



**John A. Burns School of Medicine**  
University of Hawaii at Manoa  
Honolulu, Hawaii



**2011 COBRE Mini-Symposium**  
**Pacific Center for Emerging**  
**Infectious Diseases Research**  
Medical Education Building 315, Kaka'ako  
March 18, 2011

- 12:30 pm Welcome**  
Richard Yanagihara, M.D., M.P.H.
- 12:45 pm Fatal Attraction: How Coronavirus Spike Glycoproteins Recognize the Right Host Species**  
Kathryn V. Holmes, Ph.D.
- 1:15 pm Structure and Molecular Composition of Dengue Virus**  
Richard J. Kuhn, Ph.D.
- 1:45 pm Flaviviral Host Factors: An RNA-centric View**  
Mariano A. Garcia-Blanco, M.D., Ph.D.
- 2:15 pm Matrix Metalloproteinases as Modulators of Neuronal Structure and Function**  
Katherine E. Conant, M.D.
- 2:45 pm The Evolution of the Genome Structure and Regulatory Circuits in *Burkholderia mallei* Upon Evolving from *Burkholderia pseudomallei***  
William C. Nierman, Ph.D.
- 3:15 pm Wrap-up and Networking**

**Acknowledgements**

This mini-symposium is supported in part by the Centers of Biomedical Research Excellence Program (P20RR018727), of the National Center for Research Resources, National Institutes of Health.



**Kathryn V. Holmes, Ph.D.**  
Professor Emerita  
University of Colorado School of Medicine  
Aurora, CO 80045  
[Kathryn.Holmes@ucdenver.edu](mailto:Kathryn.Holmes@ucdenver.edu)

**Fatal Attraction: How Coronavirus Spike Glycoproteins Recognize the Right Host Species**

Most coronaviruses infect only one host species, but occasionally a coronavirus jumps to a new host and causes disease outbreaks, like the animal coronavirus that caused the SARS epidemic in 2002-2003. Coronavirus spike glycoproteins recognize several different receptor proteins. Studies on coronavirus/receptor interactions suggest how coronaviruses have evolved and how receptor jumping may occur again.



**Richard J. Kuhn, Ph.D.**  
Professor and Head  
Department of Biological Sciences  
Gerald and Edna Mann Director  
Bindley Bioscience Center  
Purdue University  
West Lafayette, IN 47907  
[kuhnr@purdue.edu](mailto:kuhnr@purdue.edu)

**Structure and Molecular Composition of Dengue Virus**

A pseudo-atomic structure has been developed for dengue virus based on a combination of X-ray crystallographic structures and cryo-electron microscopy of mature virions. The maturation pathway from particle formation through virus egress and acquisition of infectivity has also been determined. Mass spectrometry is currently being employed to examine the molecular composition of virions and attempts are being made to understand the heterogeneity of individual particles. This presentation will provide an overview of all these aspects of dengue virion morphogenesis.



**Mariano A. Garcia-Blanco, M.D., Ph.D.**  
Professor, Departments of Molecular Genetics and Microbiology, and Medicine  
Director, Center for RNA Biology  
Duke University Medical Center  
Durham, NC 27710  
[garc001@mc.duke.edu](mailto:garc001@mc.duke.edu)

**Flaviviral Host Factors: An RNA-centric View**

Dengue and yellow fever viruses, two medically important mosquito-borne flaviviruses, require myriad host factors, yet only a limited number have been identified to date. Two

complementary strategies were employed for the discovery of additional host proteins required for efficient flaviviral propagation: viral RNA-affinity chromatography/ proteomics and RNA interference-based functional genome-scale screens.



**Katherine E. Conant, M.D.**  
Research Associate Professor  
Department of Neuroscience  
Georgetown University Medical Center  
Washington, DC 20007  
[kec84@georgetown.edu](mailto:kec84@georgetown.edu)

**Matrix Metalloproteinases as Modulators of Neuronal Structure and Function**

Matrix metalloproteinases (MMP) are zinc-dependent enzymes, released in a neuronal activity-dependent manner, that play a critical role in learning and memory. Substrates include synaptic adhesion molecules whose shedding can facilitate and/or promote changes in synaptic structure and function. With central nervous system infection, MMP levels may be substantially increased, with consequent effects on neurotransmission.



**William C. Nierman, Ph.D.**  
Infectious Diseases Investigator  
J. Craig Venter Institute  
Rockville, MD 20852  
[wnierman@jcv.org](http://wnierman@jcv.org)  
Professor, Department of Biochemistry and Molecular Biology  
George Washington University

**The Evolution of the Genome Structure and Regulatory Circuits in *Burkholderia mallei* Upon Evolving from *Burkholderia pseudomallei***

*Burkholderia mallei* (Bm), an obligate parasite causing glanders, whose reservoir host is the horse, is very closely related to *Burkholderia pseudomallei* (Bp), a soil saprophyte and opportunistic human pathogen, causing melioidosis. Through comparative analysis of the structure of multiple Bp and Bm strains and analysis of the quorum-sensing regulons of Bp and Bm, we have gained insights into the evolution of Bm from Bp upon niche adaptation to an obligate mammalian parasite.

