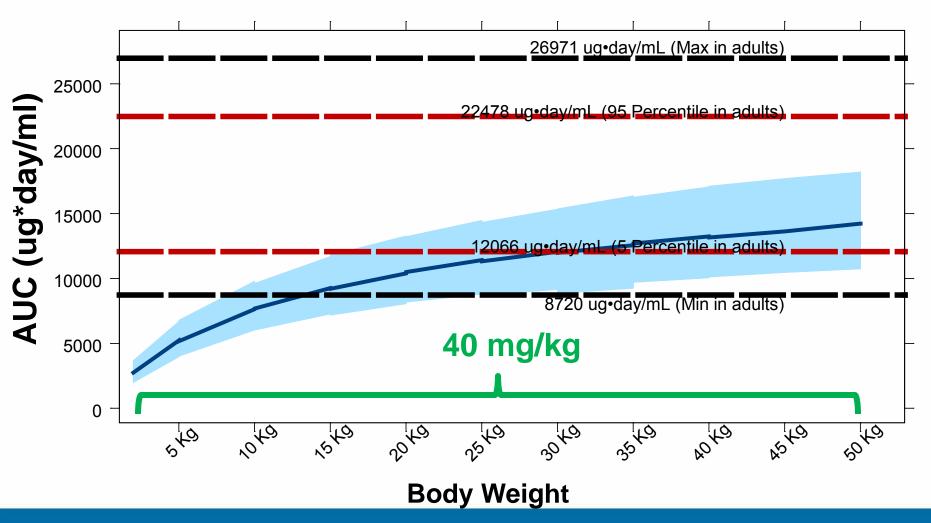


Assuming the observed relationship between PK and body weight in adults is applicable to pediatric population

- Mainly eliminated by non-specific proteolysis
- Very unlikely to be eliminated by kidney due to its large size



Simulated AUC_{inf} in Pediatric Population following Adult Dosing Regimen of 40 mg/kg





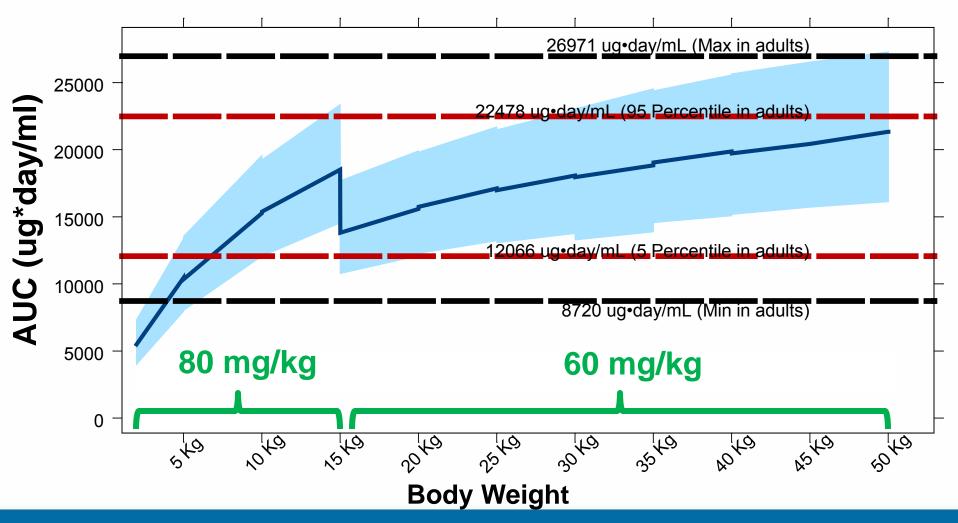
www.fda.gov

Proposed Pediatric Dosing

Body Weight	Pediatric Dose	
>50 kg	40 mg/kg	
$>$ 15 kg to \leq 50 kg	60 mg/kg	
\leq 15 kg	80 mg/kg	



Simulated AUC_{inf} in Pediatrics following the Proposed Dosing Regimen





www.fda.gov

Summary

- Assumptions
 - 40 mg/kg may be safe and efficacious in adult patients
 - Extrapolation from adults to children
 - Disease, exposure-response, PK variability
 - Relationship between PK parameters and body weight
- Criteria
 - Match the observed exposure in adults at 40 mg/kg
 - Simple to implement
- Pediatric dosing

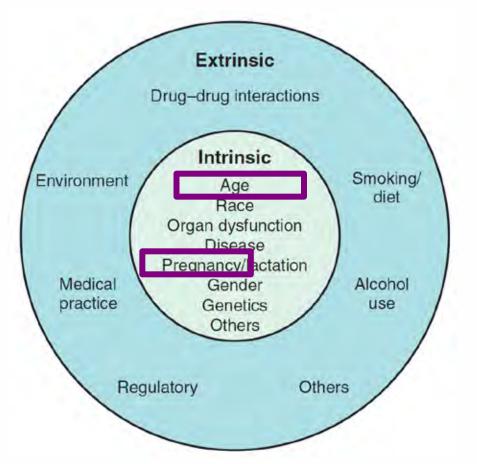
Body Weight	Pediatric Dose	
>50 kg	40 mg/kg	
$>$ 15 kg to \leq 50 kg	60 mg/kg	
\leq 15 kg	80 mg/kg	



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Case Study #2: Dosing of Amoxicillin for Post-Exposure Inhalation Anthrax





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Non-Labeled Dosing of Amoxicillin for Post-Exposure Inhalation Anthrax

- <u>Decision:</u> Dosing in the event of an intentional release of or accidental exposure to penicillin-susceptible strains of *B. anthracis*
- Amoxicillin may be considered when other antibacterial drugs are not as safe to use
- Dosing recommendations are based on the following:
 - 1. Maintain plasma concentrations above an MIC of 0.125 mcg/mL
 - 2. Dosing intervals of less than 8 hours are not practical
 - 3. Consistent dosing recommendations regardless of pregnancy status
 - 4. Same dosing frequency in adult and pediatric patients



Approach to Amoxicillin Dosing Recommendations

- Pharmacokinetic data in adults, children and pregnant women were obtained from various drug applications and literature*
- A population pharmacokinetic approach was used to characterize the concentration time-course of amoxicillin
 - Such an approach can be used to simulate dosing regimens that may not have been studied previously
- Simulations were performed at different dose levels (e.g, 500 mg and 1000 mg) and frequencies (e.g., 8, 6 and 4 hours)



Amoxicillin Dosing Recommendations: Pregnancy

Adult Recommended Dose: 1000 mg every 8 hours

		Time Above MIC (.0125 mcg/mL)		
Pregnancy Status	Trough (mcg/mL) Median [5 th to 9 th]	100% of dosing interval	75% to 100% of dosing interval	< 75% of dosing interval
2 nd Trimester	0.20 [0.06 – 0.53]	77%	23%	0%
3 rd Trimester	0.29 [0.10 – 0.71]	90%	10%	0%
Postpartum	0.29 [0.12 – 0.75]	93%	7%	0%
Non-Pregnant Adults	0.50 [0.16 – 1.36]	98%	2%	0%



Amoxicillin Dosing Recommendations: Pediatrics

Pediatric Recommended Dose: 25 mg/kg every 8 hours

		Time Above MIC (.0125 mcg/mL)			
Age Group (years)	Trough (mcg/mL) Median [5 th to 9 th]	100% of dosing interval	75% to 100% of dosing interval	< 75% of dosing interval	
12 to ≤ 16	0.52 [0.15 – 1.68]	98%	2%	0%	
6 to ≤ 12	0.53 [0.15 – 1.60]	97%	3%	0%	
2 to ≤ 6	0.44 [0.12 – 1.24]	95%	5%	0%	
1 month to ≤ 2 years	0.57 [0.16 – 1.88]	97%	3%	0%	



Conclusions

- A thorough understanding of the PK and PD data for the investigational drug or biologic is essential in selection of a dose regimen expected to be effective in humans.
- The impact of intrinsic and extrinsic factors on dosing is special populations should be considered
- Quantitative methods, such as PK modeling can be used to derive dosing of MCM products in special populations

U.S. Food and Drug Administration

REGULATORY PERSPECTIVE -- FOR --INFECTIOUS DISEASE DIAGNOSTICS -- AND --FDA-ARGOS DATABASE

BY HEIKE SICHTIG, PH.D.

Microbiology Devices | Center for Devices (CDRH) |US Food and Drug Administration Phone: +1 (301) 796-4574| Email: <u>Heike.Sichtig@fda.hhs.gov</u>

CDRH MCM Mission Space

Medical Countermeasure Approvals

• Diagnostics for CBRN threats, Pandemic Influenza and Antimicrobial Resistance

Enabling Access to Available Medical Countermeasures

- Emergency Use Authorizations (EUAs) for diagnostic tests for Ebola virus, Enterovirus D68 (EV-D68) and the Middle East Respiratory Syndrome Coronavirus (MERS-CoV)
- Pre-EUA submission process for prepositioning (DoD, BARDA, CDC and industry)

Responding to Emerging Public Health Threats

Issuing EUAs for diagnostic tests for MERS-CoV, EV-D68 and EVD

Facilitating Medical Countermeasure Development

Multiplex and Microbial Sequencing In Vitro Diagnostics Action Team

Regulatory Advice and Guidance

MCMi Regulatory Science Program

Multiplex and Microbial Sequencing In Vitro Diagnostics Action Team

This Action Team facilitates the development of multiplex and microbial DNA sequence-based *in vitro* diagnostic tests. Such diagnostics could be used to test for **multiple pathogens simultaneously** from a single clinical specimen, providing valuable information when responding to a **public health emergency**.



Disclaimer

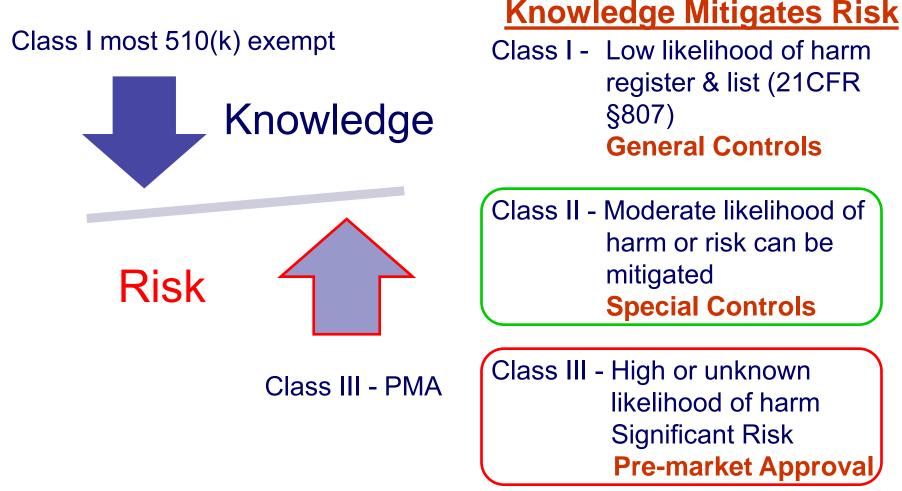
- Sequence-based diagnostic devices for the Microbiology Laboratory are raising new policy / regulatory issues; thoughts presented here are preliminary and do not represent finalized FDA policy
- Pre-submission for outstanding questions



Opinions are my own



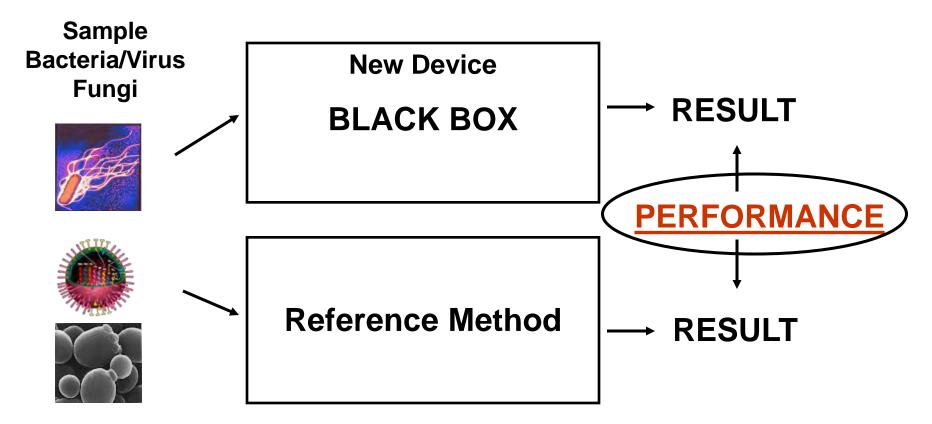
Risk Based Regulation of IVDs





Evaluation of Diagnostic Devices

FDA's general concept of diagnostic device evaluation



Problem: each possible organism needs confirmation by reference method (ref. positive or negative)

FDA Current Thinking Infectious Disease NGS Dx

Emphasis from scientific and clinical **community leaders** for **guidance** on **infectious disease**

Infectious Disease NGS Dx

Very different from human NGS:

- Absolute need for immediate and actionable result
- **Broad range** of **specimen types** (e.g., urine, blood, CSF, stool, sputum, and others)
- Large diversity of the infectious disease agents possible present within one specimen
- Dynamic nature of infectious disease agents

Public Workshop held on April 1, 2014 with FDA discussion paper

FDA Regulatory-Grade Microbial Database



FDA Regulatory Oversight

- 1. Clinical applications and public health needs: Identified specific applications where high throughput sequencing could be used for diagnosis of infectious diseases and markers of antimicrobial resistance from isolates .
- 2. **Device validation:** Developed and specified standards for the microbial genome sequencing process (from sample collection to result reporting), introduced best practices for sample/library preparation, variant identification, genome annotation, output de-convolution/results interpretation, and reporting.
- 3. Reference databases: Developed quality criteria for reference databases and database itself (FDA-ARGOS).
- 4. Streamlined clinical evaluations/trials for microbial identification: Established a new comparator paradigm for NGS as the reference method to augment or replace existing reference testing methods.

Next-Generation Sequencing

Adeyemi Adesokan², Timothy D. Minogue^{1*}

BRIEF REPORT

Actionable Diagnosis of Neuroleptospirosis by Next-Generation Sequencing

Michael R. Wilson, M.D., Samia N. Naccache, Ph.D., Erik Samayoa, B.S., C.L.S.,

Rapid Bacterial Whole-Genome Sequencing to Enhance Diagnostic and Public Health Microbiology

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Tracking a Hospital Outbreak of Carbapenem-Resistant Rapid Whole-Genome Sequencing for Detection and Characterizat Klebsiella pneumoniae with Whole-Genome Sequencing of Microorganisms Directly from Clinical Samples Evan S. Snitkin,¹ Adrian M. Zelazny,² Pamela J. Thomas,¹ Frida Stock,²

RESEARCH ARTICLE

NOSOCOMIAL INFECTION

NISC Comparative Sequencing Program,³ David K. Henderson, Tara N. Palmore,2" Julia A. Segre1"

Published in final edited form as:

sequencing

Committee

The Gram-negative bacteria Riebiello preumonior is a major cause of nosocornial infections, primarily among immunocompromised patients. The emergence of strains resistant to carbapenems has left few treatment options. making infection containment critical. In 2011, the U.S. National Institutes of Health Clinical Center experienced an outbreak of carbapenem-resistant K pneumoniae that affected 18 patients, 11 of whom died. Whole-genome sequencing was performed on K, pneumonior isolates to gain insight into why the outbreak progressed despite early Whole-genome sequencing (WGS) is becoming available as a routine tool for clinical microbiology. If applied directly on implementation of infection control procedures. Integrated genomic and epidemiological analysis traced the

outbreak to three independent transmissions from a single patient who was discharged 3 weeks before the next A distant and a

ACMG clinical laboratory standards for next-generation

Heidi L. Rehm, PhD1-2 Sherri J Bale, PhD3, Pinar Bayrak-Toydemir, PhD4, Jonathan S

Berg, MD⁵, Kerry K Brown, PhD⁵, Joshua L Deignan, PhD⁷, Michael J Friez, PhD⁸, Birgit H Funke, PhD12, Madhuri R Hegde, PhD9, Elaine Lyon, PhD5, and the Working Group of the American College of Medical Genetics and Genomics Laboratory Quality Assurance

Genet Med. 2013 September : 15(9): 733-747. doi:10.1038.gim.2013.92.



tai el al Genome Medicine 2018, 5:62

ittp://genomemedicine.com/content/5/7/62

Frank M. Aarestrup*

Interiments Descimants'

REVIEW

The human mycobiome in health and disease

Lija Cu., Allson Morris¹ and Elodie Gredin¹¹

Abstract

The mycobiome, referring primarily to the fungal biota in an environment, is an important component of the

bacteria [7]. This connotation changed in 2010, when the term 'mycobiome' (a combination of the words 'mycology' and 'microbiome') was first used to refer to the fungal microbiome [8]. Still, in a recent search of PubMed

REVIEW

REVIEW Validation of high throughput sequencing a Epidemiologic data and pathogen genome microbial forensics applications

sequences: a powerful synergy for public health

OPEN BACCESS Freety evaluable online

Development and Evaluation of a Panel of Filovirus

Sequence Capture Probes for Pathogen Detection by

Jeffrey W. Koehler¹, Adrienne T. Hall¹, P. Alexander Rolfe², Anna N. Honko³, Gustavo F. Palacios⁴,

1 Diagnostic Systems Division, United States Army Medical Research Institute of Infectious Diseases, Fort Detrick, Maryland, United States of America, 2 Pathogenica, Inc.

Boston, Massachusetts, United States of America, 3 Virology Division, United States Army, Medical Research Institute of Infectious Diseases. Fort Detrick, Marvland, United

Joseph N. Fair⁵, Jean-Jacques Muyembe⁶, Prime Mulembekani⁷, Randal J. Schoepp¹,

Henrik Hasman,* Dhany Saputra,* Thomas Sicheritz-Ponten,* Ole Lund,* Christina Aaby Svendsen,* Niels Frimodt-Meller,*

National Lood (millindo, Technical University of Dommark, Lyngby, Depreuds), Systems Bolszy, Technical University of Dommark, Lyngby, Depreuds, Systems Bolszy, Technical University, Systems Bolszy, Systems Bolszy, Technical University, Systems Bolszy, Systems Bolszy, Systems Bolszy, Systems Bolszy, Systems Bolszy, Systems Bolszy, System

samples, this could further reduce diagnostic times and thereby improve control and treatment. A major bottleneck is th

Bruch Budowle^{1,2*}, Nancy D Connell¹, Anna Bielecki-Oder⁴, Ritz R Colwell^{3,078}, Ondi R Corbett^{8 H}. Jacqueline Fletcher¹⁴, Mitti Fermion¹², Dana R Kadavy¹⁴, Alemka Markotic¹⁴, Stephen A. Marko¹¹ An all the second framework of the second second

Int. J. Mol. Sci. 2011, 12, 7861-7884; doi:10.3390/ijms12117861

OPEN ACCESS International Journal of

Molecular Sciences ISSN 1422-0067 www.mdpi.com/journal/ijms

Applications of Next-Generation Sequencing Technologies to Diagnostic Virology

Luisa Barzon 14, Enrico Lavezzo 1, Valentina Militello 1, Stefano Toppo 2 and Giorgio Palu 1

Youttin H Gent 11" and Mar Upstich 12

Molecular diagnosis in clinical parasitology: When and why?

Samson SY Wong¹, Kitty SC Fung², Sandy Chau², Rosana WS Poon¹, Sally CY Wong¹ and Kwok-Yung Yuen¹

"Department of Microbiology, The University of Hong Kong, Queen Mary Hosphal, Pok Pu Lam, Hong Kong, "Department of Pathology, United Christian Rospital, Kwun Tong of New Kowloon, Hosp Kong Corresponding author: Kwok-Yung Yuen, Email: keyuen@riku.tk.

Abstract

Microscopic detection and morphological identification of parasites from clinical specimens are the gold standards for the labora-

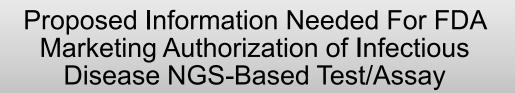
PLOS one

Direct Metagenomic Detection of Viral Pathogens in Nasal and Fecal Specimens Using an Unbiased High-Throughput Sequencing Approach

Shota Nakamura15, Cheng-Song Yang235, Naomi Sakon4, Mayo Ueda23, Takahiri Yamashita', Naohisa Goto', Kazuo Takahashi⁴, Teruo Yasunaga', Kazuyoshi Ikuti Yoshiko Okamoto², Michihira Tagami⁴, Ryoji Morita⁴, Norihiro Maeda⁴, Jun Kawa Hayashizaki[®], Yoshiyuki Nagai⁷, Toshihiro Horii^{2,5}, Tetsuya lida², Takaaki Nakaya

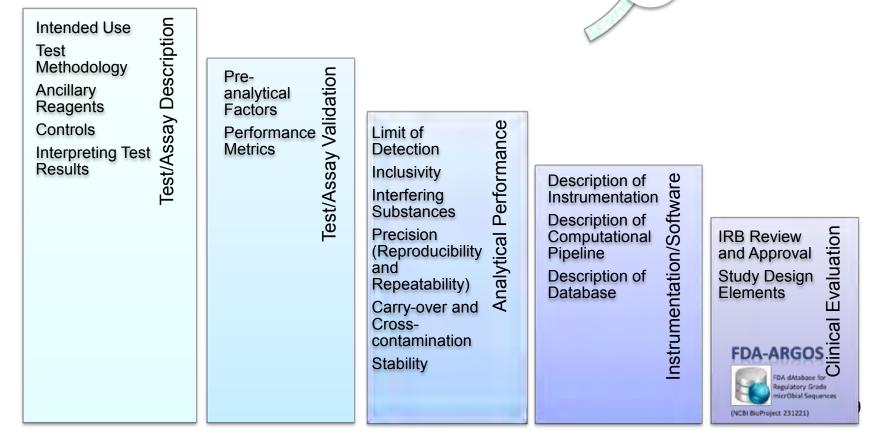
Department of Genore Informatics, Research Institute for Missibial Diseases (1998) Ocaka University, Suita, Ocaka, Japan, 2014 million and 1998) Diseases, Research institute for Microbial Diseases (RMD), Coate University, Suite, Osake, Agent, \$Department of Viology, Research In-Data Drawste, Suta Data. Agan, 4Dramment of Mectous Disease, Data Refectural Institute of Public Health, Hoadhin Molecular Protozookrys, Research Institute for Microbial Diseases RIMDI, Diaka University, Suria, Osaka, Japan, & Department of Vinde Disease, Mulatismotivana, Tokyo, Japan, 7 Center of Research Network for Infectious Disease, NREN, Chaoda, Tokyo, Japan, 80 Yokohama, Kanagawa, Japan





Targeted NGS

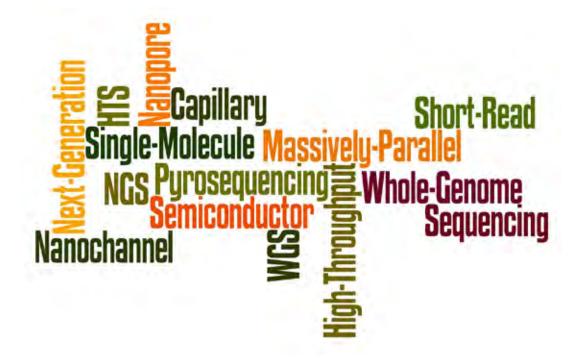
Agnostic (Metagenomics) NGS





Current Challenge:

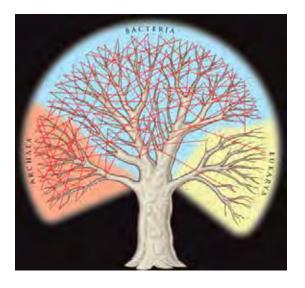
U.S. Marketing Authorization of NGS-Based Diagnostics in the Microbiology Laboratory





Current Need

Robust, Standardized, and High Quality Microbial Sequence Database in the Public Sector

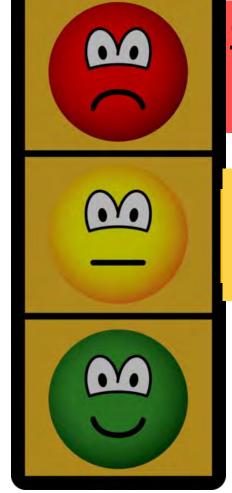


Cover illustration (Copyright © 2009, American Society for Microbiology. All Rights Reserved.)

- Representative Samples
- Metadata
- High quality raw sequences
- Assemblies
- Annotation
- Public Domain







Current Challenge:

U.S. Approval/ Clearance of NGS-Based Diagnostics in the Microbiology Laboratory

FDA Regulatory Science Efforts: Add 2000 high-quality MCM and Clinically-Relevant Pathogen Sequences



FDA ESTABLISHED AND IS EXPANDING A PUBLICALLY AVAILABLE, MICROBIAL GENOMIC REFERENCE SEQUENCE DATABASE (FDA-ARGOS)

THAT MEETS REGULATORY GRADE QUALITY CRITERIA

Critical to developers seeking to validate their candidate highthroughput sequencing-based in vitro diagnostic assays.

Collaborating with DoD, NCBI and U-MD Institute for Genome Sciences.

Geographically diverse isolate collection from agencies, public health labs, clinical labs and repositories.

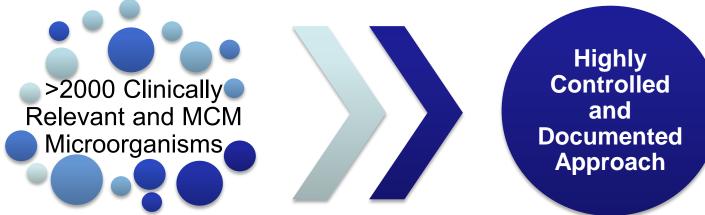
Around 2,000 isolates will be sequenced with the FDA-ARGOS project.

Antimicrobial resistance (AMR) isolates to include metadata, sequencing and registration of isolates.



FDA ARGOS DATABASE (@NCBI PRJNA231221)

- Identify "gaps" and target sequencing efforts (Funding by FDA/OCET, CRP)
 - All raw reads, assemblies, annotations, metadata sent to NCBI and accessible to the <u>PUBLIC</u>
 - Traceable results that could be reevaluated as necessary



Collaborations with Agencies, Clinical Labs and Repositories

- DoD (CRP, USAMRIID, MCS/JVAP)
- Public Health Agency Canada, Public Health Agency England
- Bernard Nocht Institute for Tropical Medicine, Germany
- National Center for Biotechnology Information (NCBI)
- National Institute of Allergy and Infectious Diseases (NIAID)
- FDA-CFSAN, FDA-CBER, FDA-CVM
- Lawrence Livermore National Lab , Los Alamos National Lab
- DHS National Biodefense Center (NBACC)
- Children's National Hospital, GWU, others
- Rockefeller University, ATCC Culture Collection

Sequencing Center (UMD IGS)

- Hybrid Approach (PacBio and Illumina)
- Deposit of Raw Reads at NCBI (SRA)
- Deposit of Assemblies at NCBI
- Deposit of Annotations at NCBI
- FDA Interface to Access Data



Project Approach

- Hybrid Sequencing Approach
 - Illumina PE HiSeq4000 (~300x cov of 5Mbp genome)/MiSeq
 - PacBio RS II (P6-C4, ~100x cov of 5Mbp genome)
 - 3-tiered viral approach (shotgun, amplicon, RACE)
 - Raw reads -> NCBI SRA
- Assembly/ Annotation
 - PacBio-only, Illumina-only, Hybrid
 - Assembly QA/QC --> "best" assembly selection
 - Automated genome annotation
 - Assembled & annotated genomes -> Genbank
 - NCBI BIOPROJECT ID: PRJNA231221
- FDA Web interface to aggregate data
- Base modification detection



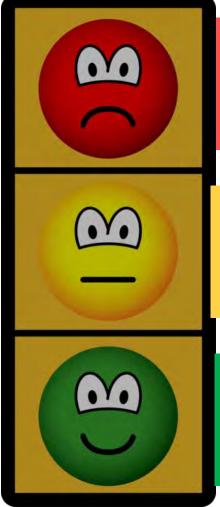


FDA dAtabase for Regulatory Grade micrObial Sequences

(NCBI BioProject 231221)







Current Challenge:

U.S. Approval/ Clearance of NGS-Based Diagnostics in the Microbiology Laboratory

FDA Regulatory Efforts: Add 2000 high-quality MCM and Clinically-Relevant Pathogen Sequences

Public Health Need: Robust, Standardized, and High Quality Microbial Comparator Sequence Database



Heike Sichtig, Ph.D. | | Microbiology Devices | Center for Devices (CDRH) | US Food and Drug Administration | Phone: +1 (301) 796-4574| Email: <u>Heike.Sichtig@fda.hhs.gov</u>



Ebola Virus, Makona

Patient No.	Age	Hospital	Date of Sampling	Outcome	Complete Genome
C5	16 F	Gueckedou	March 19	Survived	KJ660348
C7	47 F	Gueckedou	March 20	Died	KJ660347
C15	28 F	Kissidougou	March 17	Survived	KJ660346

Virus info obtained from N. Engl. J Med paper (Baize, et al 2014)

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Figure 1. Map of Guinea Showing Initial Locations of the Outbreak of Ebola Virus Disease.

The area of the outbreak is highlighted in red. The main road between the outbreak area and Conakry, the capital of Guinea, is also shown. The map was modified from a United Nations map.



IGS Ebola Sequencing Approach

- Amplicon
 - 96 amplicons, ~450bp each with 60-100bp overlaps
 - 2x amplicon coverage of the genome
 - Secondary PCR adds adaptors and barcodes
- Shotgun
 - cDNA: Nugen Ovation V2 from 5ng total RNA
 - Library: Nugen Ovation Ultralow Library V2
- 5' RACE
 - Clonetech SMARTer RACE 5'/3' kit
- All three sequenced on Illumina MiSeq



Assembly & Analysis

- Amplicon primers trimmed
- Assembled with SPAdes
- Consensus polished with shotgun data
- 5' RACE stitched on by Minimus
- Variants called by GATK



PHAC Ebola P1 Isolates

FDA ARGOS ID	Isolate Description	NCBI BioSample	NCBI SRA	GenBank
FDA_ARGOS_EBOV1	EBOV/Makona-C05 2014, P1A, 9dpi, RNA, 90 ul, PHAC harvest	SAMN03611814	SRX1023888, SRX1023889, SRX1023890	KT013254
FDA_ARGOS_EBOV2	EBOV/Makona-C05 2014, P1B, 13dpi, RNA, 90 ul, PHAC harvest	SAMN03611815	SRX1024946, SRX1024947, SRX1024948	KT013255
FDA_ARGOS_EBOV3	EBOV/Makona-C07 2014, P1A, 9dpi, RNA, 90 ul, PHAC harvest	SAMN03611816	SRX1025888, SRX1025889	KT013256
FDA_ARGOS_EBOV4	EBOV/Makona-C07 2014, P1B, 13dpi, RNA, 90 ul, PHAC harvest	SAMN03611817	SRX1025960, SRX1025961, SRX1025962	KT013257
FDA_ARGOS_EBOV5	EBOV/Makona-C15 2014, P1A, 14dpi, RNA, 90 ul, PHAC harvest	SAMN03611818	SRX1025963, SRX1025964, SRX1025965	KT013258
FDA_ARGOS_EBOV6	EBOV/Makona-C15 2014, P1B, 15dpi, RNA, 90 ul, PHAC harvest	SAMN03611819	SRX1025966, SRX1025967, SRX1025968	KT013259

P1A = 350 ul of original clinical isolate added to 5 mL DMEM medium then added to Vero E6 cells; P1B = 500 ul of P1A solution added to 4.5 mL DMEM medium



Regulatory Grade Sequencing

Ebola Makona (PHAC)

- Sequenced and Submitted to NCBI DB
 - C05
 - P1A: Amplicon, Shotgun, RACE
 - P1B: Amplicon, Shotgun, RACE
 - C07
 - P1A: Amplicon, RACE
 - P1B: Amplicon, Shotgun, RACE
 - C15
 - P1A: Amplicon, Shotgun, RACE
 - P1B: Amplicon, Shotgun, RACE
 - Received for Sequencing
 - Clinical C05, C07, C15
 - P2 of C05, C07 and C015
 - P1A of C07 for shotgun sequencing

Challenge Stocks (PHE)

- In the Pipeline for Sequencing
 - P2s
 - 2 Ebola stocks
 - 2 Sudan stocks
 - 1 Bundibugyo stock
 - 1 Tai Forrest stock
 - 2 Marburg stocks
 - P1s
 - 2 Ebola stocks
 - 2 Sudan stocks
 - 1 Bundibugyo
 - 1 Marburg Angola

Contact PI for Sequencing Requests



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DoD-MCS/JVAP

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Additional slides

MORE BACKGROUND



Summary on FDA Regulatory Efforts NGS for Infectious Disease Diagnostics

- FDA ARGOS Database (@NCBI PRJNA231221)
 - Public Regulatory-Grade Microbial Genomic Reference Database
 - Expansion as a community effort
 - Manuscript in preparation
- Microbial NGS Leapfrog Guidance (DRAFT)
 - FDA Microbial NGS Workshop (APRIL 1, 2014)
 - Targeted sequencing and Agnostic (metagenomic) sequencing
- Interagency Work Group on NGS Feasibility
 - Clinical Metagenomics Study, Results to be published
- NIST Collaboration on Microbial Reference Materials

FDA Pre-submission Process for Feedback

 Pre-submission template for infectious disease NGS-based diagnostics available (Contact <u>Heike.Sichtig@fda.hhs.gov</u>)



NIST Collaboration on Sequence-based Microbial Reference Material for NGS Validation

- Reference Material for Challenging Microbes Generated
 - List of candidate organisms (~1500 vials of gDNA):
 - Salmonella typhimurium LT2 (environmental isolate, CFSAN lab strain)
 - Staphylococcus aureus (clinical isolate from FDA ARGOS, Children's National)
 - Escherichia coli (clinical isolate from FDA ARGOS, Children's National)
 - Clostridium sporogenes (environmental isolate, CFSAN lab strain)
 - Sequencing and characterization ongoing

• FDA-NIST Workshop on Mixed Sample RMs (Oct 27/28)

- Input on defining reference materials for generation of reference data and methods
- Material will be critical to address the challenges associated with mixed pathogen detection in complex (clinical) samples using agnostic (metagenomic) and targeted sequencing