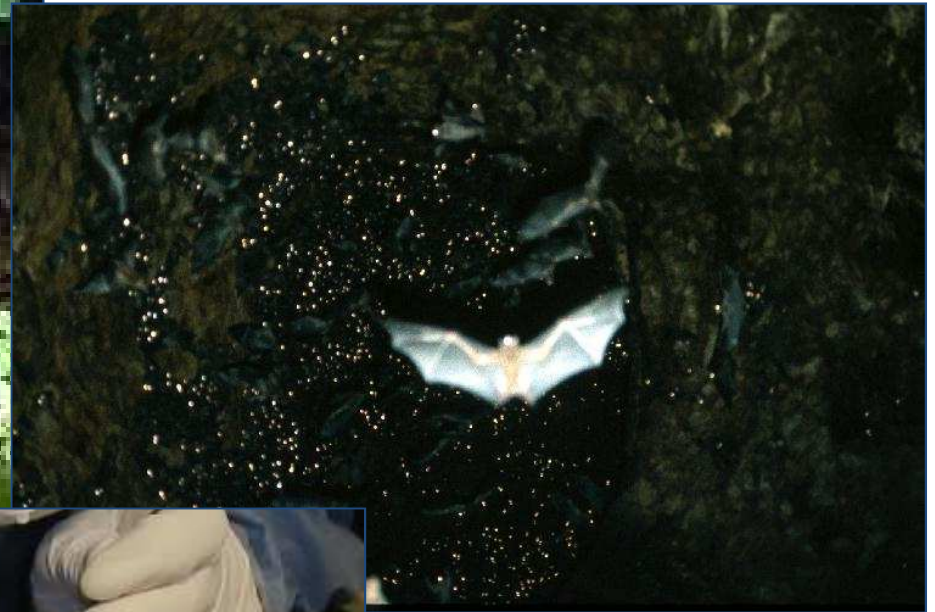


What will it take to be ready to detect and confront emerging infections?

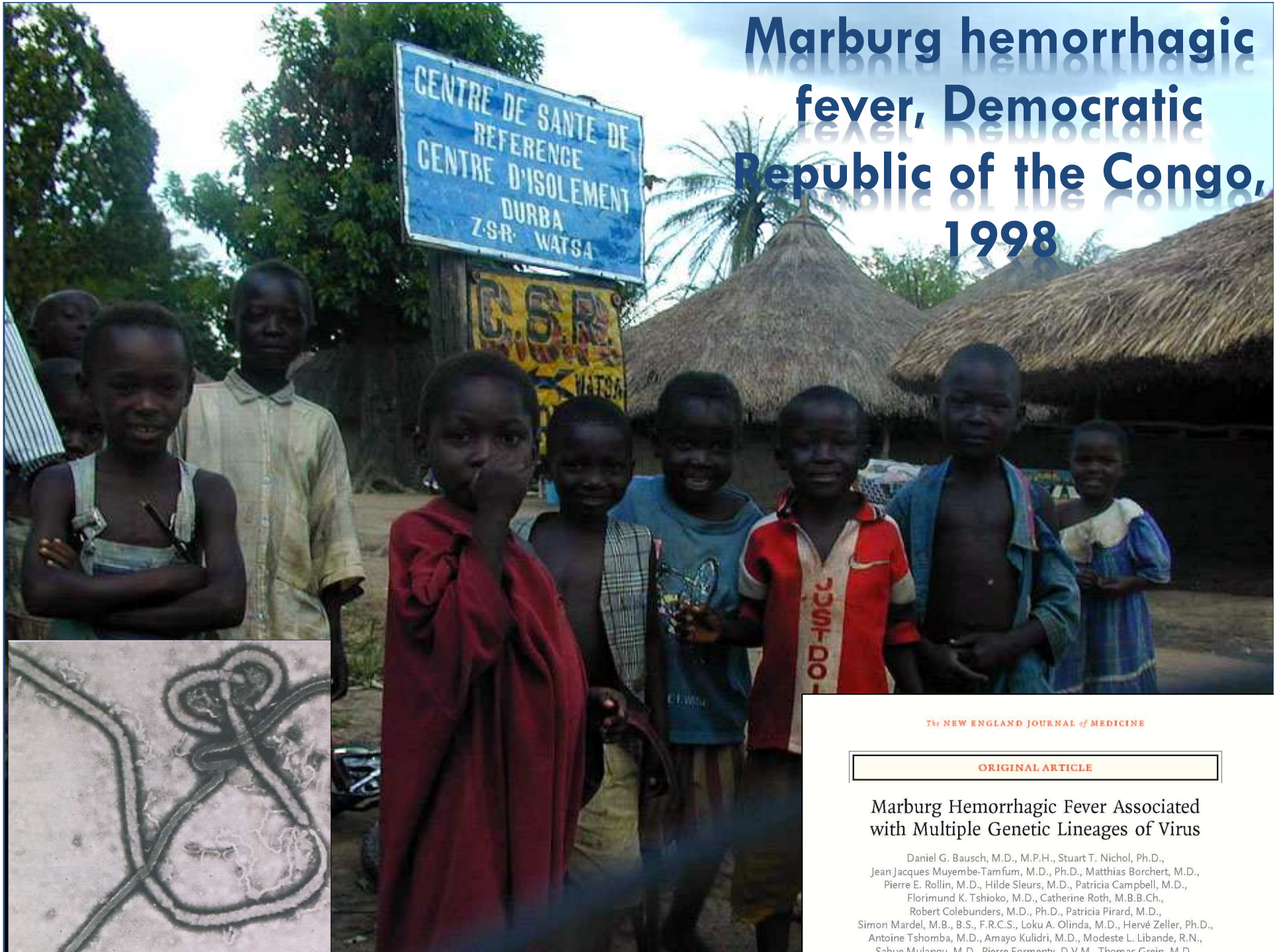
Daniel Bausch, MD, MPH&TM
Tulane School of Public Health and Tropical
Medicine, New Orleans, LA
World Health Organization, Geneva, Switzerland

Photo: Pierre Collin

EIDs \equiv Zoonoses



Marburg hemorrhagic fever, Democratic Republic of the Congo, 1998

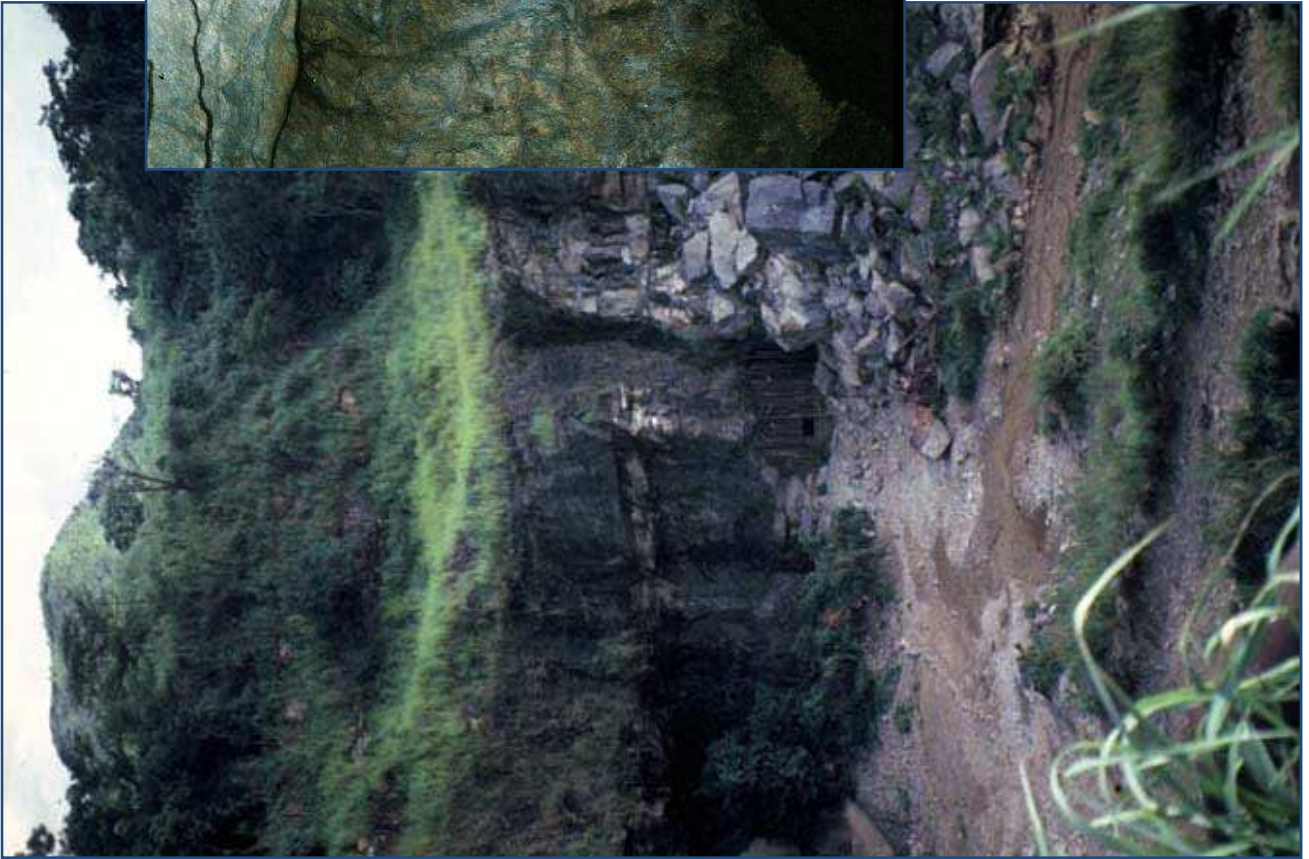


THE NEW ENGLAND JOURNAL OF MEDICINE

ORIGINAL ARTICLE

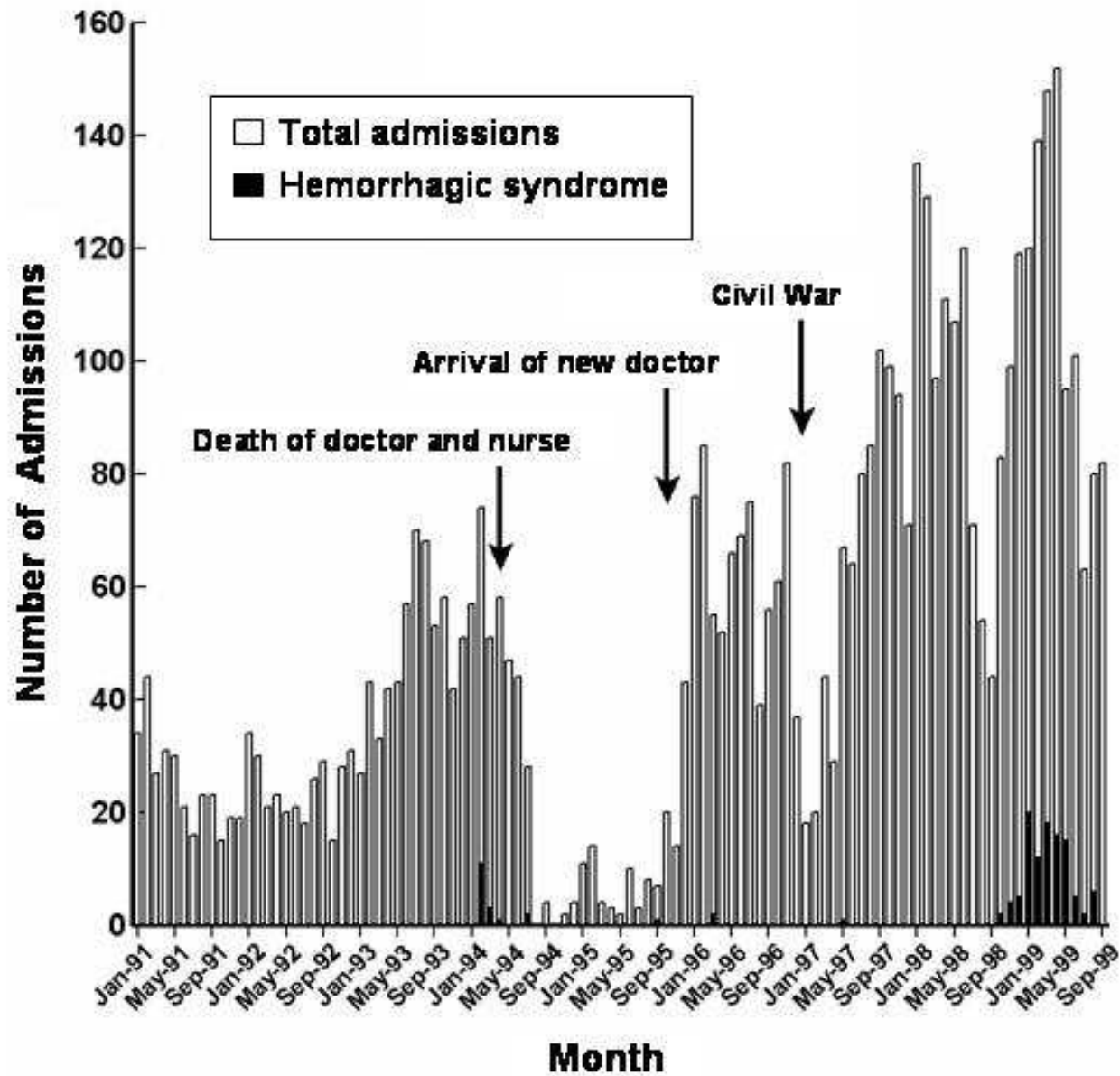
Marburg Hemorrhagic Fever Associated with Multiple Genetic Lineages of Virus

Daniel G. Bausch, M.D., M.P.H., Stuart T. Nichol, Ph.D.,
Jean Jacques Muyembe-Tamfum, M.D., Ph.D., Matthias Borchert, M.D.,
Pierre E. Rollin, M.D., Hilde Sleurs, M.D., Patricia Campbell, M.D.,
Florimund K. Tshioko, M.D., Catherine Roth, M.B.B.Ch.,
Robert Colebunders, M.D., Ph.D., Patricia Pirard, M.D.,
Simon Mardel, M.B., B.S., F.R.C.S., Loku A. Olinda, M.D., Hervé Zeller, Ph.D.,
Antoine Tshomba, M.D., Amayo Kulidri, M.D., Modeste L. Libande, R.N.,
Sabue Mulangu, M.D., Pierre Formenty, D.V.M., Thomas Grein, M.D.,

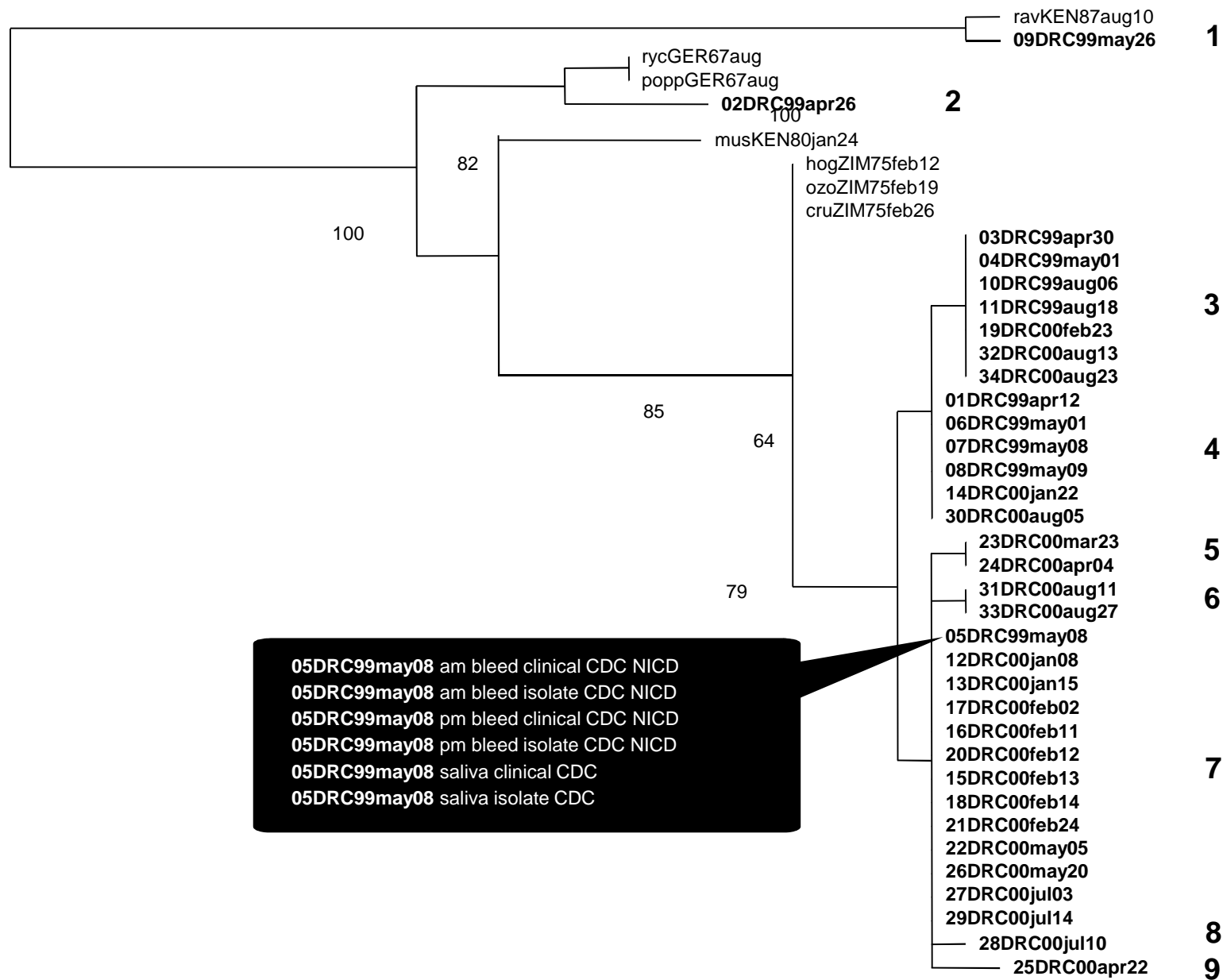








**Total admissions and febrile hemorrhagic illnesses, Durba/Watsa, DRC
Watsa General Reference and OKIMO Hospitals**



— 0.005 substitutions/site

Studies of Reservoir Hosts for Marburg Virus

Robert Swanepoel,* Sheilagh B. Smit,* Pierre E. Rollin,† Pierre Formenty,‡ Patricia A. Leman,* Alan Kemp,* Felicity J. Burt,§ Antoinette A. Grobbelaar,* Janice Croft,* Daniel G. Bausch,|| Hervé Zeller,# Herwig Leirs,** †† L.E.O. Braack,‡‡ Modeste L. Libande,§§ Sherif Zaki,† Stuart T. Nichol,† Thomas G. Ksiazek,† and Janusz T. Paweska,* on behalf of the International Scientific and Technical Committee for Marburg Hemorrhagic Fever Control in the Democratic Republic of the Congo



Photos: B. Swanepoel and P. Rollin

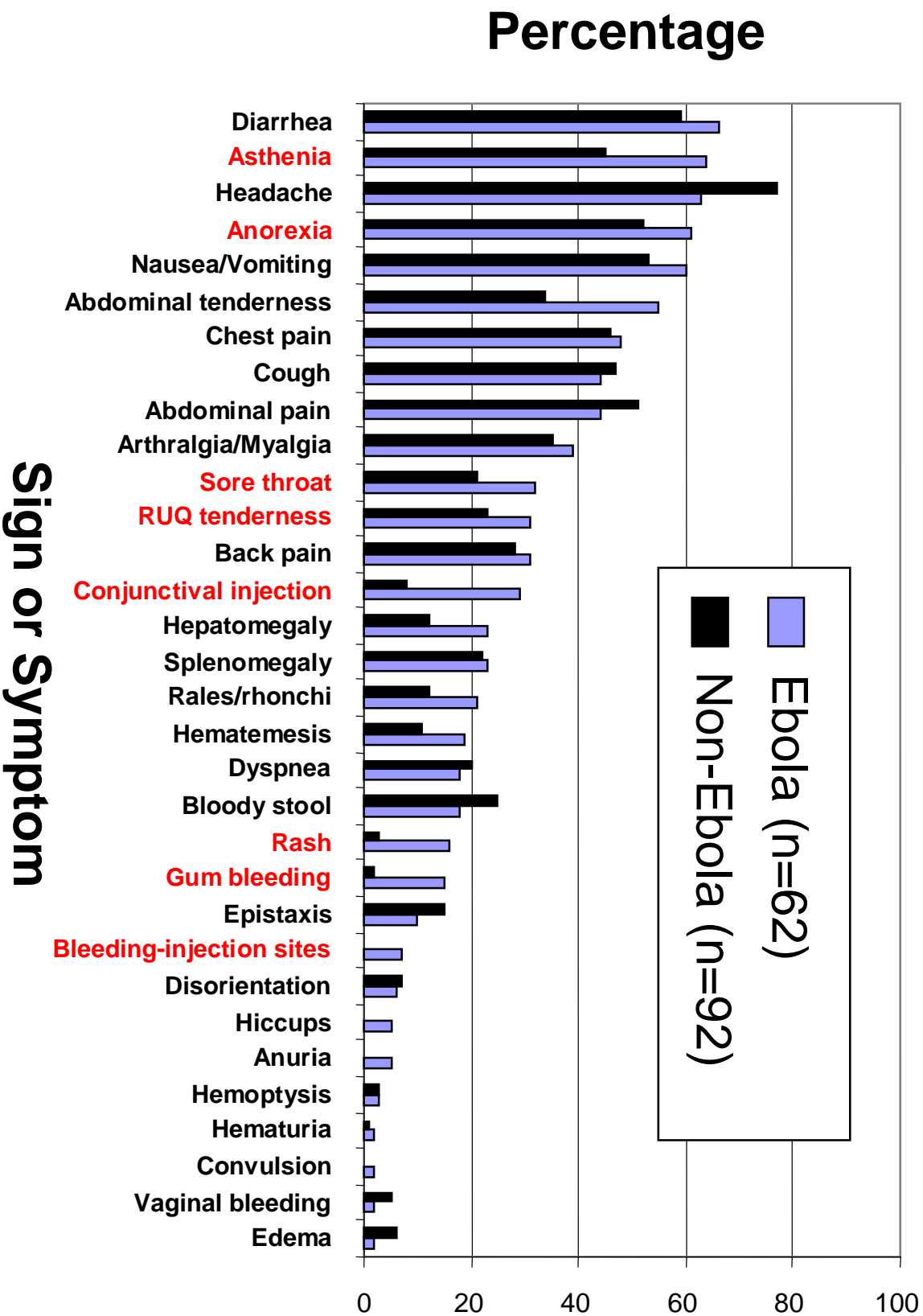
Nice Investigation: What's the Problem?

Responding to Ebola

| | DRC, 1995 | Uganda, 2000-2001 | Gabon/Congo, 2001-2002 |
|---|----------------------|------------------------------|-----------------------------------|
| Time from 1 st case to declaration of outbreak | 123 days | 46 days | 47 days |
| Duration of outbreak | 187 days | 142 days | 193 days |

Source: Bausch and Rollin, *Emerging Infections* 6, 2004

Ebola Hemorrhagic Fever: Clinical Presentation at Admission



Laboratory Diagnosis



International Center for Research on Tropical Infections, N'Zérékoré, Guinea



NAMRU-6 VIROLOGY AND EMERGING INFECTIONS DEPARTMENT

- ◉ Daniel G. Bausch, MD, MPH&TM – Director
 - Alberto Laguna, MD, PhD – Deputy Director

Vector-borne
and Zoonotic
Diseases

Pathogen
Discovery

Outbreak
Investigation
&
Response

Respiratory
and Enteric
Diseases

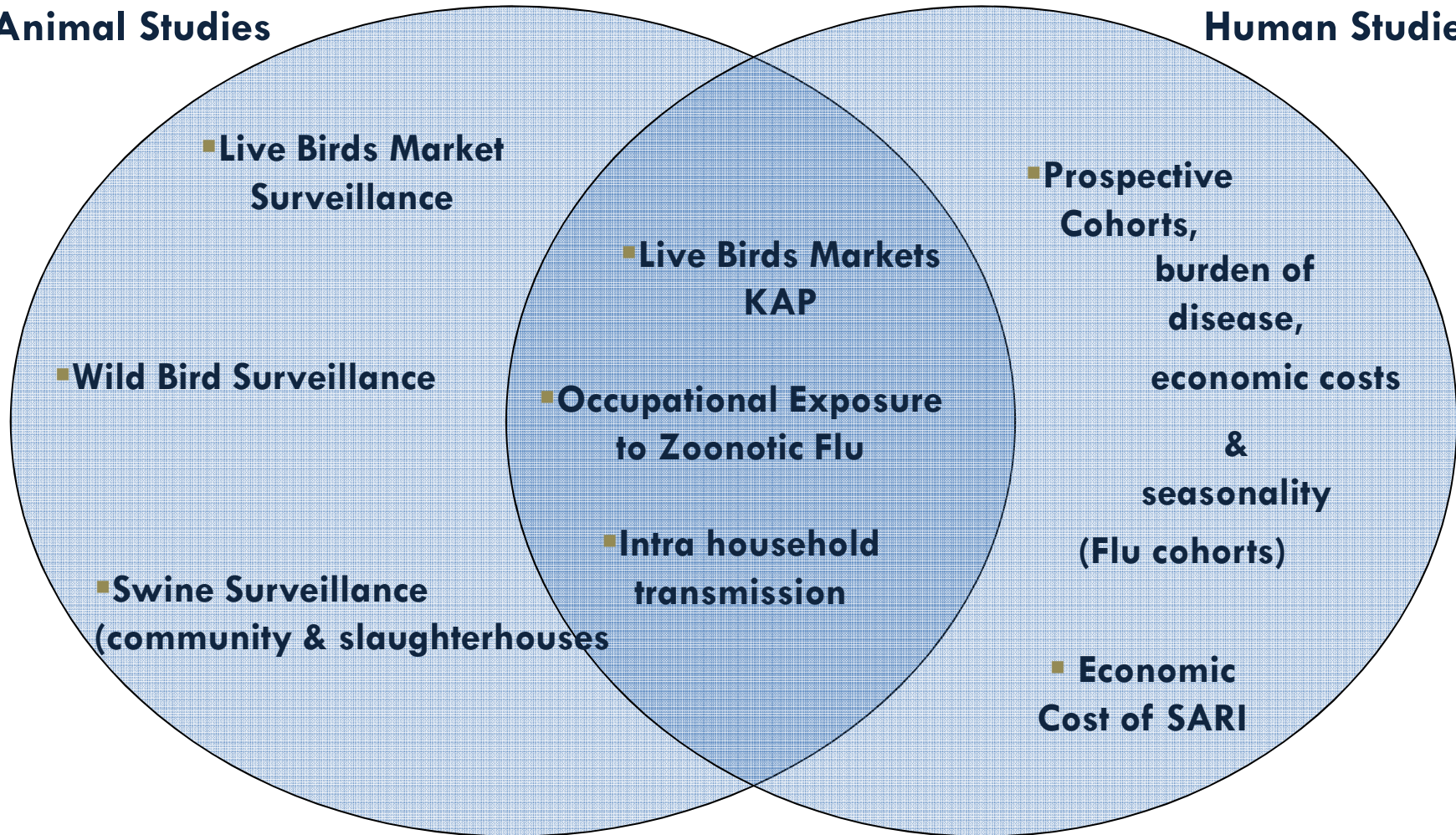
Laboratory
Diagnostics

- ◉ ~70 staff @ NAMRU-6 (MD, PhD, DVM, MS, others)
- ◉ ~80 field workers



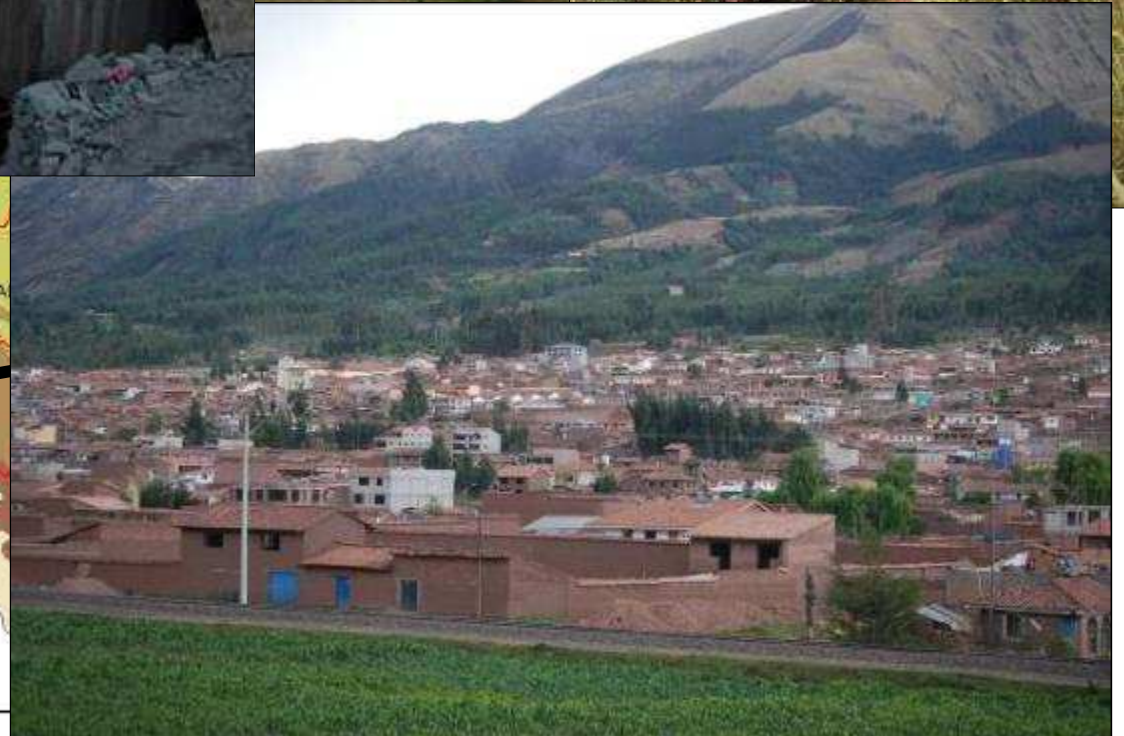
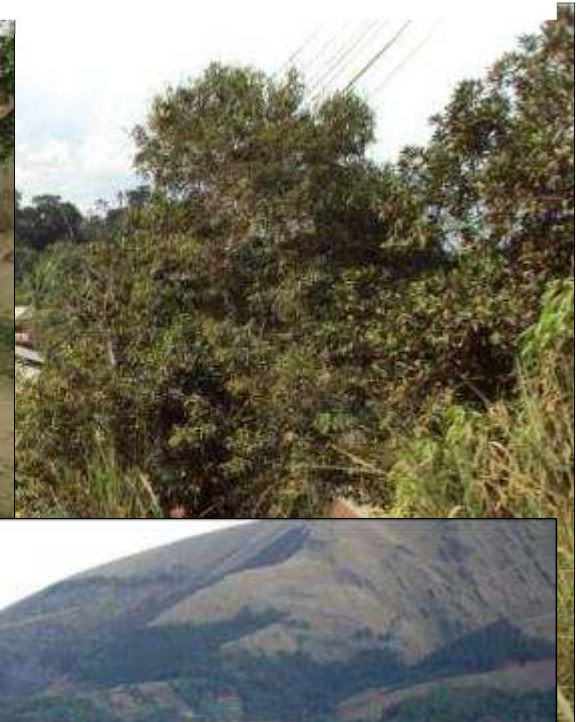
Respiratory Disease Surveillance Program Overview

Animal Studies



Human-Animal Interface Studies

Peru Influenza Active ILI Surveillance Cohorts



Cumulative summary to EW45 (2011)

- EW 45-2011 (November, 12th):

Table 1. Cumulative Number of ILI episodes per site and rRT-PCR results
June 2009 – EW 45/2011

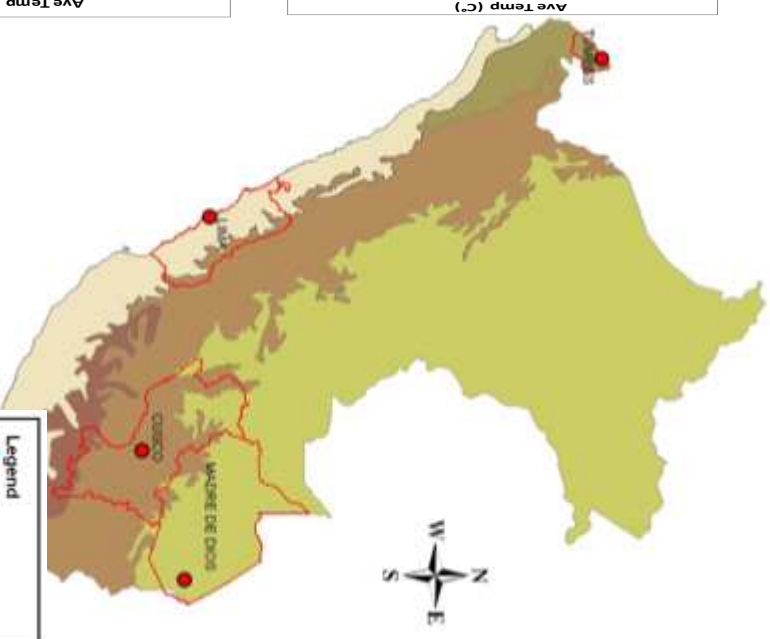
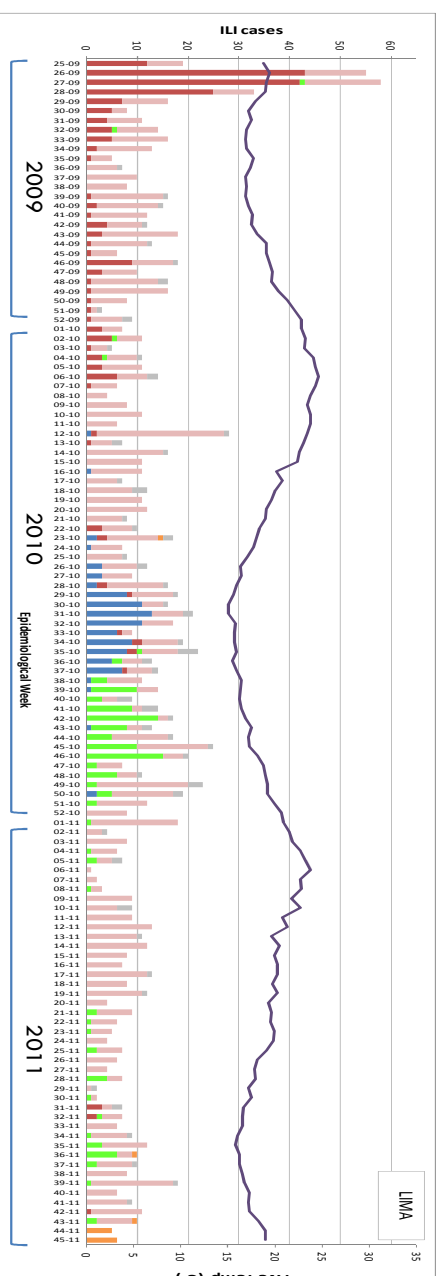
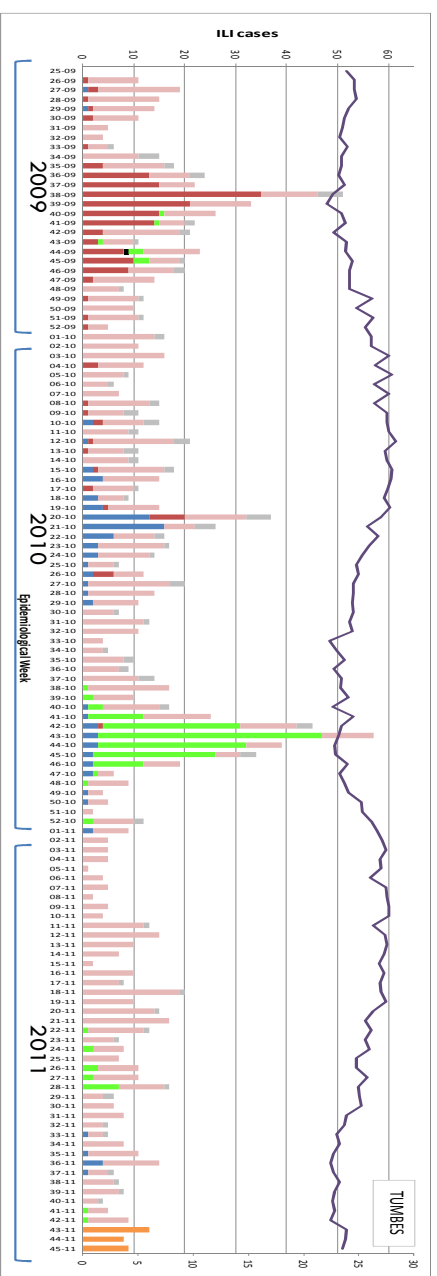
| rRT-PCR/sites | Lima | Cuzco | Tumbes | Pto Mdo | Total |
|-------------------------|-------------|-------------|-------------|-------------|-------------|
| Non Flu | 888 | 684 | 1020 | 693 | 3285 |
| pH1N1 | 225 | 83 | 189 | 95 | 592 |
| A/H1 | 0 | 0 | 1 | 3 | 4 |
| A/H3 | 129 | 139 | 181 | 171 | 620 |
| Flu B | 96 | 74 | 97 | 54 | 321 |
| Results pending | 14 | 33 | 30 | 32 | 109 |
| w/o sample | 77 | 78 | 104 | 27 | 286 |
| Total/ EW45.2011 | 1429 | 1091 | 1622 | 1075 | 5217 |

Flu Epidemic curves - Peruvian coast

TUMBES and LIMA

Weeks 25(2009)- 45(2011)

Non Flu PH1N1 A/H1 A/H3 Flu B Pend w/o samp



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Issues in the Animal-Human Interface

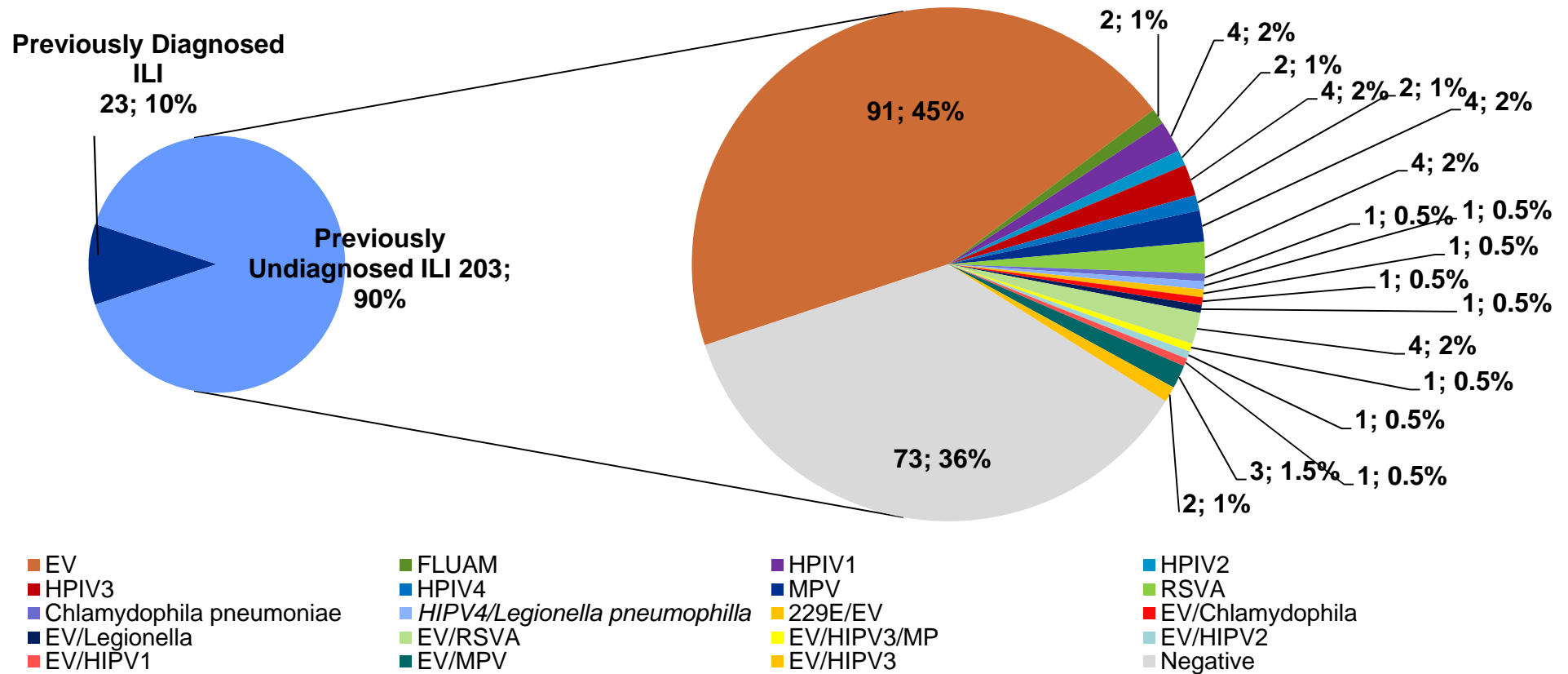
- What flu strains are circulating in Peru?
- What species are reservoirs: wild birds, poultry, pigs, guinea pigs...?
- Is there any spill over?
- What are the risks?



Other etiologies by cell culture

| ILI samples (N=1254) | | | |
|-----------------------|-----|---------------------|-----|
| ADENOVIRUS | 32 | FLU A-PARAFLU 2 | 1 |
| COXSACKIE B | 7 | FLU A-PARAFLU 3 | 1 |
| ECHOVIRUS | 1 | FLU B | 2 |
| ENTEROVIRUS | 13 | FLU B - HSV | 1 |
| ENTEROVIRUS-PARAFLU 3 | 1 | FLU B-ADENOVIRUS | 1 |
| FLU A | 394 | HMPV | 11 |
| FLU A - COXSACKIE B | 1 | HSV | 21 |
| FLU A - PARAFLU 3 | 1 | HSV-ADENOVIRUS | 2 |
| FLU A-ADENOVIRUS | 8 | HSV-ENTEROVIRUS | 2 |
| FLU A-COXSACKIE B | 2 | PARA FLU 1 | 2 |
| FLU A-ENTEROVIRUS | 3 | PARA FLU 2 | 20 |
| FLU A-HMPV | 1 | PARA FLU 3 | 16 |
| FLU A-HSV | 6 | MUESTRA CONTAMINADA | 8 |
| | | NO AISLAMIENTO | 696 |

MassTag PCR on Respiratory Samples



Genomic analysis of two novel human enterovirus C genotypes found in respiratory samples from Peru

Rafal Tokarz,^{1†} David L. Hirschberg,^{1†} Stephen Sameroff,¹ Saddef Haq,¹ Giannina Luna,² Andrew J. Bennett,^{2,3} Maria Silva,² Mariana Leguia,² Matthew Kasper,² Daniel G. Bausch² and W. Ian Lipkin¹

Correspondence
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¹Center for Infection and Immunity, Mailman School of Public Health, Columbia University, New York, NY, USA

²US Naval Medical Research Unit 6, Lima, Peru

³Tulane School of Public Health and Tropical Medicine, New Orleans, LA, USA

We report the discovery of two enteroviruses detected in nasopharyngeal samples obtained from subjects with respiratory disease in Peru. Phylogenetic analysis indicated that both viruses belong to a clade within the species *Human enterovirus C*, which includes the recently characterized human enteroviruses 109 and 104. Members of this clade have undergone significant genomic rearrangement, as indicated by deletions in the hypervariable region of the 5' UTR and the VP1 protein, as well as recombination within the non-structural genes. Our findings and review of published sequences suggests that several novel human enterovirus C serotypes are currently circulating worldwide.

INTRODUCTION

Enteroviruses (EVs) are non-enveloped, positive-sense, ssRNA viruses in the family *Picornaviridae*. They are transmitted via multiple routes (faecal–oral, oral–oral, respiratory droplets and fomites) and are amongst the most commonly diagnosed viral infections in humans. Although

picornaviridae.com). Two of these, EV-C104 and EV-C109, were detected in recent large-scale cohort studies of respiratory disease in Switzerland and Nicaragua, respectively, and represent a novel monophyletic clade within HEV-C (Tapparel *et al.*, 2009; Yozwiak *et al.*, 2010). The closest serotypes to EV-C104 and EV-C109 are CV-A1, A19 and A22 (Beaton *et al.*, 2002). Since their initial

Reservoir Studies



Predictive Model

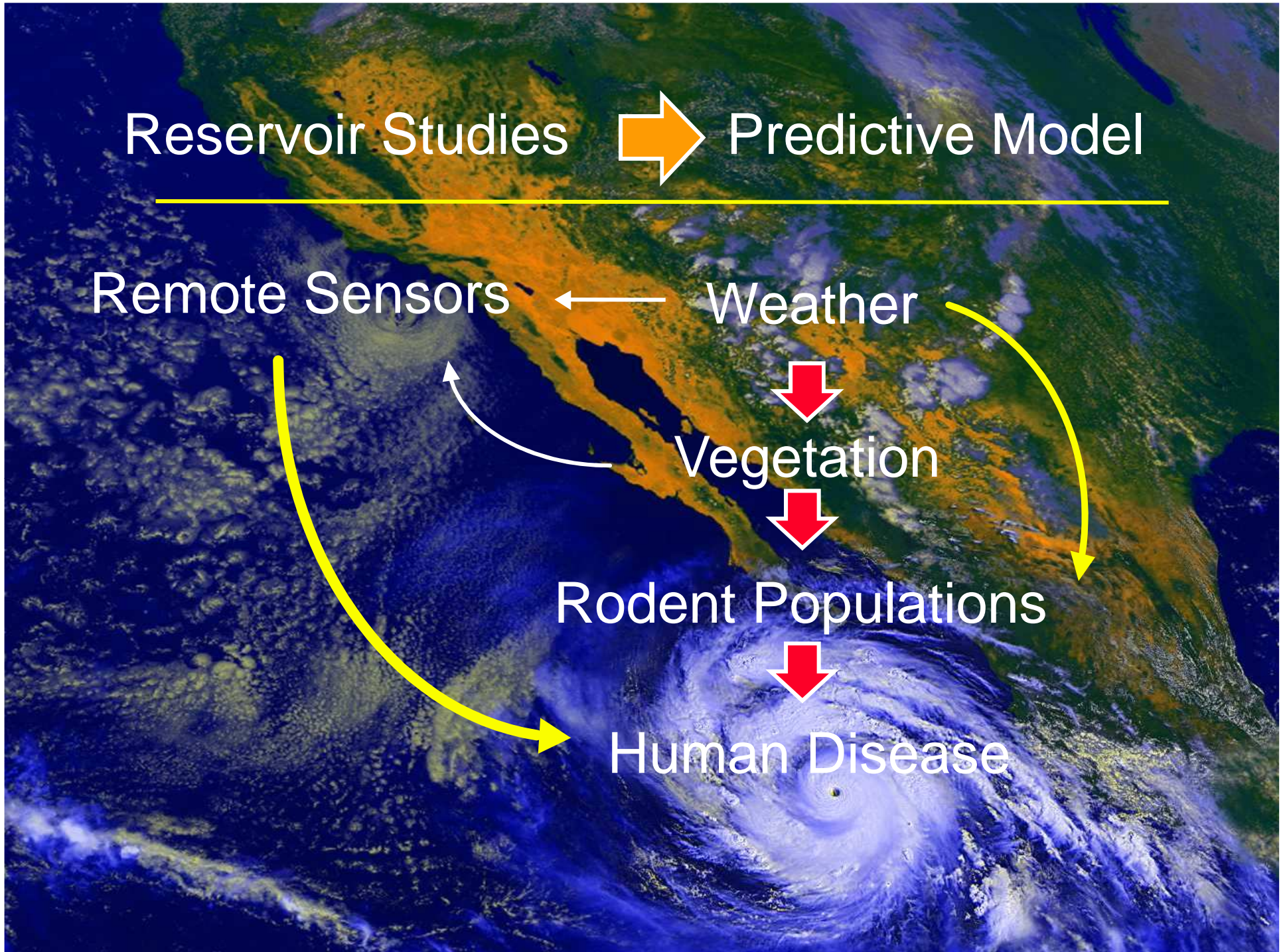
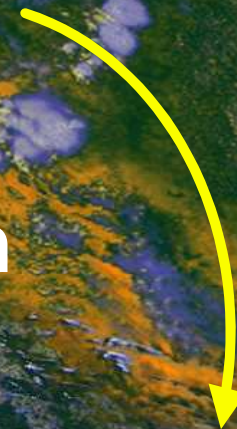
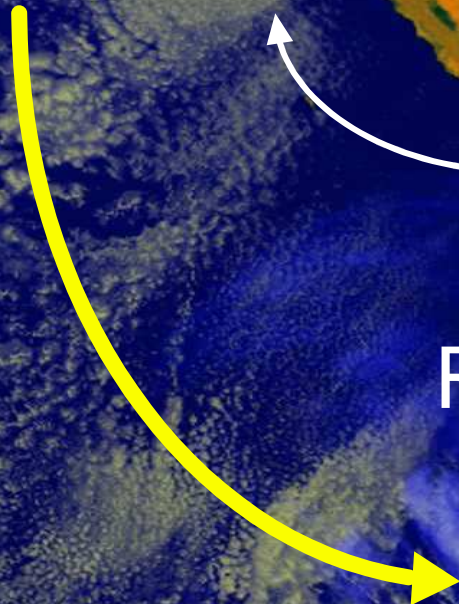
Remote Sensors

Weather

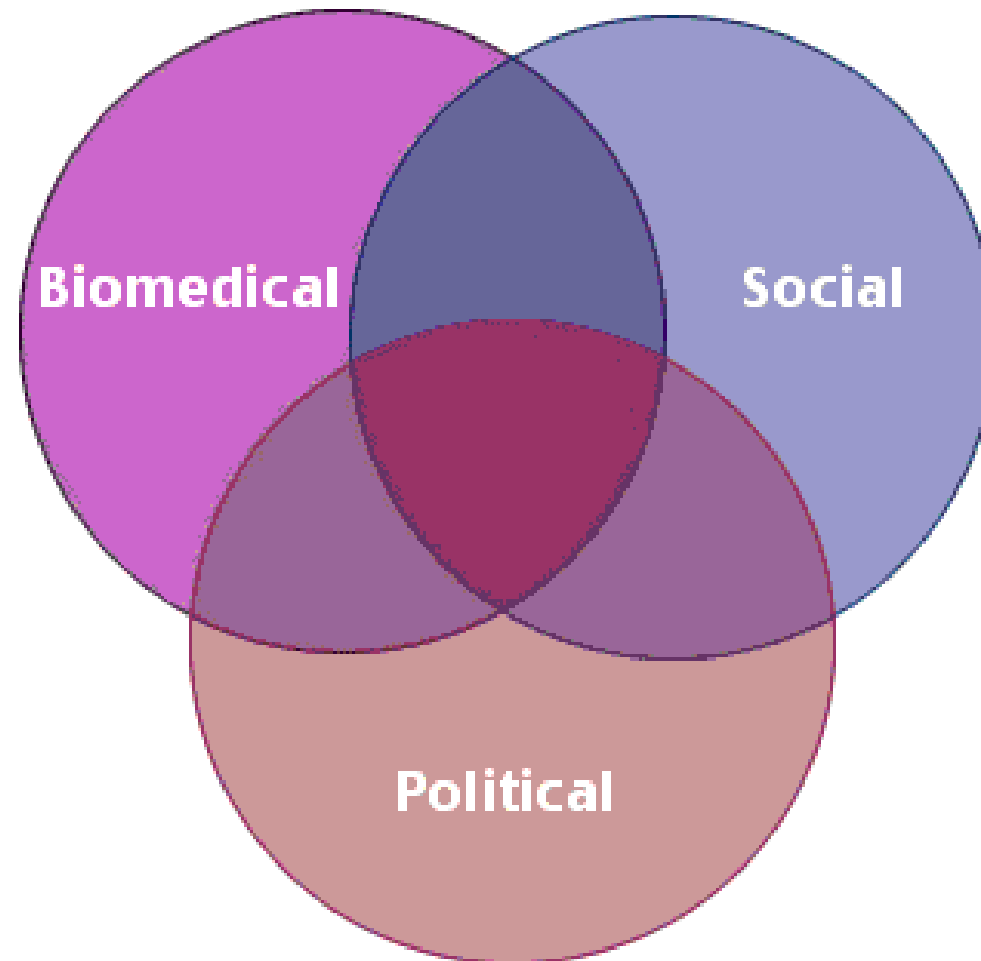
Vegetation

Rodent Populations

Human Disease



Determinants of Health



Take Home Points on Emerging Infections

1. Various types of active and passive surveillance strategies needed
2. Zoonotic interface is where the action is
3. Response “in the trenches,” not “international outbreak response,” is the rate-limiting step
4. Multiplex diagnostic strategies crucial, but astute clinicians and good epidemiologists will always be needed
5. Developing biomedical public health and research capacity in low and middle-income countries is in **everyone's** best interest
6. EIDs more likely to be in developing world and affect the disproportionately affect the poorest populations: Be proactive on social and political determinants

Partners and Funding

COLLABORATORS

- ❑ NMRCO – Peru
- ❑ San Marcos University, Veterinary School
- ❑ Cayetano Heredia University
- ❑ Cysticercosis Working Group
- ❑ JHSPH /PRISMA NGO
- ❑ Ministry of Health
- ❑ Ministry of Agriculture (SENASA)



- Schubot Exotic Bird Health Center, Texas A&M University
- Kansas University

FUNDING

- AFHSC/GEIS
- NIH - FIC
- CDC



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THANK YOU

