NANYANG TECHNOLOGICAL UNIVERSITY

School of Biological Sciences

SBS Seminar Announcement

Oceans, Climate, and Human Health: Infectious Diseases Linked to the Environment

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University of Maryland, College Park
Johns Hopkins Bloomberg School of Public Health
CosmosID™, Inc., Founder and Chairman

Abstract

During the mid-1980s, satellite sensors were developed to monitor the continents and oceans of Planet Earth for purposes of understanding climate, weather, vegetation, and their seasonal variations. During that period of time, the role of the environment in infectious disease incidence and transmission was investigated, both qualitatively and quantitatively, using those satellite sensors to document seasonality of diseases, notably malaria and cholera. This new technology revealed a very tight connection of the environment to many infectious diseases, especially waterborne and/or vector infectious diseases. With satellite sensors, relationships could be quantified, comparatively analyzed, and predictive models developed. More recent studies of epidemics have provided even more powerful models, both retrospective and prospective, for understanding and predicting disease epidemics. Epidemics of the water borne disease, cholera, can now be characterized with information from satellite monitoring of sea surface height, temperature, salinity, and chlorophyll, the latter serving as a tag for phytoplankton that seasonally precede zooplankton in abundance in coastal and river waters. Since our studies have shown that components of zooplankton (copepods and cladocerans, predominantly) carry cholera bacteria as a component of their natural flora, the data obtained by satellite sensors offer the capacity for predicting cholera epidemics. Recent studies of historical data for India on cholera deaths 1875-1948, coupled with meteorological data stored in archives for India in that time period, provide critical data from which to build a useful model to study the cholera epidemic that erupted in Haiti in 2010.

As determined from historical data for India, elevated air temperatures for two months preceding a cholera epidemic, coupled with significantly heavier rainfall at the time of onset of the epidemic, and occurrence in a geographic region where sanitation and access to safe drinking water were affected by a disruptive event, e.g., an earthquake, the probability of epidemic cholera , as opposed to endemic cholera, is high. Examples of cholera epidemics in Bangladesh, Zimbabwe, and Haiti, as well as earlier studies on *Campylobacter* are provided. Based on these studies, an early warning system for a waterborne infectious disease can, indeed, be developed, providing a powerful tool for protecting public health and for measuring effects of climate change on infectious disease agents.

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Abstract (cont.)

In parallel with environmental studies, genomic analyses of *Vibrio cholerae*, including isolates from Haiti, provide evidence of multiple sources of cholera epidemics globally. Metagenomic data of clinical samples revealed more than one pathogen, frequently four to ten different pathogens, may be present in clinical samples collected from cholera patients.

A new method for identification and quantification of bacteria to species and strains, GENIUS, was employed in metagenomic analysis of clinical samples of these cholera patients, utilizing DNA sequence data. The results indicated the necessity to redefine diarrheal disease causal agents as a community of enteric pathogens, rather than caused by a single agent. In conclusion, with the tools of satellite sensing and environmental modeling, coupled with genomic analyses, the inter-relationships of infectious disease, climate, and human health can be better understood and more effective protective measures developed.

Friday, 06 June 2014 4.00pm to 5.00pm SBS Classroom 3 (SBS-01n-23)

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