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THE EVOLUTIONARY PROCESS OF RISK DETERMINATION

to Define Surveillance Strategies and
Target Resources for Efficient Prevention and Control

BACKGROUND

Emerging diseases are a significant global threat to public health, trade, and economic growth. Among the most significant of these are diseases that emerge from animals, either wildlife (e.g. SARS) or livestock (e.g. influenza A/H1N1). Preventing and controlling emerging diseases requires significant global resources. Targeting the use of these resources requires a deep understanding of the geographical origins of new diseases, the human populations at the highest risk of being infected, and the animal populations with the highest potential for a pathogen to jump host into people. In this session, we will review the very latest techniques and approaches to better understand the high-risk interfaces where surveillance can best be targeted.

MODERATOR

Jonna MAZET

Professor & Director

One Health Institute
University of California
Davis
USA

OBJECTIVES

To present different approaches that determine the risk of emerging infectious diseases and how these might be used to best allocate global resources for prevention and control. Each speaker will cover:

- The biological/ecological nature of the risk (e.g. transmission among wildlife or livestock)
- The socio-economic aspects of the risk (e.g. cultural approaches to farming)

SPEAKERS

- *How can we predict, prevent and pay for the next pandemic?*
  Peter Daszak, President, EcoHealth Alliance, USA

- *RVC Risk assessment framework for H5N1 avian influenza in SE Asia, with special reference to the human-livestock-wildlife interface*
  Dirk Pfeiffer, Professor of Veterinary Epidemiology, Royal Veterinary College, United Kingdom

- *Assessing risk of Rift Valley Fever outbreaks using GIS, vegetation and climate*
  Pierre Formenty, Team Lead - Emerging and Dangerous Pathogens, World Health Organization, Switzerland

- *Spatial epidemiology of Highly Pathogenic Avian Influenza H5N1 in poultry: What have we learned? What can be improved?*
  Marius Gilbert, Universite Libre de Bruxelles, Belgium

Dr. Peter Daszak is President of EcoHealth Alliance, a US-based organization which conducts research and outreach programs on global health, conservation and international development. Dr. Daszak's research has been instrumental in identifying and predicting the impact of emerging diseases across the globe.

His achievements include identifyng the bat origin of SARS, identifying the causes of Nipah and Hendra virus emergence, producing the first ever global emerging disease 'hotspots' map, identifying the first case of a species extinction due to disease, coining the term 'pathogen pollution', and the discovery of the disease chytridiomycosis as the cause global amphibian declines. Dr Daszak is a member of the Institute of Medicine's Forum on Microbial Threats, and served on the IOM Committee on global surveillance for emerging zoonoses, the NRC committee on the future of veterinary research, the International Standing Advisory Board of the Australian Biosecurity CRC, and he has advised the Director for Medical Preparedness Policy on the White House National Security Staff on global health issues.

Dr Daszak won the 2000 CSIRO medal for collaborative research on the discovery of amphibian chytridiomycosis and is Editor-in-Chief of the journal Ecohealth. He has authored over 150 scientific papers, and his work has been the focus of extensive media coverage, ranging from popular press articles to television appearances.

PETER DASZAK

President

EcoHealth Alliance
USA

Dr. Pierre Formenty is a Doctor in Veterinary Medicine with a Master in Public Health. He has been working in global public health with the World Health Organization (WHO) since January 1996. At WHO, within the Department of Pandemic and Epidemic Diseases he is leading the Emerging and Dangerous Pathogens (EDP) team. The EDP team is responsible for global prevention, preparedness and response to emerging infectious diseases epidemics of international public health concern. Dr Formenty and his team are covering a large number of emerging infections: viral emerging pathogens (Ebola, Marburg, Rift valley fever, Crimean-Congo haemorrhagic fever, Lassa and Arenaviruses, Monkeypox, SARS, Hantavirus, Nipah and Hendra,…) and bacterial zoonotic diseases of epidemic importance (Leptospirosis, plague, rickettsiosis, tularemia..). In addition, their research interest include ecological studies on emerging zoonosis at the human-animal interface, viral haemorrhagic fevers, vector borne forecasting models and climate change.

Dr Pierre Formenty is a field epidemiologist specialized in Public Health and in Medical Virology with special focus on viral haemorrhagic fever. He is also a Veterinary officer, specialized in virology and epidemiology for domestic and wild animals. He has more than twenty two years' experience in both tropical animal pathology and tropical medicine.

Since 1996, Dr. Pierre Formenty has participated with WHO in field control activities of more than 35 major outbreaks of international importance. During these missions he supported outbreak response activities for the following diseases: Chikungunya, Cholera, Dengue, Ebola, Marburg, Monkeypox, Nipah, Plague, Rift Valley Fever, SARS and Yellow Fever.

He has more than 75 published papers in peer review journals.

PIERRE FORMENTY

Team Lead - Emerging and Dangerous Pathogens

World Health Organization Switzerland

Marius Gilbert graduated in Agricultural and Applied Biological Sciences at the "Université Libre de Bruxelles" (ULB, Brussels, Belgium) in 1995. He was a visiting researcher for two years at the department of Zoology, University of Oxford, and finished his PhD on the spatial ecology of the bark beetle Dendroctonus micans at the ULB in 2001. He was then a post-doctoral fellow at the "Fonds National de la Recherche Scientifique" (FNRS, Brussels, Belgium) for three years, followed by three years or research at the ULB on contract research. In 2006, he was awarded a "Research Associate" permanent academic position with the Belgian FNRS, hosted at the ULB. His research deals with the spatial epidemiology of harmful organisms, insects and animal diseases, using a range of spatial modeling and spatial statistic tools.

His work initially focused on the spatial ecology of invasive insects. In the last 10 years, he became interested in the way concepts and methods usually applied to invasion ecology could be used to improve our understanding and modeling of epidemiological study systems, and started working on several animals diseases such as Bovine Tuberculosis (BTB), Foot and Mouth Disease (FMD), and Highly Pathogenic Avian Influenza (HPAI). Much of Marius Gilbert's research over the last few years has focused HPAI H5N1 in Asia, in close cooperation with the Food and Agriculture Organization (FAO) Animal Health division (J. Slingenbergh, T. Robinson, S. Newman, V. Martin) and those lead to key publications on the spatial epidemiology of the disease across Asia. Other key collaborators are from the University of Oklahoma (Prof. X. Xiao), from the Royal Veterinary College (D. Pfeiffer), CIRAD (F. Roger, J. Cappelle), and the Departement of Zoology in Oxford (W. Wint, S. Hay).

MARIUS GILBERT

Universite Libre de Bruxelles
Belgium

He is now particularly interested in trying to better understand how changes in agricultural production, in particular intensification of animal production systems, influence the emergence and spread of animal diseases with zoonotic potential.

Jonna Mazet, DVM, MPVM, PhD,is a Professor of Epidemiology and Disease Ecology and Director of the One Health Institute and Wildlife Health Centerin the UC Davis School of Veterinary Medicine where she focuses on global health problem solving using research, training, and capacity building. She provides service to government agencies and the public faced with emerging infectious disease challenges, including U.S. Agency for International Development, U.S. Fish and Wildlife Service, U.S. Department of Agriculture, U.S. Geological Survey, OIE, National Oceanic and Atmospheric Administration, California Department of Fish and Game, National Marine Fisheries Service, and the U.S. Marine Mammal Commission. Dr. Mazet is active in international One Health research programs, especially disease transmission among wildlife, domestic animals, and people and the ecological drivers for disease emergence.

Dr. Mazet founded California's Oiled Wildlife Care Network (OWCN), the premier model wildlife emergency management system worldwide and remains a consulting expert on animal emergency preparedness and response, serving on multiple government and NGO advisory panels. Currently, she is the Principal Investigator and Co-Director of a new viral emergence early warning project, named PREDICT, that is being developed with the US Agency for International Development's (USAID) Emerging Pandemic Threats Program. PREDICT is a multi-institutional, transdisciplinary project that is establishing global surveillance for zoonotic diseases that could emerge from wildlife. She leads a network of NGOs and governmental agencies to build capacity within the participating countries to develop surveillance systems and complete the necessary research to halt the next pandemic, like influenza, SARS, Ebola, and HIV that have preceded the program. Inless than three years, PREDICT has implemented surveillance in 20 developing countries, trained over 1000 professionals in field and laboratory techniques and biosafety, and discovered over 200 novel viruses. In addition, Jonna is active in intensiveOne Health research programs, such as tuberculosis in Africaand pathogen pollution of California's coastal waters.

JONNA MAZET

Professor & Director

*One Health Institute,
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DIRK PFEIFFER

Professor of Veterinary Epidemiology

*Royal Veterinary College
United Kingdom*

Dirk Pfeiffer graduated in Veterinary Medicine in Germany in 1984. He obtained his PhD in Veterinary Epidemiology from Massey University, Palmerston North, New Zealand in 1994.

He worked as an academic in New Zealand for 9 years and has been holding the Chair in Veterinary Epidemiology at the Royal Veterinary College (RVC) since 1999. Dirk has been involved in epidemiological research since 1985 and worked on animal health issues in developing as well as developed countries. He has published 175 peer-reviewed publications, and currently holds research grants as principal investigator with a total value of about £5Mill. He currently is the Head of Veterinary Epidemiology & Public Health Group within RVC comprising 11 academic staff and about 35 PhD students and research assistants.

Dirk is also Head of the newly designated FAO Reference Centre for Veterinary Epidemiology at the RVC. He teaches epidemiology at undergraduate and postgraduate levels and has designed and taught international training courses in veterinary epidemiology, risk analysis and spatial analysis in Europe, North America, Australasia and Africa. At RVC, he co-directs an MSc in Veterinary Epidemiology as well as one in Veterinary Epidemiology & Public Health by Distance Learning.

He is the lead author of a textbook on spatial epidemiology, author of the chapter on spatial analysis in the key veterinary epidemiology textbook 'Veterinary Epidemiologic Research' and the author of a new textbook 'Introduction to Veterinary Epidemiology'. His particular interest is the epidemiology and control of infectious diseases, and the science-policy interface.

His technical expertise includes field epidemiological and ecological research methods, advanced epidemiological analysis, spatial and temporal analysis of epidemiological data, risk analysis, computer modelling of animal disease and development of animal health surveillance systems. Dirk provides scientific expertise to various national and international organizations including the European Food Safety Authority, the European Commission, the UK Department of Environment, Food and Rural Affairs, the Food and Agriculture Organization of the United Nations, the World Organisation of Animal Health, as well as various national governments.

RISK ASSESSMENT FRAMEWORK FOR H5N1 AVIAN INFLUENZA

in South-East Asia, with Special Reference to the Human-Livestock-Wildlife Interface

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SUMMARY

Risk assessment has been widely used in South-East Asian countries to inform the development of control policies for highly pathogenic avian influenza (HPAI) H5N1. The understanding of the disease's epidemiological parameters can probably now be considered adequate, and broadly effective diagnostics and vaccines have been developed. But the inability to eradicate the infection from the region has led to the realization that the occurrence of HPAI H5N1 is influenced by a complex interaction of environmental, epidemiological and social factors that are spatially heterogeneous and interconnected across the region and beyond. Sustainable and effective control will need to take account of the holistic nature of the system. A major challenge will be to understand the influence of human behaviour and to develop effective mechanisms leading to appropriate behaviour change where necessary.

CONTEXT

Initially large and now small-scale outbreaks of highly pathogenic avian influenza (HPAI) H5N1 have occurred in South-East Asia since late 2003. While some countries, e.g. Thailand, have been able to eradicate it, others, e.g. Viet Nam, still experience outbreaks on a regular basis. The threat of a global pandemic which justified the major multi-national efforts towards control of HPAI H5N1 in the region is still just as relevant, given the continuing virus spread and the associated risk of genetic change [1]. The current situation is dangerous, in that most stakeholders have become less aware of this still present risk. In addition, the widespread use of vaccination in Viet Nam (and in China) without being able to eradicate the virus due to insufficient vaccination coverage may accelerate the emergence of resistant virus mutations.

RISK MANAGEMENT OF HPAI H5N1

Risk management of infectious diseases such as HPAI H5N1 is ultimately aimed at elimination of infection from a population sub-nationally, nationally, regionally or even globally. Given the presence of the virus in wild waterbird species and domestic poultry in South-East Asia and neighbouring countries which are connected through wild bird migration and poultry-associated trade, elimination from South-East Asia will not be feasible for the foreseeable future with the currently available disease control tools. This reality needs to be recognised and the objectives of risk

management within the region may have to be re-defined in some countries. One objective should be to minimise the risk of genetic change in the virus and if it does indeed occur to detect such changes early. A second objective will be to minimise the risk of human exposure since infection can be fatal. The third objective is to eliminate the virus from defined populations for trade purposes. The fourth objective is to minimise infection risk for domestic poultry to reduce mortality.

The resulting risk management policy needs to be part of an integrated risk governance (or analysis) framework that includes risk assessment, risk communication and surveillance [2, 3]. Given the transboundary nature of the system within which the virus is transmitted, long-term effectiveness of risk management requires a regional approach to the problem. It is also important that the risk management policies are informed by integrated risk assessment taking account of the holistic nature of the underlying system.

RISK ASSESSMENT OF HPAI H5N1

The understanding of the ecological, epidemiological and sociological system within which HPAI H5N1 exists is one of the factors influencing the development of risk management policies. Scientific risk assessments are now widely accepted as the most appropriate tool for synthesizing knowledge about risks such as infectious diseases in a structured way. They also allow expressing the absolute risk in quantitative or qualitative terms and to prioritise different risk pathways which in turn provides guidance for risk mitigation strategies [3].

For HPAI virus (HPAIV) H5N1 in South-East Asia, structured scientific risk assessments based on the OIE risk analysis framework [3] were conducted in support of national policies, for example in Thailand and Viet Nam. The process was facilitated by a project funded by the UK Department for International Development (DfID) and led to a series of reports tailored to the needs of national policy makers [4, 5]. The risk assessments included a variety of information sources and analytical tools. Data- as well as knowledge-driven modelling approaches were used [6]. The data-driven approaches were based on existing surveillance data, and resulted in identification of many specific but also large numbers of proxy variables for environmental, epidemiological and sociological risk factors [7]. Key outcome of this research was the identification of the importance of rice-paddy production systems with their mix of poultry and ducks connected through live bird markets and free grazing ducks for local maintenance of HPAIV H5N1 [8-11]. Furthermore, cross-border trade played an important role as a source for continued introduction into the region and between countries within the region [1]. Knowledge-based approaches were applied to produce maps of suitability for HPAIV in Asia [12] and to model the infection dynamics [13-15]. The risk assessments were complemented by socio-economic studies which emphasized the importance of economic drivers influencing the occurrence of HPAI H5N1 [16-19].

LESSONS LEARNED

The complexity of systems associated with disease emergence has been recognised for some time now [20-22]. The inability to regionally control HPAI H5N1 in South-East Asia and elsewhere has demonstrated the need for

an interdisciplinary approach towards dealing with infectious disease challenges [23]. Most of the research conducted so far uses a single or multidisciplinary approach, primarily involving the bioscientific disciplines. The resulting very resource-intensive risk management policies have led to a major reduction in HPAI H5N1 outbreak occurrence in SE-Asia control without being able to eradicate HPAIV H5N1 from the region [18, 24-27]. The challenge for now and the future will be to establish more effective and sustainable processes and practices for participatory and cross-sectoral approaches embedded within a sound risk governance framework in SE- Asian countries, and elsewhere [28, 29].

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SPATIAL EPIDEMIOLOGY OF HIGHLY PATHOGENIC AVIAN INFLUENZA H5N1 IN POULTRY:

What have we learned? What can be improved ?

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Highly pathogenic avian influenza (HPAI) H5N1 has spread to more than 60 countries, covering a variety of agro-ecological, economic and environmental conditions. Whilst the disease has been eradicated from most regions to which it was introduced, it persists in others, where it continues to affect the livelihoods of smallholders, to constrain development of the poultry sector, and to cause occasional human fatalities. For several years, the spatio-temporal patterns of HPAI H5N1 outbreaks (or indicators of virus presence such as positive identification) has been studied with two main aims. First, to identify risk factors associating with the presence of the virus such as to guide intervention and changes in prevention measures and policies. Second, to map the geographical distribution of the risk of HPAI H5N1 virus presence, so that surveillance and control could be better targeted.

OF DUCKS, RICE... AND TRUCKS

Some of the first publications on the distribution of HPAI H5N1 risk were produced about the situation in Thailand (Gilbert et al. 2006) and Vietnam (Pfeiffer et al. 2007) because those countries experienced strong epidemics and quickly established efficient disease surveillance systems allowing those analyses to be done. The analyses identified the density of domestic duck as key risk factors associating with the presence of HPAI H5N1, and this supported the results of previous laboratory work highlighting that domestic duck could make asymptomatic infections (Hulse-Post et al. 2005) and spread the virus silently. Follow-up work showed that domestic duck husbandry was closely associated with intensively cropped rice (Gilbert et al. 2007), and that the remote sensing of those areas with double or triple annual production of rice could be carried out using satellite imagery, and that these data could help better mapping the distribution of HPAI H5N1 risk in the Mekong region (Gilbert et al. 2008 p. 1).

However, follow-up studies carried out in other countries such as Indonesia (Loth et al. 2011), Bangladesh (Loth et al. 2010; Ahmed et al. 2012) and South Asia (Gilbert et al. 2010) showed a

different pattern, with domestic duck density not showing up as a significant risk factor, whilst other factors where found comparatively more important. A plausible explanation, already suggested in Gilbert et al. (2010) was that the difference was caused by differences in duck production systems. This hypothesis was tested by going back to the Thailand data set, separating chicken and duck data extensive and intensive production systems (Van Boeckel et al. 2012b), and testing those new variable against HPAI H5N1 risk in Thailand. In Thailand, it was found that the variable most strongly associated with HPAI H5N1 risk was the duck raised intensively, with large flock having a median of approximately 5000 birds per owner (Van Boeckel et al. 2012a). Those used to be transported by truck over long distance throughout the country to be fed in rice paddy fields (Songserm et al. 2006) at the time of the epidemic, before new policy banned those long-distance movement in the absence of a negative test. In contrast, ducks raised extensively by smallholders with a flock size of 10 birds per owner where not showing a strong association with HPAI H5N1 risk, a situation that resembles that observed in Bangladesh, India and Indonesia where duck farming is largely dominated by backyard production. In China, where duck production was drastically intensified over the last few decades (Fig. 1), and where HPAI H5N1 emerged (Li et al. 2004), a recent study by Martin et al. (2011) showed that factors relating to HPAI H5N1 presence detected through active surveillance in markets also correlated with domestic waterfowls density and typical habitat.

OTHER FACTORS

Many other authors have since analyzed risk factors associating with the presence of HPAI H5N1 virus, and those we recently reviewed in Gilbert & Pfeiffer

(2012). The review aimed to identify common risk factors amongst spatial modelling studies conducted in different agro-ecological systems, and to identify gaps in our understanding of the disease's spatial epidemiology. Three types of variables with similar statistical association with HPAI H5N1 presence across studies and regions were identified: domestic waterfowl, several anthropogenic variables (human population density, distance to roads) and indicators of water presence. Variables on socio-economic conditions, poultry trade, wild bird distribution and movements were comparatively rarely considered. Surprisingly, the density of chicken did not show a consistent association with HPAI H5N1 risk across studies and scales. This variable may cover a diversity of types of farming with extremely variable levels of bio-security, hygiene and disease prevention practices. Differences of the type of chickens (native vs. improved breeds), how they are raised (backyard vs. commercial), and how these differences were, or were not, accounted for in the studies considered in the review likely explains the differences obtained across studies. Here again, better accounting for the difference in production system may shed some light on this effect.

Three types of factors have been poorly addressed in the reviewed studies, especially if one considers their potential impact on disease transmission: i) socio-economic factors, ii) poultry trade factors, and iii) factors related to wild bird distribution. The common feature of all three factors is that there are technical difficulties in data collection . Socio-economic data (e.g. purchasing power per capita, land value, price indices) are often aggregated at a relatively coarse level, and can hence not be easily integrated into spatial modeling.

Similarly, poultry trade variables are notoriously difficult to obtain. When available, these data ignore illegal trade, which can be very significant within and between countries, and that can be further exacerbated under HPAI H5N1 epidemic conditions. Furthermore, trade patterns are extremely dynamic and can change according to production / demand discrepancies and price differences between geographic regions. A trade flow observed in a year between two regions could stop, or even reverse the following year as a result of changes in price differences between the regions. Difficulty in obtaining pertinent spatial data is also one of the main reasons explaining why so few studies have formally integrated information on wild birds in HPAI H5N1 spatial modeling. In the wild avifauna, migratory water birds of the Anatidae family are those thought to have been implicated in long-distance transmission of HPAI H5N1. However, this family includes a large number of migratory species that have an inherently dynamic distribution. Data on their distribution in space and time are hence difficult to obtain at high resolution. Furthermore, although some sites are known to harbour large wintering populations, the precise locations where birds will actually stay may vary from year to year, depending on the specifics of the water level and food availability. One can then only predict areas where the birds are likely to be, rather than where they actually are. Massive efforts have been directed toward better characterization of waterfowl migration patterns and habitat preference in the context of HPAI H5N1, and this has resulted in important advances in understanding their potential capacity to spread the virus over long distances. However, these data provide information on individuals that cannot easily be used to predict the distribution at the population level at a fine spatial scale.

FUTURE WORK

Future work could improve upon previous findings in several ways.

First, we have highlighted the importance of separating poultry data into production systems, so that the respective role of smallholders, semi-intensive and industrial farming can be better disentangled. What was recently shown for Thailand is probaly true also for other countries, i.e. different type of production systems are not associating with the risk equally. The current body of studies that only rarely provides adequate differentiation of poultry data into different production system categories has not provided a robust evidence base to inform the debate about their respective role in the epidemic.

Second, the same can be said about the respective role of wild birds and poultry trade in the spread of HPAI H5N1. We recognize the challenge of integrating these factors within the most commonly used modeling frameworks, and the challenge of obtaining pertinent data. However, with the emergence of the "One health" concept, that aims to more holistically integrate the key factors of the human and animal dimensions influencing emergence of infectious diseases, future work should aim at better integrating those overlooked factors into spatial models.

Third, the integration of two other dimensions of ecological system within which HPAI H5N1 occurs should also be considered in future modeling efforts: time and evolution. With few exceptions, time has been ignored in previous

studies and would deserve to be better accounted for in temporally explicit statistical modeling, where both the dependent variable and the predictors are explicit in space and time. This could help quantifying the space-time association between the distribution of water, cropping or eco-climatic variables and HPAI H5N1 risk, and help developing hypotheses on the seasonality that was observed in HPAI H5N1 epidemic curves. Along those effort, a shift from data-driven statistical modelling to more mechanistic mathematical modeling will be useful so that more explicit hypotheses can be tested. Finally, all HPAI H5N1 cases have been considered molecularly and pathogenetically identical in the spatial modeling studies, whilst the virus has evolved into a number of clades over time that could be linked to variations in pathogenicity and transmission. A better integration of phylogeographic and risk-factor type of studies, whilst methodologically challenging, would also provide much insight into the evolutionary conditions of emergence of this unprecedented panzootic.

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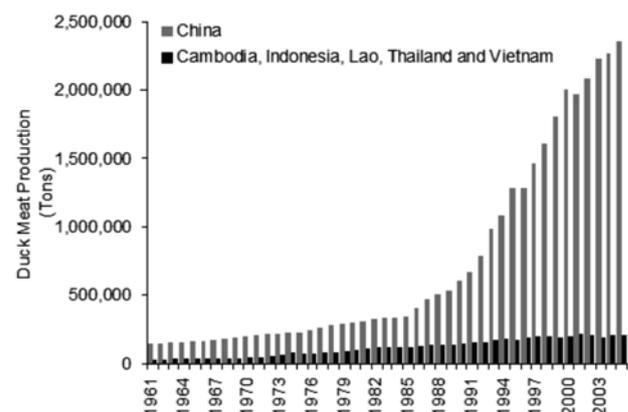
Fig. 1 Total production of duck meat in China (grey) and summed over Cambodia, Indonesia, Lao, Thailand and Vietnam between 1961 and 2006 (source: FAOSTAT 2006)

HOW CAN WE PREDICT, PREVENT AND PAY FOR THE NEXT PANDEMIC?

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SUMMARY

The emergence of novel pandemics causes substantial mortality, morbidity and economic loss. Recent analyses show that disease emergence is linked closely to human activity such as deforestation, agricultural intensification and other forms of rapid economic development. Predictive models show that diseases emerge from EID 'hotspots' in the tropics, and that they gravitate to the richer countries via the global network of travel and trade. Dealing with this threat will require 1) a 'Smart Surveillance' strategy that uses predictive modeling to target hotspots for pathogen identification and programs that alter high risk behaviors; and 2) a way to levy payments to insure against pandemic emergence. This payment system will most likely need to be an insurance program that incurs cost on the high-risk activities responsible for disease emergence and the countries most at risk.

CURRENT REALITIES:

New pandemics have emerged repeatedly in the last few decades causing substantial mortality, morbidity and economic loss. These are caused by pathogens that 'spillover' from their wildlife hosts (e.g. SARS), that evolve resistance to antibiotics (e.g. XDR TB), that are carried to new regions with their vectors (e.g. West Nile virus), or that emerge from intensive agriculture and global food delivery networks (e.g. influenza A/H1N1 & A/H5N1). Even when these diseases do not lead to significant mortality, they can cause substantial economic damage through disruption of trade networks (e.g. drop in travel to SE Asia during SARS outbreak) or through the public response to the negative publicity surrounding a new pathogen (e.g. the drop in pork consumption during H1N1 'swine' flu outbreak) (Brahmbhatt, 2005).

Analysis of all disease emergence events for the past 6 decades reveals a number of predictable patterns (Jones et al., 2008): 1) Disease emergence is strongly linked to human societal activity on the planet such as land use change, intensification of agriculture and other forms of economic development; 2) The number of new emerging diseases is increasing annually even after correcting for increased surveillance; 3) Diseases with the most potential to become pandemic emerge from regions in the Tropics with high biodiversity and intense human activity.

Using this information, we can develop maps of the regions on the planet most likely to propagate

the next emerging disease. These EID 'hotspots' are the major sources of new pathogens with pandemic potential. However, due to intensely interconnected patterns of global travel and trade, pathogens are able to spread rapidly and threaten lives and economies globally. In fact, emerging pandemics will rapidly gravitate to richer economies with higher levels of trade and air travel (Fig 1, below).

OPPORTUNITIES AND CHALLENGES:
We have two unique opportunities to deal with the pandemic threat in our generation. First, our understanding of the process of disease emergence has developed rapidly so that we can predict the regions on the planet most likely to be the origin of a new disease and the populations most likely to be affected. Second, new methods for pathogen discovery make it possible to identify a substantial proportion of the unknown pathogens harbored by animal hosts before they emerge in people.

However, progress in developing a global strategy to deal with new EIDs is hampered by a lack of international capacity, even following the development of the World Health Organization's International Health Regulations. National surveillance programs in the developing countries where diseases often first emerge are usually less effective than those in the developed countries where their impact is highest. Trade in animals and their products is poorly regulated for the spread of novel emerging pathogens, despite the OIE regulations for known agents. Finally, there is a significant urgency to developing a global program to deal with the pandemic threat. Our analysis of the economic costs of pandemics suggests that, given a continued rise in the annual number of new diseases, there is a window of between 3 and 34 years to address the threat before it becomes too costly.

Disease emergence is therefore a classic tragedy of the commons dilemma whereby their emergence in one country (often a developing country) can have the highest impacts on another country once a pathogen enters the globalized travel and trade network. Developing a global strategy to deal with them will be costly and there is significant uncertainty around who should pay for this and how much it will cost.

One solution to predicting the next emerging zoonosis is a 'Smart Surveillance' strategy that uses predictive models to identify where zoonoses will most likely emerge. Targeting these regions for surveillance of wildlife for new pathogens, food animals and people for antibiotic resistance will enable the best use of scant global resources. These regions would then need to be targeted for programs to develop alternatives to behavior with a high risk of disease emergence.

However, to prevent the next pandemic will require dealing with the underlying drivers of disease emergence which will be costly. For example, road building, deforestation, dam building, trade in livestock, development of intensive farms all involve a modest risk of propagating a new pandemic. Dealing with this risk will levy a cost on these activities, unless local governments or intergovernmental agencies pay. One solution may be an insurance approach whereby a cost is levied by a local government on the private sector involved in these activities. However, if the impact of pandemics is principally on countries distant to the origins, it could be argued that these countries should pay some form of insurance. A workable solution might be a system whereby largescale development projects are required
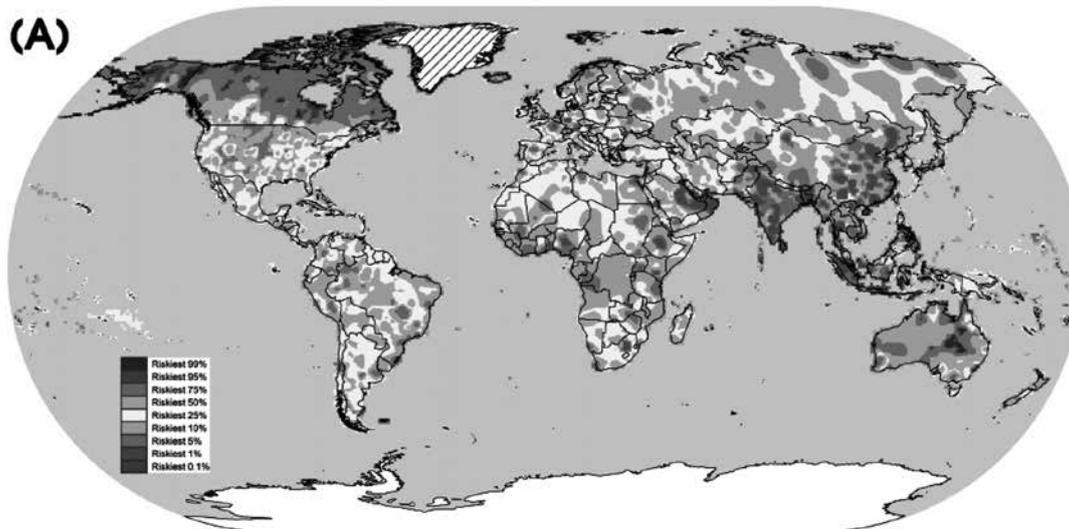
Figure 1: A map of global vulnerability to emerging diseases. This map is based on analyses in Jones et al. (2008) which show that global human activity and biodiversity are the key drivers of novel disease emergence. This map incorporates measures of global travel and trade, and countries' abilities to deal with early outbreaks and prevent them. The red color represents countries where diseases will most readily emerge and spread globally.

to assess the risk of a novel EID as part of a Health Impact Assessment. Measures to deal with the risk could then be put in place as part of the funding for these projects.

POLICY ISSUES:

Recent advances have shown that emerging diseases 1) emerging with increasing frequency; 2) originate in mainly Tropical regions, with high wildlife biodiversity and growing human populations; 3) are causing increasing economic impact; and 4) once they are in the human population rapidly gravitate to those countries with the most active travel and trade networks (North America, Europe, Australia and other high-GDP countries). The critical policy needs are to identify:

- A coordinated global early warning system for EIDs that uses predictive modeling to allocate resources to the regions most likely to propagate new pandemics, and develops surveillance strategies to identify them rapidly, and behavior change programs to deal with underlying risk.

- Efforts to insure against cost of an EID that allocate the payments fairly among the industries and activities driving novel diseases to emerge (e.g. livestock trade, road building, mining activities) and the countries most at risk (e.g. those where travel and trade routes bring in novel pathogens most effectively).

- A commitment from intergovernmental agencies spanning One Health, International Development, Conservation and Trade. This would mean a wider remit than the tripartite One Health agreements among OIE, WHO and FAO, and bring in UNDP, IUCN and others to address emerging diseases as a complex issue.

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ASSESSING RISK OF RIFT VALLEY FEVER OUTBREAKS USING GIS, VEGETATION AND CLIMATE:

Remapping Rift Valley Fever Outbreaks in Africa and the Middle East

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Rift Valley Fever (RVF), is a viral zoonosis that primarily affects animals but that also has the capacity to infect humans. Infection can cause severe disease in both domestic animals (cattle, sheep, goat, and camels are amplifier hosts during major outbreaks) and humans. Vaccines for animals are available and experimental vaccines have been developed for humans. RVF is endemic throughout sub-Saharan Africa; the disease has occasionally spread to Egypt, Saudi Arabia and Yemen. The major mode of transmission to humans is direct contact with infected animal blood or organs, but the virus can also been transmitted by mosquito bites and laboratory contamination. Several different species of mosquito are able to act as vectors for transmission of the RVF virus. To date, no human-to-human transmission has been documented.

From end 2006 to date, major RVF outbreaks have started in Eastern Africa and are still on-going in Southern Africa. According to WHO, in Kenya, Somalia and Tanzania alone, a total of 100,000 human infections can be estimated. During this wave, RVF transmission has been reported in contrasted eco-epidemiological patterns.

Joint WHO/FAO field investigations in most of the affected countries provided an opportunity to review the ecology of RVF major outbreaks and to distinguish two ecologically distinct situations: primary and secondary emergence sites. At primary foci sites, RVF virus spread through transmission between vectors and hosts and maintains between outbreaks through vertical transmission in Aedes mosquitoes. During major outbreak in primary foci, the disease can spread to secondary foci through livestock movement or passive wind-borne dispersal of mosquitoes. At secondary foci sites RVF virus spreads between naïve ruminants via local competent mosquitoes like Culex and Anopheles that act as mechanical vectors. Irrigation schemes, where populations of mosquitoes are abundant during long periods of the year, are highly favourable places for secondary disease transmission.

An innovative RVF primary versus secondary area map is proposed, based on expert opinions and review of historical and recent outbreaks. A joint FAO/WHO database including approximately 2000 records from official and unpublished data has been developed. These data are now used to improve the models for the determination of RVF suitable areas and real-time monitoring developed by collaborative centres, with the final objective of improving RVF outbreak forecasting and early warning.

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