

**RISK ASSESSMENT AND
QUANTITATIVE SIMULATION
MODELING IN PUBLIC
VETERINARY SERVICES:
IS IT A GOOD APPROACH?**

Mo Salman

m.d.salman@colostate.edu



Global Health and Official Veterinary Services (OVS)

[Acha, P. N. A strategy for Veterinary Services to meet the requirements of a changing world. Rev Sci Tech Off Int Epiz. 1987; 6(4):925-945.]

"In recent years, delegates to the OIE have voiced concern about the situation of many Official Veterinary Services (OVS). There is broad agreement on **the obsolescence** of many OVS in regard to the demands of the animal industry."



Worthy Global Health Events



Zika Virus

Transmitted by **mosquito bite**

ABOUT 1 in 5 people infected will become ill

SYMPTOMS normally last **2-7 days**

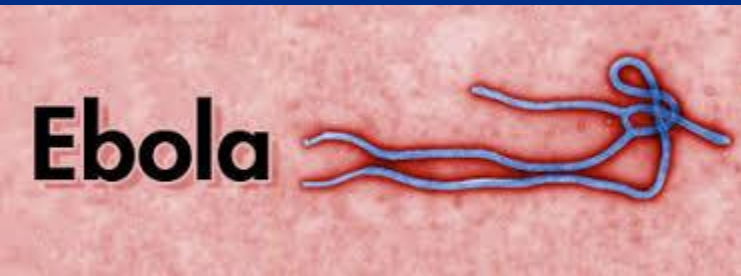
SYMPTOMS: fever, rash, joint pain, conjunctivitis (red eyes)

ILLNESS is usually mild and **death is rare**

Mosquitoes known to transmit the virus are **not present in Canada**

No treatment or vaccine is available

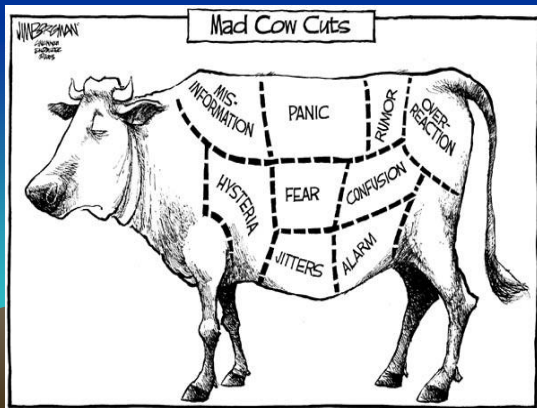
Health Canada / Centers for Disease Control and Prevention



MERS-CoV

Middle East Respiratory Syndrome Coronavirus

Also termed as Camel Flu or EMC/2012



Significant Issues

- These health events in the news involve animal health authorities;
- Public Health agencies attempt to control or eradicate these diseases;
- Opportunities instead of troubles.



Preparing for terror



**Policy, strategies,
regulations, and
authority**



**National Animal Health
Services**



surveillance

Field and Clinical Operations

**Diagnostic and
Investigation Operations**

**Prevention, treatment,
vaccination, awareness**



Laboratory, field response



What are the drivers for implementation of animal disease surveillance systems including risk assessment?

- SPS agreement
- Spotlight on Animal Health Programs
- New Terms:
 - Comprehensive surveillance
 - Quantitative disease indices and modelling
 - Scientific based risk analysis



Have we achieved successful animal disease surveillance systems?

- Yes but with qualified limitations;
- Attentions to health events with social and/or media coverages;
- Regulations and/or enforcement of specific health events have more successful than those diseases without enforcement;
- Here to say vs. scientific evidence – Verification
- **Limited use of surveillance data**

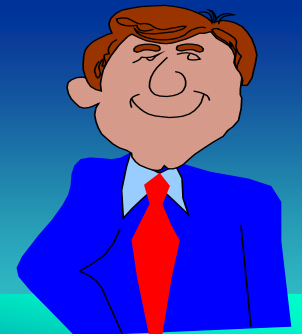


Surveillance and its link to risk assessment

- Reporting of findings from surveillance systems is one of the output components of the system – **Risk communication option**;
- Analysis of the observations is essential part of an effective surveillance system – **Risk Analysis as a tool**;
- Scientific communications using surveillance data are essential component for risk assessment process – **Risk Assessment process is needed.**

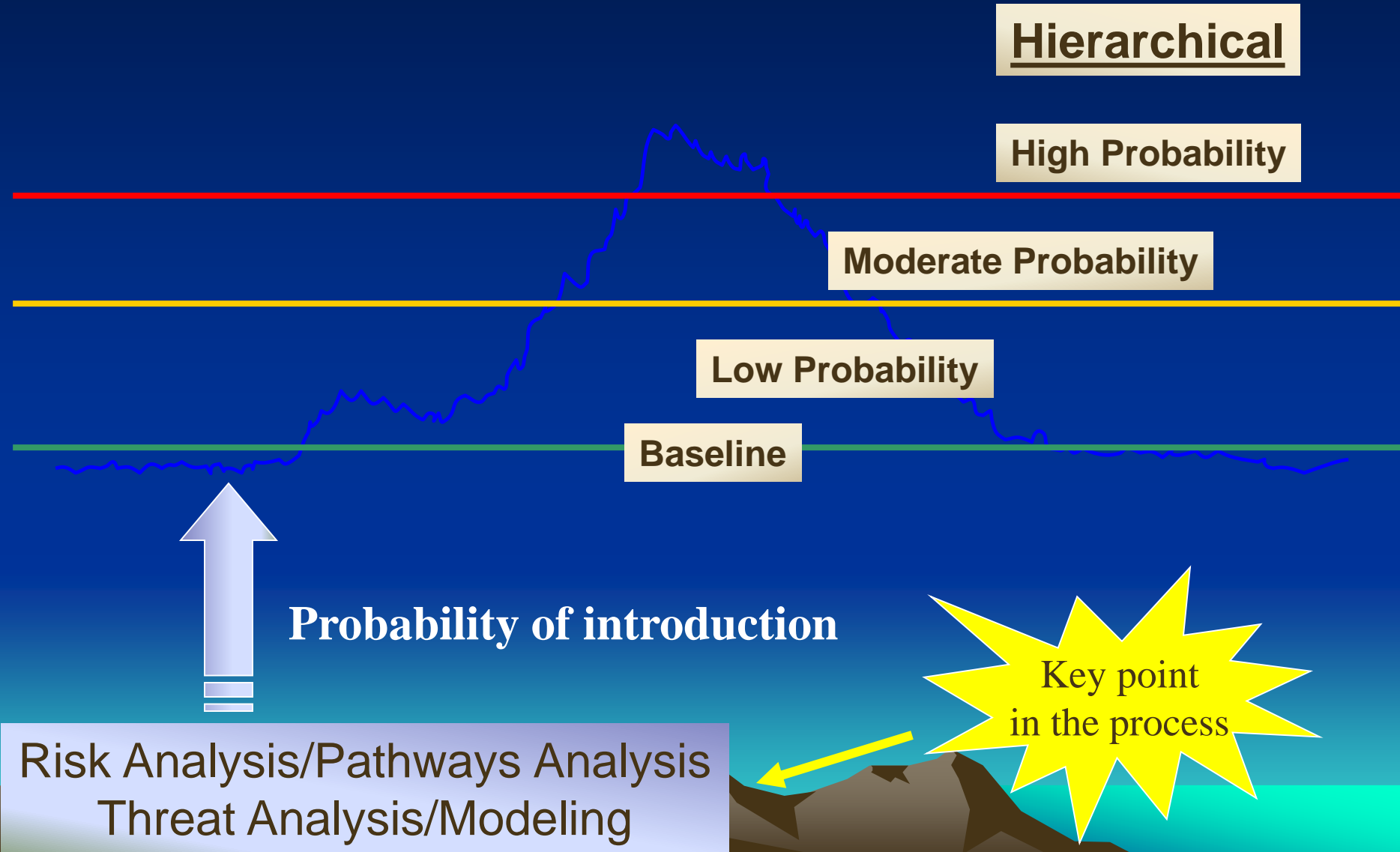
How is a surveillance recognized by the decision makers?

- No surprise with limited embarrassment;
- Involvement and awareness of the various stages of the system;
- Regular reporting of the outcome and early warning system;
- Options with their potential consequences instead of a single action plan.



Probability Based Surveillance *

* Bates and Thurmond, 2003

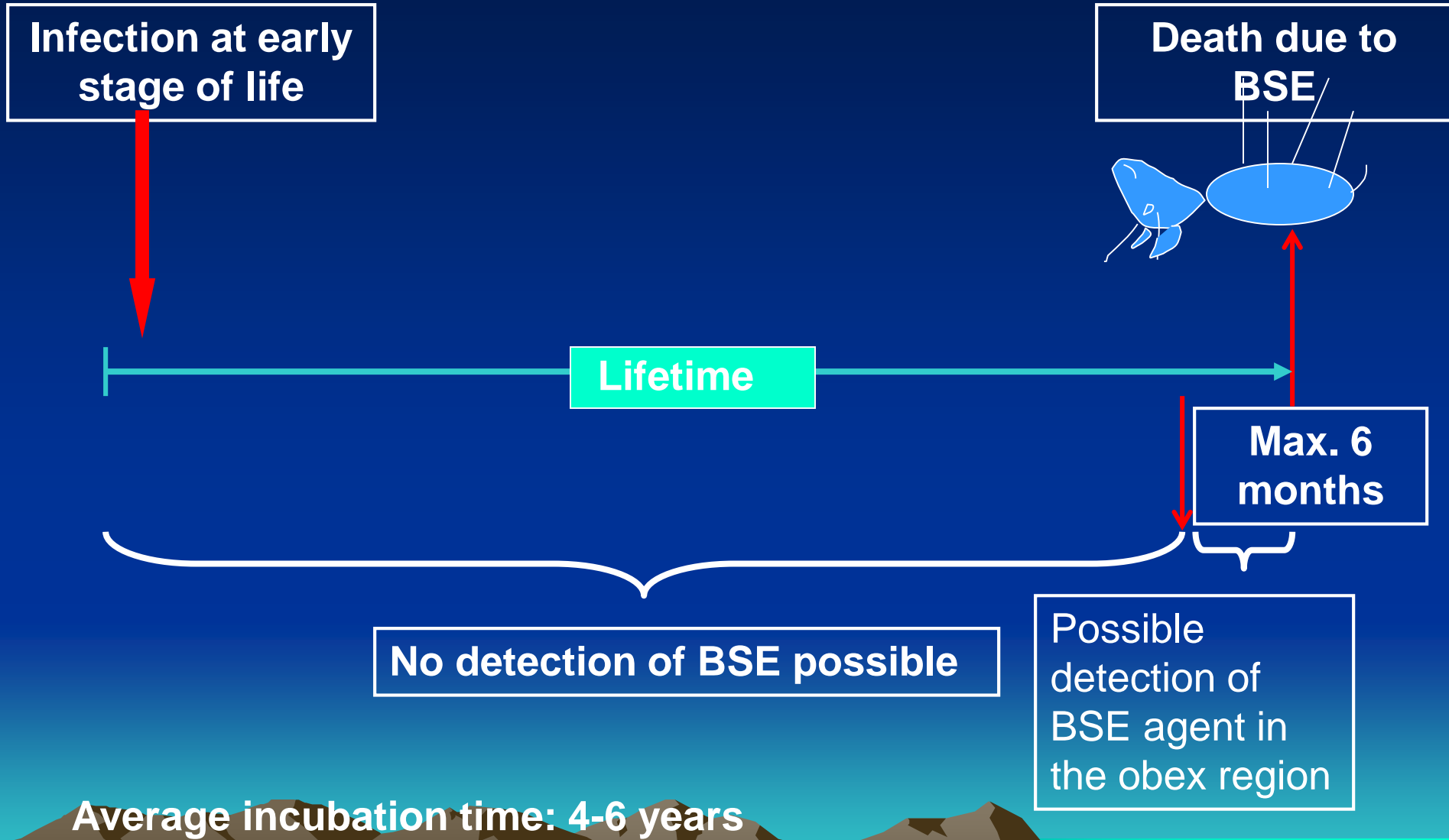


What are the lessons we gained from the national control programs of the following diseases?

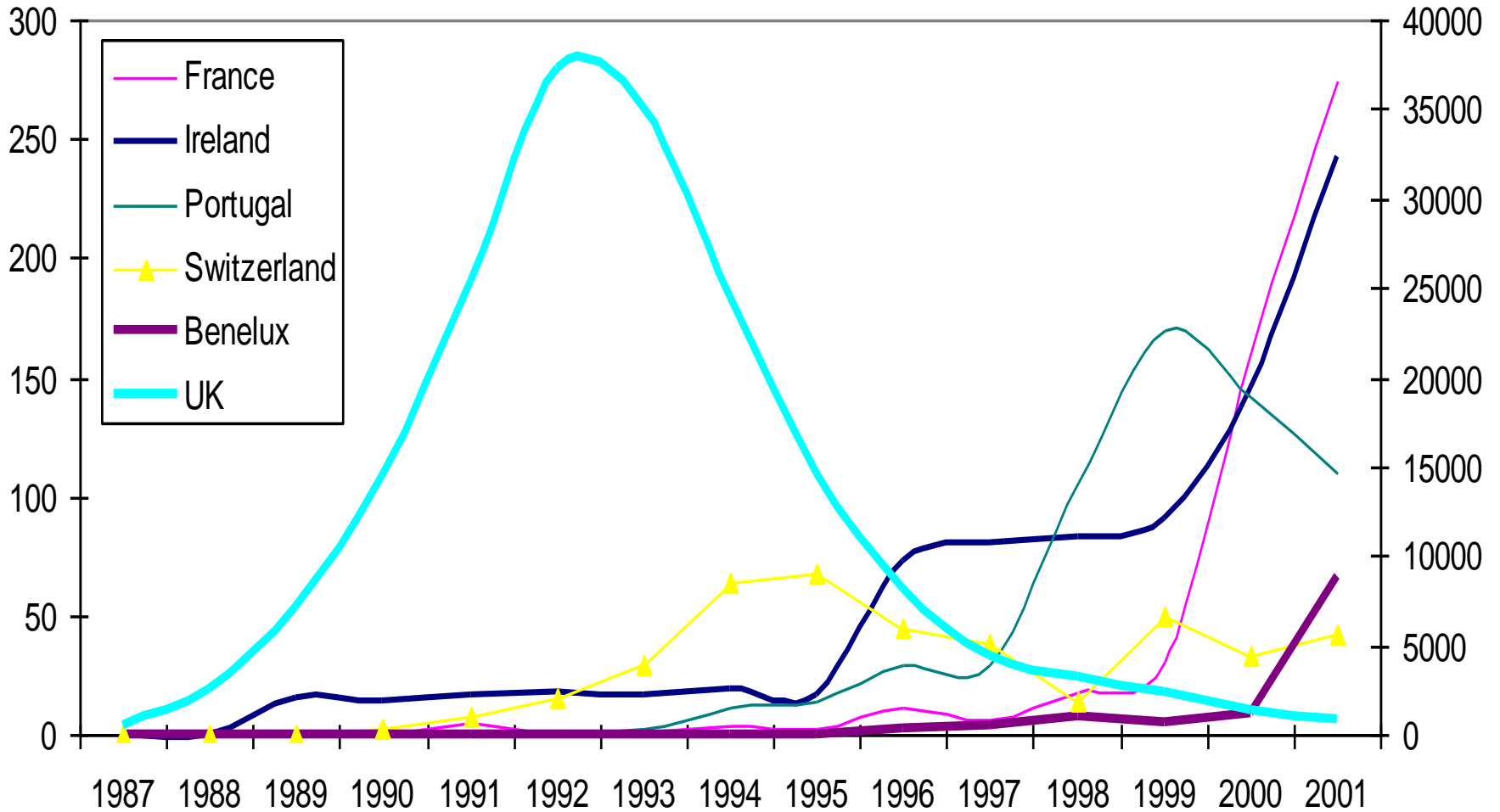
- BSE
- Rabies
- Emerging viruses



BSE-Infection

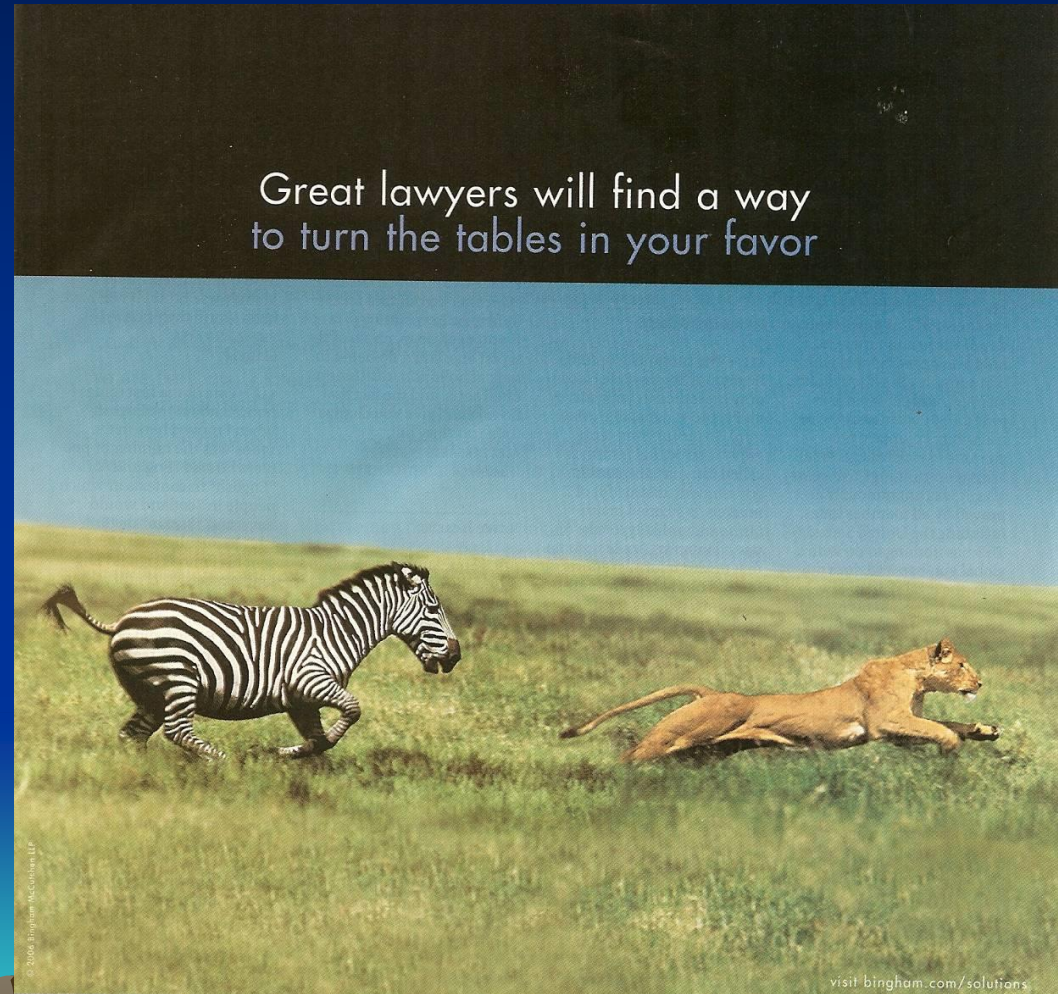


Development of BSE in Europe



Simulation Modelling

Approach to
Prediction,
Prevention and
Control for BSE in
Europe



Simulation modelling - Outcome

Predicting the Unpredictable

Graham F. Medley

Disease predictions have reached epidemic proportions (1–5). Predicting the course of a disease in a population certainly fulfills a morbid fascination, but predictions that vary by two or three orders of magnitude are, for all intents and purposes, meaningless. Three papers published this week by *Science* (1–3) attempt to predict patterns of disease caused by the infectious agent responsible for bovine spongiform encephalopathy (BSE) in cattle and sheep, and its counterpart in humans called variant Creutzfeldt-Jakob disease (vCJD). To date, there have been 111 confirmed cases of vCJD in the UK. In their analyses of the UK vCJD epidemic, Huillard d'Aignaux *et al.* (page 1729) (1) and Valleron *et al.* (page 1726) (2) use statistical approaches to predict future numbers of cases. Both groups predict a long incubation period, with the numbers of predicted cases varying from several hundred (2) to hundreds of thousands (1). In their study of BSE in sheep, Kao and colleagues (3) “retrodict” the past epidemic, their princi-

pal interests being the extent to which this epidemic has increased human exposure to the BSE agent and its current prevalence in sheep. They predict fewer than 20 clinical cases of BSE in sheep this year (assuming a maternal transmission rate of 10%), but retrodiction of the peak number of infections varies between 25 and 25,000 (3). In each study, the width of the confidence intervals (or range of outcomes from different scenarios) can only be described as unhealthy. Why can't we do better?

In essence, the calculation is simple. The numbers of vCJD cases diagnosed during 2002 will be a convolution of the time of infection and the incubation period distribution (IPD), expressed as [(number infected in 1987) × (probability of progressing to disease during 15th year after infection)] + [(number infected in 1988) × (probability of progressing to disease during 14th year after infection)] + (etc.). Age, sex, and genetic predisposition to infection are among the factors that might complicate this relationship, but they do not change it.

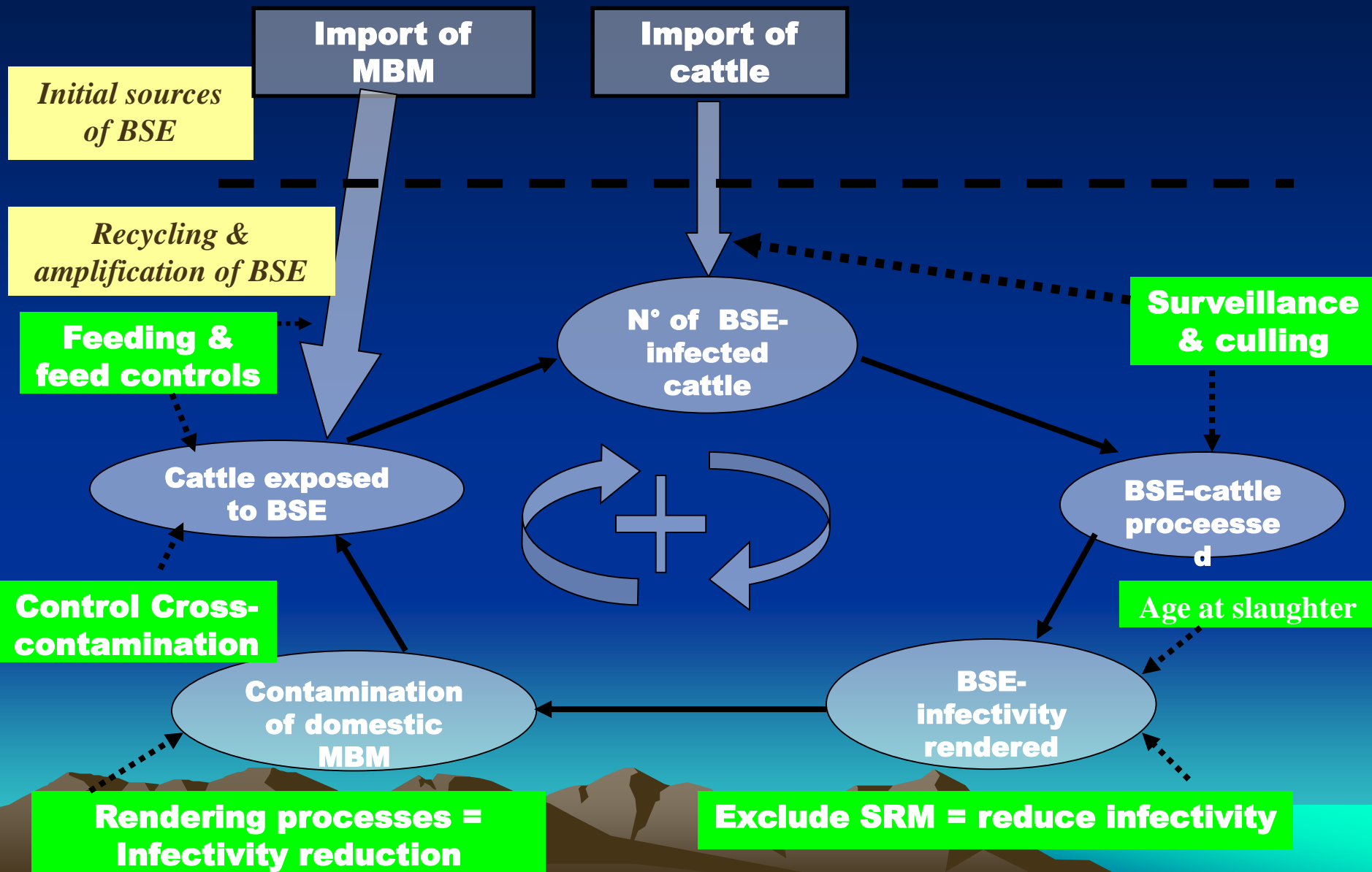
Knowledge of any two of these three quantities (time of infection, IPD, and number of cases) allows the other to be estimated. For the current vCJD epidemic, we

know neither the numbers infected nor the IPD in humans. In order to make predictions, one must be able to estimate these values simultaneously from case data, which is clearly impossible. For example, the current case data could have arisen from a small number of infections and a short IPD (predictions will be small) or a large number of infections and a long IPD (predictions will be large). Pick a prediction, and a suitable choice of infection rate and IPD will justify it. In contrast, accurate predictions of AIDS in the UK were possible because the pandemic was asynchronous. In that case, estimates of the IPD were available from cohort studies in which the time of infection of individuals was known or could be imputed, and infection times predated the UK epidemic [e.g. (6)].

Several approaches have been adopted to overcome these problems (1, 2, 7), but they require that strong assumptions be made. First, universally, the IPD is described as a parametric function. More cautious investigators have used extremely flexible functions (with large numbers of parameters) and have performed sensitivity analyses to extend the range of their predictions. However, any IPD estimate is conditional on the observed data, and the IPD is an (unsupported) extrapolation with no supporting data (8). Second, demography curtails the upper end of the prediction range: More than 5 million people have died in the UK since 1990 from non-vCJD causes, but some of them would have been infected.

The author is in the Ecology and Epidemiology Group, Department of Biological Sciences, University of Warwick, Coventry CV4 7AL, UK. E-mail: graham.medley@warwick.ac.uk

BSE/CATTLE SYSTEM





Contents lists available at SciVerse ScienceDirect

Preventive Veterinary Medicine

journal homepage: www.elsevier.com/locate/prevetmed



Geographical BSE risk assessment and its impact on disease detection and dissemination

Mo Salman^{a,*}, Vittorio Silano^b, Dagmar Heim^c, Joachim Kreysa^d

^a Campus Stop 1644, Animal Population Health Institute, College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins, CO 80523-1644, USA

^b European Food Safety Authority (EFSA), Largo Natale Palli 5/A I, 43100 Parma, Italy

^c Swiss Federal Veterinary Office, Schwarzenburgstr. 155, 3097 Bern-Liebefeld, Switzerland

^d European Commission, Joint Research Centre, Institute for Health and Consumer Protection, Via Enrico Fermi, Ispra (VA), Italy

ARTICLE INFO

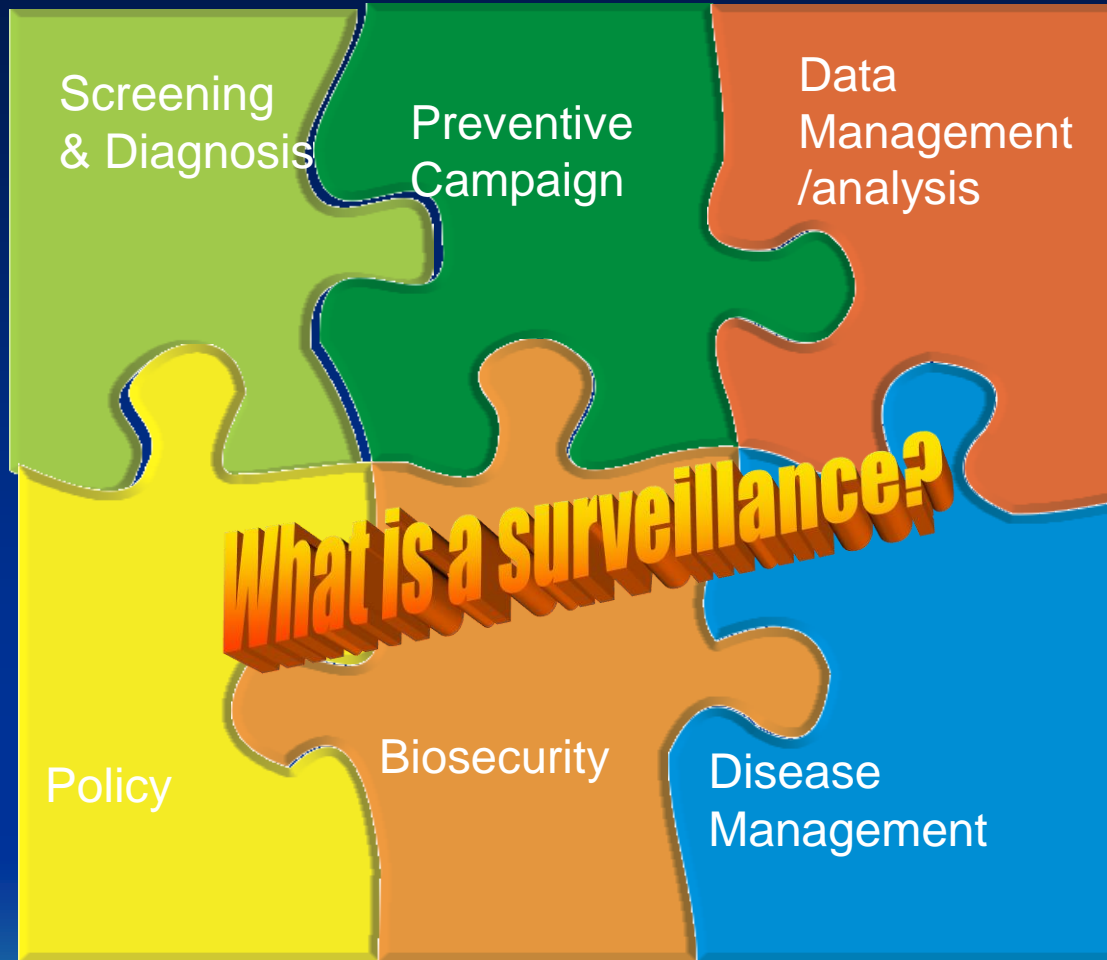
Keywords:

BSE
Risk assessment
Geographical risk assessment
TSE

ABSTRACT

Bovine Spongiform Encephalopathy (BSE) rapidly evolved into an issue of major public concern particularly when, in 1996, evidence was provided that this disease had crossed the species barrier and infected humans in the UK with what has become known as “variant Creutzfeldt Jakob Disease” (vCJD). The aim of this paper is to describe the European Geographical BSE risk assessment (GBR) that was successfully used for assessing the qualitative likelihood that BSE could be present in a country where it was not yet officially recognized. It also discusses how this can lead to risk-based and therefore preventive management of BSE at national and international levels.

Lesson gained – BSE



Lessons gained

- Risk assessment is a critical component of the entire risk analysis in epidemiology;
- Risk assessment is not qualified to be labeled as a discipline. It is an integration of several approaches;



Lessons gained

- Animal health risk analysis cannot be done without surveillance data and observations;
- Understanding the means of disease transmission require observations through the surveillance system;
- Mitigation measures require knowledge about the effectiveness of these measures.

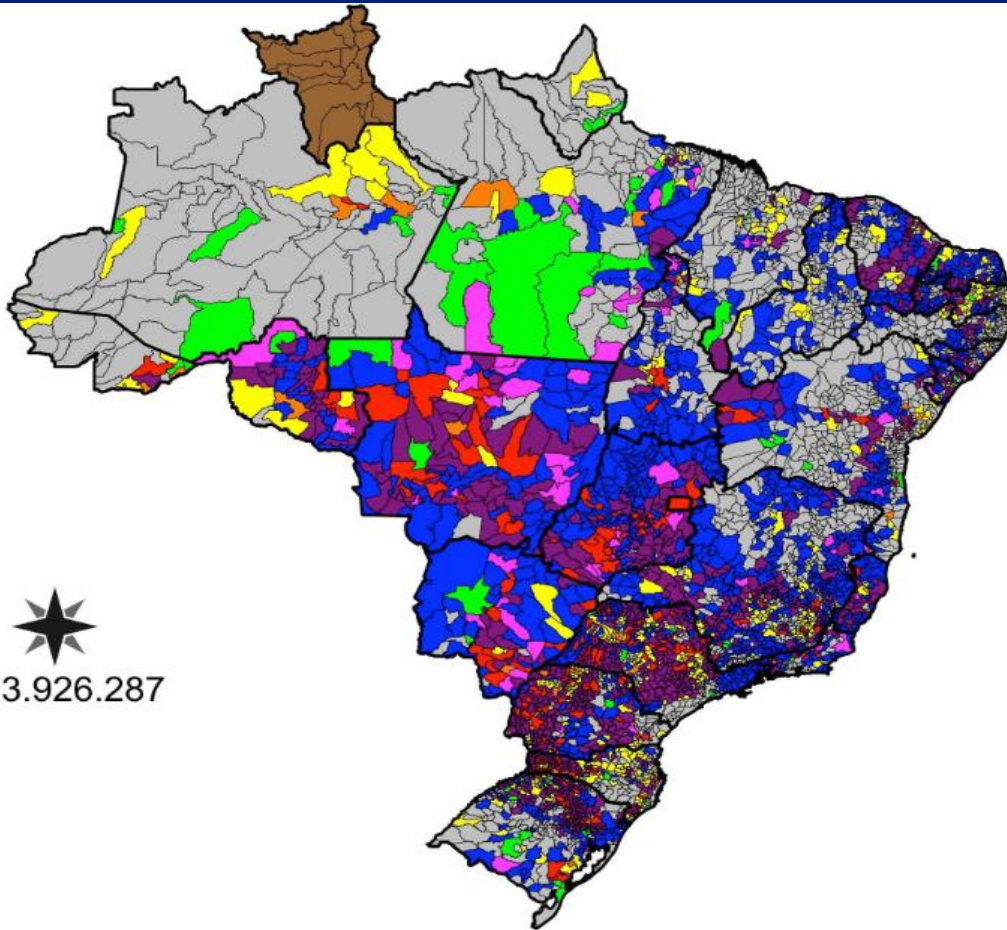


Lessons gained

- Reporting outcomes from a surveillance system is an essential step in maintaining the interest in the surveillance.
- Database management of surveillance data is NOT the entire surveillance system.



Risk factors in bovine feeding related to BSE - 2015



Risk	Description	Nº counties	% counties
A	Potential use of concentrate feeds to ruminants	1,538	27.6%
B	Potential risk of cross-contamination / poultry litter in ruminant feed	506	9.1%
C	Potential risk of contamination with MBM in ruminant feed	70	1.3%
D	A + B	1,290	23.2%
E	A + C	79	1.4%
F	B + C	46	0.8%
G	A + B + C	198	3.6%
H	No risk factor identified	1,829	32.8%
I	No answer	15	0.3%
Total		5,571	

Rabies – Challenging Questions

- Is it a NAHP or NPHP?
- How should priority for inclusion of rabies be assigned?
- Is rabies more important than brucellosis?
- Is the global interest more important than national interest?
- What is the link to trade?
- Is there a room for risk assessment process for a rabies surveillance system?

Prioritizing surveillance activities

A suggested approach



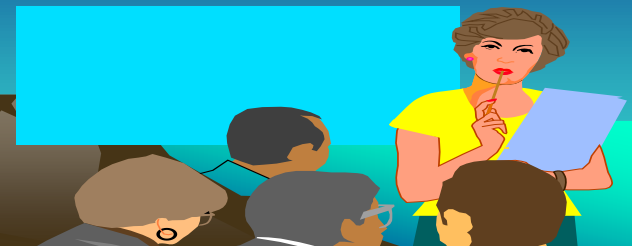
A proposal to prioritize diseases

- Based on scoring diseases considering a set of defined criteria including social and political interests
- Scores are assigned for each criterion using a matrix

COUNTRY	CRITERIA							
	Impact on trade							Likelihood of reproduction
	Public Health	Production impact	Feasibility of control	Animals	Products	Public perception	Social impact	
	Weights							
Scores	3	2	2	1	1.5	1.5	2	
H=3		D				D		1
M=2			D	D				0.5
L=1					D		D	0.25
N=0	D							0

Lessons gained

- The surveillance system should include an early warning system for unexpected events – **Effective communications with preparedness plans**
- Prioritizing of inclusion of diseases in a surveillance system should be assessed with prior established criteria agreed upon by all involved parties – **Buy in by all stockholders**



Emerging New Viruses– Challenging Questions

- Is it a NAHP or NPHP?
- How should priority be assigned?
- Is CCHF more important than lumpy skin disease?
- Is the global interest more important than national interest?
- Is there a room for Risk Assessment process for an emerging viruses surveillance system?



What are the roles of the following approaches in Emerging viruses?

- Spatial Analysis – **Hot spots!!!**
- Simulation models – **Lack of certainty;**
- Social and ecological science and tools – **Reliability of the data;**
- Genetic analysis of the isolated viruses – **Limitations in external validations**
- Surveillance data – **Limitations in current use .**



Genetic Analysis Vs. Surveillance Data for predicting virus emergence

Downloaded from <http://rsob.royalsocietypublishing.org/> on October 29, 2017

OPEN
BIOLOGY

rsob.royalsocietypublishing.org

Perspective



Cite this article: Geoghegan JL, Holmes EC. 2017 Predicting virus emergence amid evolutionary noise. *Open Biol.* **7**: 170189. <http://dx.doi.org/10.1098/rsob.170189>

Received: 2 August 2017

Accepted: 24 September 2017

Subject Area:
microbiology

Keywords:
emergence, evolution, phylogeny,
virus, spill over, virosphere

Predicting virus emergence amid evolutionary noise

Jemma L. Geoghegan¹ and Edward C. Holmes²

¹Department of Biological Sciences, Macquarie University, Sydney, New South Wales 2109, Australia

²Marie Bashir Institute for Infectious Diseases and Biosecurity, Charles Perkins Centre, School of Life and Environmental Sciences and Sydney Medical School, The University of Sydney, Sydney, New South Wales 2006, Australia

ECH, 0000-0001-9596-3552

The study of virus disease emergence, whether it can be predicted and how it might be prevented, has become a major research topic in biomedicine. Here we show that efforts to predict disease emergence commonly conflate fundamentally different evolutionary and epidemiological time scales, and are likely to fail because of the enormous number of unsampled viruses that could conceivably emerge in humans. Although we know much about the patterns and processes of virus evolution on evolutionary time scales as depicted in family-scale phylogenetic trees, these data have little predictive power to reveal the short-term microevolutionary processes that underpin cross-species transmission and emergence. Truly understanding disease emergence therefore requires a new mechanistic and integrated view of the factors that allow or prevent viruses spreading in novel hosts. We present such a view, suggesting that both ecological and genetic aspects of virus emergence can be placed within a simple population genetic framework, which in turn highlights the importance of host population size and density in determining whether emergence will be successful. Despite this framework, we conclude that a more practical solution to preventing and containing the successful emergence of new diseases entails ongoing virological surveillance at the human–animal interface and regions of ecological disturbance.

Modelling and decision making process

Epidemics 15 (2016) 10–19



Contents lists available at ScienceDirect

Epidemics

journal homepage: www.elsevier.com/locate/epidemics



Decision-making for foot-and-mouth disease control: Objectives matter



William J.M. Probert^{a,b,k,*}, Katriona Shea^{a,b}, Christopher J. Fonnesebeck^c, Michael C. Runge^d, Tim E. Carpenter^e, Salome Dürr^f, M. Graeme Garner^g, Neil Harvey^h, Mark A. Stevensonⁱ, Colleen T. Webb^j, Marleen Werkman^{l,k}, Michael J. Tildesley^k, Matthew J. Ferrari^a

^a Center for Infectious Disease Dynamics, Department of Biology, Eberly College of Science, The Pennsylvania State University, University Park, PA, United States

^b Department of Biology and Intercollege Graduate Degree Program in Ecology, 208 Mueller Laboratory, The Pennsylvania State University, University Park, PA, United States

^c Department of Biostatistics, Vanderbilt University, Nashville, TN, United States

^d US Geological Survey, Patuxent Wildlife Research Center, 12100 Beech Forest Rd, Laurel, MD, United States

^e EpiCentre, Institute of Veterinary, Animal and Biomedical Sciences, Massey University, Palmerston North, New Zealand

^f Veterinary Public Health Institute, University of Bern, Bern, Switzerland

^g Animal Health Policy Branch, Australian Government, Department of Agriculture, GPO Box 858, Canberra 2601, ACT, Australia

^h Department of Computing and Information Science, University of Guelph, Guelph, ON, Canada N1G 2W1

ⁱ Faculty of Veterinary Science, University of Melbourne, Melbourne, VIC, Australia

^j Department of Biology, Colorado State University, Fort Collins, CO, United States

^k School of Veterinary Medicine and Science, University of Nottingham, Leicestershire LE12 5RD, United Kingdom

^l Central Veterinary Institute, Wageningen University and Research Centre, Houtribweg 39, 8221 RA Lelystad, The Netherlands

Lesson Gained

- Simulation models – limited in controlling the diseases or infection but they can be great aid in the preparedness ;
- Genetic analysis has confused the issues – N1H5 lack of link to observational data ;
- Lack of scientific verifications for the proposed plan of action – Zika ;
- Surveillance data were either incomprehensive or data analyses were not utilized – MERS CoV

General Conclusions

- Surveillance system is the core of NAHP;
- Veterinary Public Services play major role in the social and economic wellbeing of a country;
- Scientific tools for assessment and implementation of disease control measures should be continued to be the drivers for reliable NAHP;



General Conclusions

- Simulation models are not predicator of health events; rather they are tools with limited applications in assessing control strategies;
- Simulation models should be treated with precautions and understanding their assumptions;



General Conclusions

- Epidemiology, risk assessment including risk communication are ONLY tools and should not be considered as the expected outcome for a reliable NHAP;
- Field observations, common sense, and practical approaches should be treated equally with scientific research findings;
- Academic curiosity is good and healthy dialogue but should not be considered as a solution for an adverse health event.

Any questions?

