

TRAVEL REPORT FORM

출장보고서

결 재	팀장	부서장	원장	
	05/22 김광형	05/22 김형진	05/22 정홍상	
협 조				

I. Reporter 보고자

Department 소속	Position 직위(직급)	Name 성명	Travel Date 날짜	Note 비고
응용사업본부 사업기획팀	팀장	김광형	2016.05.22	

II. Major Activities 주요업무 수행내용

1. Main Contents and Activities 주요내용 및 활동

1. Workshop on mathematical models of climate vairability, environmenta change and infectious diseases

가. 일정: 2017.5.15. - 2017.5.16. (2일간)

나. 주요내용: Policies and mechanisms of intervention to prevent or reduce the spread of infectious diseases related to environmental change and future prospects for tackling emerging and neglected diseases.

2. IECID 2017 컨퍼런스

가. 학회일정: 2017.5.17. - 2017.5.19. (3일간)

나. 주요내용

○ 학회명: Impact of Environmental Change on Infectious Diseases (IECID) 2017

○ 목 적: 기후변화에 따른 감염병 발생 환경 변화를 감지할 수 있는 병발생 모형의 개발 및 활용에 대한 다양한 연구발표와 토의를 목적으로 함

○ 발표명: Development of seasonal rice pest outlook using a rice tungro epidemiological model in the Philippines

2. Relevance to APEC Climate Center's Activities 결론 및 소감

- 기상기후정보를 활용한 인수 감염병 모델링이 현재 다양한 질병을 대상으로 활발하게 이루어지고 있으며, 특히 개도국에서 가장 문제가 되는 Vector-born diseases에 대한 연구가 주를 이루고 있음

- IRI의 Dr. Thomson에 의해 발표된 내용에 따르면 기후정보를 바탕으로 보건분야 의사결정을 지원하는 시스템이 연구개발을 넘어서 실제 활용분야로까지 그 가능성을 넓히고 있지만, 여

전히 많은 검증과 성능의 향상이 필요한 실정임

- 감염병의 발생 자체가 기상기후조건 뿐만 아니라 굉장히 많은 여러 가지 인자에 영향을 받기 때문에 역학조사가 우선적으로 이루어지고, 다른 사회경제적 정보와 기상기후 정보는 역학조사 결과를 참고적으로 지원하는 논리로 활용이 되고 있음

- 따라서 현재 기후변화 시나리오를 바탕으로 평가가 이루어지는 많은 감염병 발생에 대한 영향평가에 문제점을 다루었고, 이러한 것들이 보다 정확한 정보를 전달하기 위해 역학적으로 고려되어야 하는 모든 요소들을 활용하는 모델링 기법이 개발되어야 할 필요가 있음이 지적됨

- 과거에 비해서는 많은 학자들이 기상기후정보를 활용하려고 시도하고 있지만 여전히 감염병 발생에 기여하는 보다 중요한 인자들이 우선적으로 고려되고 있고, 기상기후정보는 하나의 작은 function으로 머물러 있는 듯한 인상을 받음

- 결과적으로 감염병의 발생과 환경적 요인을 고려한 발생의 예측 및 모니터링, 평가 등이 제대로 이루어지기 위해서는 다학제적인 접근이 반드시 필요하며, 현재의 기술 수준에서는 여전히 많은 제약이 존재하고 있다는 결론에 도달함

- 통계적인 방법 역시 기상기후 이외에도 고려해야 될 수많은 요소들이 있기 때문에, 해당 자료의 QC부터 올바르게 분석할 수 있는 통계적 기법에 이르기까지 해결해야 될 문제가 많아 보임

- 향후 APCC가 보건분야로 그 영역을 확대하기 위해서는 보건분야를 백그라운드로 기상기후적 접근을 시도한 전문가를 영입하는 것이 가장 필요할 것인데, 이를 위해 본 conference에 참석한 전문가 그룹에 대한 지속적인 모니터링과 해당 그룹에서 수학한 인재를 관심있게 지켜보는 것이 필요할 것임

III. References 참고사항

(with attachment of any information or report in case of attendance of conferences, workshops and meetings) 학술대회, 워크숍, 회의 등 참석 시 관련 정보 및 문서 첨부

1. Presented and Collected Materials 주요 수집자료

2. Suggestions and Remarks 건의사항

[INV01]

Dengue transmission- interaction of environmental and human factors

L. Ching NG*

National Environment Agency, Singapore

Dengue, transmitted by *Aedes* mosquitoes, has become the most rapidly growing mosquito-borne disease globally. Comprising four different serotypes, the Dengue virus causes 20 to 40 thousands deaths a year, incurring high economic and social costs to societies inflicted by epidemics which is increasing in frequency and intensity. The primary vector, *Aedes aegypti*, thrives in tropical and subtropical climate; and adapts to human dwellings, particularly the urban environment. Riding on environmental and human behaviour changes, the virus and the vectors have, in the last decade, increased their activities and expanded geographically to temperate regions, rural communities and higher altitudes. While most historically endemic areas fail to reduce the burden of the dengue, the disease continues to scorch new communities and regions. This presentation will explore the role of environmental and human factors that impact the epidemiology of dengue; and the potential implication of the various epidemiological features on disease control and management.

[INV02]

Predicting global emergence and spread of zoonotic diseases

K. Jones*

University College London, UK

Human infectious diseases are a significant threat to global human health and economies (e.g. Ebola, SARs), with the majority of infectious diseases having an animal source (zoonotic). Despite their importance, the lack of a quantitative predictive framework hampers our understanding of how spillovers of zoonotic infectious diseases into the human population will be impacted by global environmental stressors. Although empirical statistical analyses of human infectious diseases has been successful in understanding the spatial environmental correlates of initial outbreaks, a mechanistic understanding of these patterns is lacking at a global scale. Here I present some latest research attempting to merge both empirical and mechanistic approaches at a global scale using data from a poorly understood disease, Lassa fever. I show that macro-scale environmental conditions play an important role in driving the spatial extent of Lassa virus and that any future habitat change to agricultural systems may facilitate a range expansion. I also expand this approach to model zoonotic diseases more generally and examine the impact of future environmental and habitat change on the emergence and spread of zoonotic diseases.

[INV03]

From modeling key drivers of cholera transmission dynamics to new perspectives on parasitology

A. Rinaldo^{*1,2}

¹*Ecole Polytechnique Fédérale de Lausanne, Switzerland,* ²*Università di Padova, Italy*

Hydroclimatological forcings, the mobility of susceptible/infected individuals, and large-scale treatment are key drivers of waterborne disease transmission. The direct inclusion of these factors into spatially explicit mathematical models of epidemic cholera has proved effective in real-time prediction of unfolding epidemics. These models have the potential to account for heterogeneous disease drivers and thus to portray complex patterns of disease dynamics. Also, remotely acquired information on human settlements and mobility, waterways along which pathogens/hosts disperse, and relevant hydroclimatological processes has proven particularly valuable and directly exploitable. Current scientific and technological advancements allow for a widespread and relatively straightforward application of general spatially explicit modeling techniques. Large-scale hydroclimatological and anthropogenic drivers (or their proxies) are key to spatial descriptions of waterborne disease dynamics and can often be inferred by satellite imagery and the tracking of human mobility via mobile phones. Moreover, spatial information provides insight into the course of ongoing epidemics and can aid in emergency management and the assessment of alternative interventions, mobilizing a large set of tools from applied mathematics like e.g. data assimilation, Bayesian parameter calibration and optimal control frameworks. Spatially explicit approaches also allow us to unearth the geography of endemic diseases via suitable eigenvector analysis of proper Jacobians -- large block matrices derived from the metacommunity framework now fully assessed for a broad spectrum of disease. In fact, many viral or parasitic waterborne infections share the same drivers and substrates as cholera. However, they are characterized by vastly different disease dynamics and pathogen life cycles.

In this Lecture I shall discuss how recent advances in cholera research are expected to impact the study of parasitic waterborne diseases of medical and veterinary interest, especially those -- like proliferative kidney disease in fish -- where the impact of environmental changes on infectious disease will be particularly acute.

[INV04]
A malaria early warning system for the Amazon
W. Pan*
Duke University, USA

Reported cases of malaria in the Peruvian Amazon have increased 5-fold since 2011, from 11,779 to 60,254 in 2015. Given the increase in the rate of detection in 2016 during high transmission periods, the number of cases are likely to exceed 70,000 in the region of Loreto. Responding to this epidemic has been challenging given the reduced financial support from the Peruvian government combined with large-scale environmental impacts that have affected Peru, including massive flooding in 2012, “mega” El Nino in 2016, and continued natural resource extraction via logging and mining. An underappreciated driver of malaria transmission is the human-environment interface resulting in increased human contact with high-risk transmission environments. With support from NASA, a team of investigators from the US, Peru and Ecuador are developing a 2-component system that will improve detection of high-risk environments using large-scale prediction models (consisting of both malaria and human population models), followed by application of focused agent-based models (ABMs) to predict local transmission dynamics and simulate potential intervention strategies. This presentation will provide an update of the system after two years of development. Data include: weekly case detection reports for 2000-2015 from all health posts in the region of Loreto in the northern Peruvian Amazon; satellite-derived estimates for meteorology, land cover, hydrology, and eco-region; and estimates of population density. The large-scale model identifies districts with high spatial and temporal clustering. The small-scale ABMs, described in Pizzitutti et.al. 2015, have been improved to incorporate human mobility. This long-term project has both scientific and policy challenges that will be discussed.

[INV05]

Population dynamics and evolutionary response of an emerging avian pathogen

A. Dobson*

Princeton University, USA

Mycoplasma gallisepticum emerged as a new disease of wild birds in the United States in 1993.

In the 25 years since emergence, it has spread from an isolated location on the east coast to cover most of the United States. As the hosts have no economic importance, there have been no attempts to control the pathogen, so we have been provided with an opportunity to observe its dynamics and evolutionary changes in virulence- similar conditions rarely arise for other pathogens as they are quickly eradicated and much speculation exists about whether their virulence will evolve. We have also been able to monitor the pathogen and hosts response to different climates from the strong seasonal climate of New England to the deserts of the south-eastern US.

The model system provides many insights that are relevant to the response of other pathogens to emergence and climate variability. These will be emphasized in this talk.

[INV06]

Decision tool for climate disasters and infectious disease at subnational level in India ensuring a paradigm shift in health planning from prevalence to vulnerability

N.K. Dogra^{*1}, P.K. Taneja², S. Bhadwal³, R. Akhtar¹

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Health sector planning in India has traditionally focussed on prevalence of disease, in other words on cases emanating from the government health system. This can be particularly erroneous in developing countries like India, where a large number of cases are seen by private health providers, traditional healers or treated at home by self medication. On the other hand, if planning is done on the basis of vulnerability, taking into account both government and community factors, it is more likely to be accurate. The Intergovernmental Panel on Climate Change (IPCC) framework of vulnerability defines it as a function of exposure, sensitivity and adaptive capacity. Vulnerability indices utilizing this framework have been applied widely outside the health sector such as for natural hazards in South East Asia (Yusuf and Francisco, 2009) and the double burden of globalization as well agriculture (O'Brien et. al. 2004). More recently these methods have also been applied to the health sector in India, such as for cyclones in the east coast of India (Shukla and Dogra, 2012) and in Haryana State (subnational level) in North India (IIHMR, 2013). A similar exercise was done for 15 districts in the Eastern India State of Bihar which are at a high risk of floods. The final tool involved as many as sixteen different socio-economic, health and disaster indicators. A key finding, as anticipated, was that vulnerability did not coincide with the disease prevalence. Reasons for this difference in the context of visceral leishmaniasis (a common vector-borne disease in the region) and diarrhoea are presented. The relevance of this tool in ensuring a paradigm shift in health planning is also mentioned.

Keywords: climate disasters, vulnerability, adaptation

[INV07]
Fine-scale urban climate projections with the UrbClim model
D. Lauwaet*
VITO, Belgium

Cities tend to be warmer than their rural surroundings, a phenomenon called the 'urban heat island'. Because of the urban temperature increment, cities are particularly vulnerable to heat waves during summer, exposing urban residents to much higher levels of heat stress than people living in the nearby rural areas. At the same time, climate projections indicate that the frequency, intensity, and duration of heat waves is very likely to increase and it is expected that in the future cities may become more often exposed to extreme heat stress. In order to investigate this issue, urban climate modelling is increasingly considered a relevant tool for the evaluation of the impact and efficiency of urban (infrastructural) design measures aiming at the improved climate resilience of cities.

Therefore, the urban climate model UrbClim has been developed at VITO, designed to cover individual cities and their nearby surroundings at a spatial resolution of a few hundred meters. UrbClim is an agglomeration-scale model, with a modest level of complexity, but because of that capable of doing relatively long and/or numerous simulations. The model has been set up in cities all over the world (e.g. Barcelona, Brussels, Delhi, New York, London, Rio) and has been validated extensively regarding its urban-rural temperature differences, humidity, land surface temperatures, wind speeds and energy fluxes.

At the moment, the UrbClim model is deployed in several national and international projects, focusing on projections of the heat stress and UHI situation towards the end of the century. Therefore, the model is nested in an ensemble of global climate models from the IPCC assessment and run for 20-year periods. Also the effect of adaptation and mitigation measures from local authorities are investigated. A large focus in these projects is on health and economic impacts.

[INV08]

Climate change, schistosomes and snails: Past trends and future prospects

A-S. Stensgaard*

University of Copenhagen, Denmark

Numerous studies have documented how climate change is already changing plant and animal species' distribution and phenology as they attempt to adapt or track their climatic optima. Climate change is also affecting the occurrence and distribution of many infectious diseases, but the exact outcomes depend to a large degree on the form of climate change and the specifics of the host-pathogen system. For the three main species of snail-borne schistosomes that infect humans, *Schistosoma haematobium*, *S. mansoni* and *S. japonicum*, climate-induced shifts in phenology and geographical range of both parasite and intermediate host snails, are likely to affect disease dynamics. However, the socio-economic context and multifactorial nature of schistosomiasis make it difficult to detect climate-mediated changes, and it is unclear whether range shifts, contractions, or expansions are the most likely outcome for the human *Schistosoma* species. Accurate predictions of these outcomes and their geographical location will play an important role in alerting health authorities to potential future risks, and have important implications for the feasibility of schistosomiasis control and elimination goals. Hence, there is an urgent need to review our current understanding of the effects of climate change on schistosomiasis and our capacity to project future impacts. To this end, I here summarize the principal findings and specificities of empirical and experimental studies investigating the effect of climate and climate change on the main species of human schistosomes and their intermediate host snails. The main results are synthesized and some caveats about the most common approaches used to estimate future risk of schistosomiasis at continental and sub-continental scales presented. Finally, I highlight several challenges for future research both in theoretical and applied realms. Overall, this review shows that current predictions are very variable, depending on the method, geographical realm and scale, and species of snails and parasites considered.

Keywords: schistosomiasis, snails, climate change, modelling

[INV09]

Interactions between climatic changes and malaria intervention effects on the spatio-temporal disease dynamics

P. Vounatsou^{*1,2}

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In the past decade, malaria morbidity and mortality have been decreased mainly due to the scaling up of vector-control measures, such as insecticide-treated bednets and indoor residual spraying. Malaria indicator surveys (MIS) gather information about key malaria indicators through national representative household surveys. We analyse data from countries with repeated MIS and present Bayesian spatio-temporal models which quantify the effects of malaria interventions on the spatio-temporal disease dynamics and take into account interactions with climatic changes. Geostatistical variable selection methods are used to identify the most relevant insecticide-treated bednet measures for reducing malaria risk. Spatially varying coefficients of intervention coverage indicators enable estimation of their effects at subnational level.

[INV10]

Evolutionary and ecological insights into the emergence of arthropod-borne viruses

M. Marklewitz¹, A. Kopp¹, F. Zirkel^{1,2}, K. Hermanns¹, C. Drosten¹, S. Junglen^{*1}

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The prevalence of arthropod-borne viruses (arboviruses) is increasing worldwide. Arboviruses undergo cyclic transmission between arthropod and vertebrate hosts. In order to understand arbovirus emergence processes, we need more insight into the biodiversity and ecology of viruses that are carried by arthropods but do not, or not yet, undergo arboviral dual-host transmission.

In studying the biodiversity of mainly mosquito-associated viruses, we have detected an extremely wide spectrum of previously unknown RNA viruses. These viruses establish novel genera within known virus families, or even novel virus families such as the first insect-associated nidovirus Cavally virus, the type species of the family *Mesoniviridae* (order *Nidovirales*). Within the family *Bunyaviridae*, which is considered the most diversified family of RNA viruses, we identified four proposed novel viral genera that all seem to be restricted to insects and are in sister relationship to major pathogenic arboviral genera. We have been able to isolate these viruses in cell culture and obtained further insight into phenotypic properties such as host cell tropism. Combining phenotypic and phylogenetic studies of live insect-specific bunyaviruses, we found evidence for the hypothesis that arboviruses within the family *Bunyaviridae* have evolved from arthropod-specific progenitors. It becomes increasingly clear that insects carry a huge biodiversity of RNA viruses that may exceed and antedate the diversity of pathogenic vertebrate viruses.

Arbovirus evasion from primary habitat may be driven by ecological change. Tropical rainforests show the highest level of terrestrial biodiversity and may be an important contributor to microbial diversity. Exploitation of these ecosystems and accompanying loss of biodiversity may foster the emergence of novel pathogens. At present, however, we lack an understanding of the biological mechanisms that drive the emergence of specific pathogens.

Analyses of virus diversity and infection rates studied along disturbance gradients in tropical Africa and the Neotropics showed a decrease in genetic diversity of viruses from natural to modified habitat types. Interestingly, infection rates of mosquitoes with specific viruses from several different families increased along disturbance gradients. Knowledge on the interplay between vector diversity and virus infection rates could provide innovative approaches for epidemic risk assessment and intervention strategies.

Keywords: arbovirus, insect-associated virus, evolution, biodiversity

[INV11]

Climate-driven modelling of bluetongue disease: Assessing the current and future threat

A.E. Jones*, J. Turner, C. Caminade, M. Wardeh, A.E. Heath, A.P. Morse, M. Baylis
University of Liverpool, UK

Bluetongue (BT), a disease of ruminants which is endemic in many tropical and subtropical areas of the world, has expanded its range considerably in recent years, occurring for the first time in northern Europe in 2006 and spreading to the UK in 2007 and as far as Norway by 2009. Bluetongue virus is transmitted by *Culicoides* spp midges with increasing efficiency as the environmental temperature rises, and there is strong evidence from climate-driven disease models that anthropogenic climate change may have played a role in its recent expansion. Following another outbreak in France in 2015, and overwintering of the disease to 2016, BT now appears to be an ongoing threat in Europe. Here we use two different epidemiological modelling approaches to analyse the climate component of this threat, and how it may change in the future.

First, using a mathematical model of the relationship between the basic reproduction ratio for BT transmission and temperature, we quantify climate suitability for BT transmission in northern Europe. Observed temperature data are used to assess the past and current risk, and future scenarios are considered using downscaled projections to the end of the 21st century from five global climate models. Second, we use a spatially-explicit, stochastic-dynamic model of BT transmission to explore the potential spatial and temporal variability of BT outbreaks for the specific case of the UK. The stochastic-dynamic BT model incorporates both temperature-sensitive on-farm disease dynamics and transmission between farms via vector dispersal and livestock movements. Temperature data from the UKCP09 5km archive are used to drive the model to simulate and examine the 2007 UK outbreak, and also to consider the potential range in size, duration, extent and frequency of outbreaks under current climate conditions. Finally, we use climate projections to drive the stochastic-dynamic BT model and explore the potential severity of future outbreaks, and then discuss the implications for disease control.

Keywords: bluetongue, climate change, vector-borne disease, epidemiology

[INV12]

Climate and public health connection: A working process

G. Mantilla*

Columbia University, USA

The impact of climate (variability/change) on public health as well on the environment is significant and has been documented profusely by IPCC and researchers during the last decades. Although the connection of public health and climate is known not only on communicable and non-communicable diseases scope, the patterns, and/or, their relationships are still a matter of significant research efforts, because under a changing climate the spatial-temporal issues of public health and climate are becoming more relevant than ever.

For instance, infectious diseases related to changes in vector biology associated with climate anomalies; water, and food contamination due to flooding or drought; respiratory and cardiovascular disease related to worsening air pollution and heat waves; injuries and fatalities related to severe weather events; nutritional shortages related to changes in food production connected to changes in precipitation on local and regional patterns; allergic symptoms related to increased spatial-temporal allergen production; anxiety and depression connected to extreme weather and climate events and its consequences of mass migration and regional conflicts, are pressing the challenge for public health actions to anticipate, manage, and ameliorate the public health burdens they will impose at regional and local levels.

A natural way to go is to develop climate-based tools and methodologies e.g. early warning systems at the community level, which requires a clear framework and partnerships built between those who supply data and information, those who use it and those who understand the societal consequences of both negative and positive impacts of climate. To date those relationships have been hard both to build and to maintain because of so many factors associated with the way epidemiologists, public health officials, researchers and policy makers work to tackle the problem. Uncertainties regarding: weather/climate predictions; health interventions cost and its impacts; research results usability; lack of relevant or appropriate climate and epidemiological data are part of the issues that the actors mentioned above address with different approaches leading to successful or unsuccessful policy actions. In this context it is necessary to increase the public health and climate community's capacity to understand the role of climate on disease and public health outcomes in order to be able to develop a productive partnership that will help to prevent and control diseases and risk factors.

[KEY01]

Title to be announced

D. Hollingsworth*

University of Warwick, UK

[KEY02]

One health collaborations addressing interactions among environmental change, reduced biodiversity, and disease emergence in wildlife

A. Alonso Aguirre*, V. Beasley, P. Echaubard, B.A. Wilcox

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According to WWF's Global Living Planet Report 2016, declines in vertebrate populations averaged 58% between 1970 and 2012, including losses of 36%, 38%, and 81% in marine, terrestrial, and freshwater environments, respectively. Humanity has much more to learn about the critical roles that these species play in both complex ecological processes and health, and thus much to lose letting these species go extinct. As wild habitats have been fragmented and lost, rivers have been dammed, toxic chemical and nutrient pollution have spread, species have become stranded in isolated and degraded habitat remnants, inbreeding has compromised genetic diversity, and health problems have begun to resemble those seen in zoos, concentrated livestock, and aquaculture. Wildlife is increasingly impacted by encroachment, malnutrition, toxicants, and emerging diseases shared with domestic animals and humans. Infectious and non-infectious diseases can be catastrophic to already stressed populations. Amphibian chytridiomycosis, white nose syndrome of bats, Tasmanian devil facial tumors, Ebola in great apes, nutrient-driven hypoxic dead zones impacting fish and shellfish, and mites, microbial pathogens and neonicotinoids in honeybees are a few examples of infectious and non-infectious agents becoming leading factors in species declines and extinctions. While compelling, the human health justification for wildlife conservation is extremely anthropocentric, and an urgent need is to address how biodiversity depends on us.

One Health collaborations in research, intervention, and education should think on coincidental health problems and risks in areas of spatial and temporal overlap among species and stressors including—crowding, pathogens, metals, nutrients, biotoxins, anthropogenic chemicals, and climate change. Collectively countering such stressors can restore ecosystem services that protect humans and non-humans alike. Transdisciplinarity, integrative research, and capacity building are core elements in establishing One Health interventions that address extant, emerging, and re-emerging pathogens and toxicants that harm humans, wildlife, and other components of biodiversity. These should be both “bottom/local up” and “top/national/

international down.” Innovative participatory methodologies that operationalize knowledge flow among stakeholders should consensually and sustainably address major “real-life” problems that confront society. The One Health approach requires practical, sustainable and effective solutions with a keen understanding of local socio-economic factors as well as a solid grasp of complex regional, national and international health and environmental policies. One Health offers time-sensitive opportunities for practitioners to apply their expertise to give rise to simultaneous benefits for humans, animals, and the environment. Such nested efforts are underway and should be expanded and built upon with great determination and vigor.

Keywords: biodiversity loss, one health, transdisciplinarity, wildlife disease

[KEY03]

Waterborne and food borne diseases: A need for further efforts on reducing environmental health exposure risks

G. Cisse*

Swiss TPH, Switzerland

The effective burden of water and foodborne diseases is difficult to establish. The recent WHO estimates indicate that the global burden of foodborne diseases for 31 selected hazards was 33 million DALYs in 2010 and that 40% of the foodborne disease burden was among children under 5 years of age. Animal contact, water and soil were found contributing relatively more to food borne disease burden in low and middle-income countries (LMICs), in comparison with high income sub-regions. The highest burden per population of foodborne diseases was observed in Africa, followed by South-East Asia and the Eastern Mediterranean sub-regions. Unsafe water used for the cleaning and processing of food is one of the important factors contributing to foodborne diseases. Water contribution to the general burden of diseases deserves a great attention, particularly in LMICs, as it goes beyond the only food chain. Of note, for the year 2012, water, sanitation and hygiene was responsible for 842,000 annual deaths from diarrhea. Water related infectious diseases are a major cause of mortality and morbidity, while additionally to the classical water related pathogens, there is a rise of newly recognized emerging pathogens, increasing the challenges for the public health sector. The need of investing more in improving the environmental conditions impacting on the water and foodborne infectious diseases is not yet receiving enough consideration in LMICs and there is insufficient focus on environmental health exposure risks within the more vulnerable communities. WHO estimates that all together, improvements related to drinking-water, sanitation, hygiene, and water resource management could result in the reduction of almost 10% of the total burden of disease worldwide. There is a need of multi-stakeholder engagement and multi-sectorial collaborations for relevant research-action and integrated interventions at both community and household levels.

[KEY04]

Accounting for human drivers of seasonal epidemics

C. Buckee*

Harvard University, USA

The pronounced seasonal dynamics that characterize many infectious diseases, particularly those that are vector or water-borne, are in many cases clearly correlated with environmental variables such as rainfall and temperature. Seasonal patterns of human aggregation and travel may also play a significant role in driving seasonal peaks of disease incidence, and as rural-to-urban migration continues, the importance of city structure and human dynamics will be of increasing concern. Disentangling key drivers of epidemics is critical for the design of effective interventions, however these human dynamics are more difficult to measure in many settings than environmental variables. Here I will discuss the use of mobile phone data as a new approach to measuring human aggregation and travel patterns that underlie epidemics, as well as the feasibility of using these data sets for sustainable implementation of forecasting and containment in national control programs.

[KEY05]

Climatic and landuse change as drivers of infectious disease resurgence

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Climate change poses large risks due to multiple exposure pathways through which increases in climatic extremes can threaten human and animal health. Vector- and water-borne diseases are particularly affected. From temperature effects on the extrinsic incubation period of pathogens and vector biting rates, to precipitation altering the abundance of breeding sites, climate extremes can cause mosquito-borne disease epidemics to fluctuate beyond normal seasonal levels. Case studies will be presented on malaria and arboviruses, including recent findings on the northward expansion of chikungunya virus, and on the 2015-16 El Niño event's relationship to Zika virus emergence in South America. Temperatures were well above a 30-year average, and parallels El Niño and dengue fever epidemic patterns in Southeast Asia.

Landuse change affects the hosts or vectors of disease and, subsequently, the pathogens and parasites that breed, develop, and cause disease. Landscape impacts such as deforestation, human settlement sprawl, industrial development, road construction (i.e., linear disturbances), and large water control projects (e.g., dams, canals, irrigation systems, reservoirs) have been accompanied by global increases in emergent and re-emergent infectious disease. Some extractive industries, such as mining, not only alter landscape structure but also present a myriad of introduced contaminants that further degrade ecological integrity. New encroachments into wildlife habitat and new trade routes also pose health risks by introducing animals, plants and pathogens into new regions. This presentation will particularly provide a detailed case study of the relationship between deforestation and resurgent malaria in the Amazon region.

[KEY06]
Sustainable food systems for resilient and healthy societies

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Prevailing food systems today have become dysfunctional. The nutrition situation is worsening, socio-economic disparities are increasing and food production contributes to, and is being affected by, climate change. The persistence of silo approaches - in particular the persisting gap between food and agriculture on the one hand and health on the other - generates inconsistency of policies and regulatory frameworks, resulting in increased vulnerability of the poorest sections of society, including to infectious diseases, and further environmental degradation. And prevention and management of infectious diseases can undermine development sustainability.

Sustainable management of natural resources at territorial level is a prerequisite to public health, and sustainable livelihoods - including appropriate lifestyles and living conditions - are essential to ensure resilience to, and management of infectious diseases. Agriculture must nurture healthy ecosystems and processors and retailers should align their practices with public health and environmental goals. And prevention of infectious diseases must take into account impacts on environment and livelihoods. Comprehensive health strategies should therefore be systematically associated with food and agriculture strategies: it is essential to reorient local food systems and ensure their effective articulation with regional and global food systems.

Development approaches so far have been among the drivers of urbanization and migration, which in turn have been driving the spread of infectious diseases. Localization and integration of Sustainable Dietary Goals within the 2030 Agenda will lead to more sustainable development, including prevention and management of infectious diseases. And consumers ultimately have a key role to play in addressing the issues of climate change, food security, nutrition and health.

The presentation will introduce a variety of recent global and local initiatives and advocate for relocalization and joint planning of development approaches as well as vertical and horizontal articulation of practices and policies.

Keywords: Sustainable food systems, Place-based development, Health in all Policies

[KEY07]

In search of a better life? Urbanization low income countries and implications for health

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The majority of people in Africa and Asia predominantly live in rural areas although the two regions are urbanizing faster than any other region in the world. By 2050, Africa will see the share of its urban population increase from the current level of about 40% to 56% and for Asia, the percentage urban will increase from 48% to 64%. In terms of numbers, by 2050, over 70% of the 6.3 billion urban population will be concentrated in Asia and Africa only. Rapid urbanization brings advantages and many challenges for health. Specifically, the growth of mega cities, with high population densities and increasing temperatures, may promote the rapid spread of infections; and the growth of slum settlements, which are characterised by social marginalisation, poor housing, environmental pollution, and poor basic amenities, is eroding the “urban advantage” for many health outcomes. This paper will begin by giving an overview of patterns of urbanization in Africa and Asia and insights into socio-political factors that have implications for the health and wellbeing of the urban poor. This will be followed by examples of research from Africa to demonstrate the health realities for rural-to-urban migrants and the urban poor especially. The paper will discuss the links between place of residence (slum, other urban, and rural living) and HIV prevalence, child health, and use of health services. The paper will conclude by examples of why a simple urban/rural dichotomy can be misleading, and highlight some implications for policies.

[KEY08]

Spatio-temporal epidemiological approaches to quantifying environmental change and its impact on infectious diseases, using the example of echinococcosis in China

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Echinococcoses are parasitic diseases of major public health importance globally. According to recent estimates, the geographical distribution of *Echinococcus* spp. infections is expanding and becoming an emerging and re-emerging problem in several regions of the world. Using geographic information systems and remote sensing technologies, we explored the role of environmental factors in determining the spatiotemporal variation of human echinococcosis risk in Ningxia Hui Autonomous Region, which is a hyper-endemic province for echinococcoses. Data on echinococcosis cases were obtained from a hospital-based retrospective survey undertaken between 1 January 1994 and 31 December 2013. Land cover maps of the region were created using a range of high-quality remote sensing images with approximately 30-meter spatial resolution. Data on climatic factors were obtained from 11 local meteorological stations. The inverse distance weighted interpolation method was applied to obtain data for those locations where there were no meteorological observations locally available. Bayesian spatiotemporal conditional autoregressive models were developed at the township-level to quantify the relationship between monthly cases of human echinococcoses and environmental factors. The results of the study indicate that the land cover patterns and landscape characteristics in the province were greatly altered during the study period. We also found a significant spatial heterogeneity in the prevalence of human echinococcoses across the province. Models revealed significant positive association between human cystic echinococcosis infection and mean temperature in winter (lag-10), and also negative associations between human alveolar echinococcosis and moving averages calculated for bareland, mean temperature and mean temperature in winter. Environmental determinants of human echinococcoses can be used to develop and refine initiatives local and national initiatives to reduce the medical, social and economic burden of the infection.

[KEY09]

It's a bug's life: The impact of future environmental changes on vector borne infectious disease dynamics in people and animals: An overview

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Going back to basic biology, this paper will explore points where climate changes can directly and indirectly influence vector behaviour and susceptibility. It will then review how natural and deliberate adaptations by organisms, microbial and parasitic, as well as animal and human, to climate changes can also influence the Climate Change – Vector Borne Disease – Animal and Human health nexus.

[KEY10]

Climate change destabilizes many infectious diseases from the arctic to the equator: A call for action

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This presentation reviews the different pathways through which the various components of climate change - increase in flooding, temperature increase, rainfall amounts (up and down) and patterns - on a wide range of infectious diseases. The typical example are vector-borne diseases, as vectors' body temperature are not temperature controlled, so their biting behavior and their reproductive behavior are strongly influenced by temperature increases. Further, the reproductive cycle of the pathogen, e.g. the protozoon *Pl. falciparum* is shortened, so that one vector can transmit more than once during their life-time. Such diseases include Zika, Dengue, Leptospirosis, malaria and many more. The second group of infectious diseases are those where the pathogen resides in the water, such as cholera. A third group is food-borne, e.g. salmonella, and a fourth group finally is air-borne, e.g. epidemic meningitis. After reviewing the expected impact of climate change on a wide range of infectious diseases, adaptation measures will be presented, which can be grouped into (i) early warning and surveillance systems; (ii) priority development of new drugs and vaccines for climate sensitive IDs; application of existing control tools and (iv) strengthening health services in low and middle income countries for early diagnosis and correct and prompt treatment. Finally I describe as an illustrative example my own research on a satellite-guided early warning system for changing breeding site patterns in rural Burkina Faso and BTi-based integrated larval source management as an additional tool for malaria control.

[PLN01]

Climate information in health decision-making - from research to practice

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There is an ever-growing scientific basis for understanding the climate impacts on health outcomes and a pressing global need for countries to protect vulnerable populations from climate variability and change (including sea level rise, warming temperatures and increasing hydrometeorological extremes). Today, more than ever, public health strategies, policies and practices designed to improve climate sensitive health outcomes, must to be informed by concrete evidence of climate-related risks. Once these risk have identified information on the past, current or future climate may be used to help mitigate risks and identify new opportunities for improved health outcomes.

To date research supporting the development of climate informed health decisions has been largely piecemeal. In bringing two very different communities together with the aim of building policy relevant evidence many obstacles are made apparent. Both climate and health communities need to understand each other's policy context, disciplinary norms, language, modeling approaches and data in order to collaborate successfully. In particular, sources of uncertainty in model input data, model choice and parameterisation and predictands must be made explicit.

This presentation will focus on the incorporation of climate information into 1) routine epidemiological surveillance systems for climate-sensitive diseases 2) Disaster risk reduction strategies for health outcomes 3) nutrition planning. It will present new and innovative mechanisms for 1) strengthening climate observations, data management and sharing in development of relevant climate services, 2) intersectoral collaborations and 3) training and capacity building needs and 4) the identification of new research opportunities.

[PLN02]

Impact of environmental and demographic changes on schistosomiasis

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Schistosomiasis is a parasitic disease that affects more than 250 million people, mainly school-aged children in sub-Saharan Africa. Transmission is complex, as it is governed by the interplay of humans, specific aquatic or amphibious snails and human-water contact patterns. Demographic and environmental changes impact on schistosomiasis. Hence, the distribution of schistosomiasis is highly focal, both in space and time, and this has important ramifications for targeting prevention and control measures. I will present an approach for integrated risk profiling of human schistosomiasis at different scales. The role of systematic reviews and meta-analyses to quantify changing patterns of schistosomiasis will be demonstrated, placing particularly emphasis on major ecological transformations, such as large dams and irrigation systems in Africa. Recent examples of population movement and migration and how this alter the risk of schistosomiasis – also in Europe – will be presented.