

ESF Exploratory Workshop on

# New Approaches To Horizon Scanning For Emerging And Infectious Viruses In Europe

Egham (UK), 6-7<sup>th</sup> July 2010

Convened by:  
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## SCIENTIFIC REPORT

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## 1. Executive summary

Horizon scanning, as applied here, is the approach to predict the next virus to emerge in animal and/or public health, both in terms of its route(s) of transmission and its origins (i.e. country and source reservoir). The main aim of the workshop was to develop an approach to horizon scanning that not only drew together all possible pathways but also allowed for change in the key drivers in virus emergence, namely socio-economic, environmental (including climate) and wildlife. Expert opinion is typically limited to asking experts about known viruses. The next virus to emerge, however, may not even be in the text books as yet. Thus, many viruses discussed in the workshop were segmented RNA viruses which can evolve rapidly through genetic drift and shift to fill new niches created by change in routes, hosts and interactions. For this reason, there was considerable emphasis in the workshop on how to build in the potential for adaptation and evolution of viruses and also to predict the human immune response using neural nets, for example. The approaches discussed included genomic and proteomic technologies. Mathematical concepts of trait space and fitness in relation to reproductive ratio (R0) were considered in relation to the emergence of new infections.

The emergence of a new virus typically involves a combination of events. The introductory presentation raised the question of whether diseases such as BSE in cattle and transmission of highly pathogenic avian influenza (HPAI) virus to backyard chickens through frozen duck meat could have been predicted if persons with the appropriate expertise had been “gathered together in a room beforehand”. Predicting the emergence of new viruses is complicated by the involvement of complex chains of events (so called complex scenarios). An example of a complex scenario was given; namely the collapse in vulture populations (due to misuse of a veterinary drug) leading to an increase in cattle carcasses which provided food for feral dogs, which in turn increased in abundance leading to an increase in dog bites and hence the risk of rabies transmission to humans.

The approach to horizon scanning for viruses developed in the workshop is exploratory and novel. The development and use of spidergrams to generate the complex scenarios is central to the horizon scanning process. The spidergrams are produced by randomly linking factors which may directly or indirectly affect the emergence of diseases. The factors were chosen from a database under eight header categories (as defined by the participants). These were:-

1. Human demographics and behaviour/biology
2. Socio-economic
3. Non-human biology
4. Habitat use
5. Environmental factors/Climate change
6. Political
7. Technology/Medical Care/Medicine
8. Farming practice.

Many thousands of scenario chains can be produced by this method and most may be irrational. However, the approach enables the testing of combinations not previously considered but which would be tested in nature. The workshop sought to consider approaches to test the various chains and thereby identify new routes and pathway combination scenarios of potential significance in the emergence of new viruses.

There were three primary outputs from the workshop:-

- 1) development of a prototype data base of factors (under the eight header categories listed above)
- 2) generation of prototype spidergrams for selected viruses using the factors in 1)
- 3) consideration of mathematical approaches to apply to 1) and 2)

The outputs were obtained through participants contributing to breakout groups. The workshop brought home the importance of taking a global perspective and considering wildlife, food and environmental reservoirs. The workshop emphasized the wide variety of interacting factors in the emergence of viruses, and the spidergram approach provided a framework for tracing all elements of the complex pathways. During the breakout groups, spidergrams were developed for five viruses, namely Nipah virus, avian influenza virus, hantavirus, Dengue fever virus and hepatitis E virus. The generation and mathematical analysis of spidergrams during this two day workshop gave some notable results:-

- 1) provided an insight as to how spidergrams could be useful for developing case-control studies for diseases with no obvious reason for certain epidemiological observations. For example, there are numerous potential reasons why hantavirus prevalence increases in the elderly. The break-out group on hantavirus used the spidergram to identify new reasons and routes for exposure and susceptibility of the elderly to hantavirus. Those routes could be used to fine tune and design a questionnaire for a case control study.
- 2) Demonstrated how Nipah virus emergence *could* be linked to temperature through a range of seemingly unrelated factors including migration, deforestation and war.
- 3) In terms of mathematical analysis, one approach is to look for critical feedback loops in the scenario chains. These give non-linear dynamics. A useful way to present the risk for a given scenario is to determine how many "links away" the scenario is from human-to-human transmission, for example. This is similar to looking for ecological niches which are waiting to be filled by an emerging virus.

Overall the participants were very positive about the proposed approach which provides a framework for how different factors could interact, irrespective of the disease. The spidergram approach developed here could be set up as a web forum where participants add to a universal set of factors and upload their spidergrams for other researchers to build on or use. This was not discussed at the workshop but could be taken forward with ESF. It was agreed that the convenors would write and publish an opinion (or paper) to take the approach forward.

The meeting was held at Royal Holloway, University of London, Egham over two days (6/7 July 2010). Participation numbered 22 people for 10 countries. Each day included a series of presentations by experts followed by break-out groups in which the expertise and ideas of the participants were gathered. The first day of the workshop focused on the biological/virological aspects and was devoted to the development of spidergrams to link complex scenarios for the emergence of new viruses. The focus was on the combination of seemingly unrelated events. The second day explored mathematical approaches to process and interpret those spidergrams. Additional informal interaction and discussion took place in the working lunches and also over dinner and in the bar afterwards.

## 2. Scientific content of the event

Examples of complex chain scenarios given in the introductory talk include the decline of vultures (due to the drug dichlofenac) in India resulting in an increase in dog bites (due to increased dog abundance through supply of cattle carcasses meat). Other examples included the increased transmission of West Nile virus through stagnant swimming pools becoming mosquito breeding sites in the USA after the economic crash and the increase in house repossessions. A new complex chain was presented based on the retreat of glaciers (due to climate change) on the island of South Georgia allowing rats to gain access to seabird nesting areas. The resulting decline in giant petrel and skua numbers may result in dead seal carcasses littering the beaches which together with warmer conditions may result in botulism outbreaks.

Day 1 of the workshop, which focused on the ecological/virological factors highlighted the following points:-

- 1) The need to consider food-borne transmission in any emerging virus. Most new viruses have a foodborne link, (e.g. SARS virus, filovirus in pigs, Nipah virus (through palm oil) and hepatitis E virus). The increasing demand for animal protein may shift food production to the undeveloped world. A potential concern is Reston Ebola virus in pigs. Nipah virus can be transmitted through food, and person-to-person transmission of Nipah virus is a high concern.
- 2) The need to consider spread on a global scale even in local markets. For example outbreaks of a herpes virus in French oysters (from a change in the way oysters were produced) have resulted in the French importing oysters from China, Japan and Korea. These contain different noroviruses and the possibility of recombination could generate virulent strains to which Europeans are immunologically naive.
- 3) The interaction of seemingly unrelated events. In Africa, outbreaks of RVFV related to climatic conditions result in losses of large numbers of sheep so the local populations resort to eating bush meat (e.g. fried fruit bat meat).
- 4) With regard to pathogen emergence there is a close relationship between human, wildlife and livestock populations. Wildlife biodiversity is a source of emergence of zoonotic diseases. While

wildlife are undoubtedly sources of viruses, there is evidence that high local biodiversity reduces zoonotic transmission of hantavirus in Panama and also West Nile virus in the USA. Biodiversity is also important within an organism. The concept of the microbiome within the human gut was presented with reference to molecular warfare between the different bacteria. Emergence of more pathogenic microbes or antibiotic resistant strains through falls in biodiversity in the gut should be considered.

5) Transmission routes for rodent borne diseases include vectors, excreta, bites, direct contact and consumption of rodent meat (bush meat). General predictions on the emergence of rodent-borne pathogens are difficult, even impossible, because of the complexity of interactions between them, their reservoirs and the biotic and abiotic environment. These include masting, landscape structure, fragmentation and landscape changes and biodiversity. Some rodent viruses have no clear host, but others co-evolve with one host species. Outbreaks of a certain hantavirus associated with a single rodent host in a certain part of Germany in 2007 and 2010 correlate with fruiting of beech trees in -1yr which correlates with climatic variables (summer and autumn temperature) in the -2yr.

6) The outbreak of chikungunya virus in Italy demonstrates how globalisation of trades and trans-continental movement of people spread vector-borne disease. The speaker outlined how the globalisation of vectors and the globalisation of virus lead to a dangerous combination. Furthermore that outbreak also demonstrated how vectors (notably the mosquito *Aedes albopictus*) can adapt to new environments and how arboviruses can adapt to new vectors.

7) Emergent viruses in European pigs include pestiviruses, influenza A virus, porcine reproductive and respiratory syndrome virus, Foot-and-mouth disease virus and hepatitis E virus (HEV). For an emergent infection the virus has to transmit under new circumstances, e.g. a new host species or a new route. Evolutionary changes in traits of viruses are at the heart of the process. A virus transmitting in a new situation is already different from the dominant type. Further adaptation to the new situation will occur subsequently. It is important to understand how selection works and what the  $R_0$  is under the new circumstances. The  $R_0$  for pig-to-pig transmission of HEV is 8.8.

8) Recently two flaviviruses, namely Usutu virus and West Nile virus (WNV), have emerged in places where they were not previously known. Since 1999 WNV has swept across the USA and then into Argentina using new mosquito vectors and bird hosts. Flaviviruses infect a range of animal species including frogs, crocodiles, humans and horses. There are 62 known species of mosquito vector. Birds (crows and blue jays) are the first to die during an outbreak, but only 2/3 weeks in advance of humans. It is estimated some 1 million individuals were asymptotically infected with WNV in the USA. This created a potential problem for blood transfusion. Quarantining birds no good because mosquitoes get through cages. Introduction of WNV into Europe may be due to ticks on birds. Ticks survive for longer than mosquitoes. High temperatures were an important factor in the lineage 2 WNV outbreak spreading through Europe. Dead falcons and goshawks were indicators.

9) The workshop highlighted the issue of changes and creating new niches waiting to be filled by an emerging virus. For example, in the human immunodeficiency virus (HIV) epidemic there was an increase in herpes cases preceding the HIV epidemic consistent with changes in sexual behaviour.

10) There are some 1,400 species of bats worldwide. There is huge biodiversity and bats are important for pollination, seed dispersal and insect regulation. Bats in Texas ingest pests of cotton crops and corn and over the season save the industry one spray of the crops with pesticide. Not many species have been tested for Nipah virus, and other species could be reservoirs.

Day 2 of the workshop, which focused on the mathematical aspects highlighted the following points:-

1) When a nuclear weapon was lost in a plane crash in North Carolina (Broken Arrow) five of the 6 safety devices failed. This represents the non-linearity of the perfect storm. The focus for complex scenario chains should therefore be on how many links a system is away from the perfect storm. Percolation thresholds and clustered networks vs. random could also be considered.

2) The complex scenarios should take into account seasonal effects. This was illustrated with H3N2 antigenic drift and population susceptibility. The proportion of population which is susceptible depends on whether the virus is similar to last year's, which depends on the antigenic drift. Fade out is because of diminution of susceptibles. If there are more susceptibles the epidemic is early. The probability of developing symptoms is greater if the epidemic is late (Oct/Nov) because of low susceptibility at the beginning of the season.

3) Data driven predictions of how immunologically prepared we are and how susceptible is the population to a new virus. Predictions of the fit for presentation of AI peptide sequences (nonopeptides) by the MHC II can be made. This can allow for the screen for resistance to emerging

viruses. Virulence could be predicted using neural nets if we had 100 examples of a virulent virus and a 100 examples of a non-virulent virus.

4) Ecological changes may lead to increases in  $R_0$ . Other factors include density, migration, host heterogeneity, behavioural changes and changes in ecological community structure. For more heterogeneously dispersed populations, there is less chance of emergence compared to homogenous populations. Adaptation allows the emergence of mal-adapted pathogens.

The mathematics session of the workshop revealed some basic but fundamental points of prediction and horizon scanning. Firstly, disease outbreaks and disease emergence are a mixture of chance and necessity, or in the jargon of mathematical modelling, have stochastic and deterministic aspects. To fully evaluate and appreciate the possibility of a future event, both these aspects need to be taken into consideration.

In how far can we predict the emergence of a disease, and in how far are such predictions useful and practical? It is tempting to take past events as a guide and organise our thinking around historical outbreaks. We can, in retrospect, always argue that we should have been able to foresee a certain particular event. For horizon scanning the issue is not if we could have foreseen one particular event, but what the likelihood of a particular event is to take place. This is useful because if there are a large number of events that all can happen with a small and roughly similar probability it is not realistically possible to identify certain scenarios that should be heeded more than others. Under such a scenario it is also unlikely we can learn much about what the next event is from past events. In contrast, if a particular event is much more likely than others we can identify this event as one that is waiting to happen, and if needed, attempt to put measure in place to prevent it.

A further observation is that for a disease to appear or reappear, there are two possible factors that matter. Firstly, the environment (in the wider sense) can have changed and this could have been one of the main causes that triggered the emergence. Secondly, a disease outbreak is in itself a process that, even if the environment is conducive to this, need not happen. It is essential to be aware of this, and this dichotomy is helpful in organising predictions. Such predictions are difficult, but not necessarily impossible. A methodology for horizon scanning could start with deconstructing changes in the environment into chains of smaller events. If we can assess what the probability that sequences of small chances take place, we can in this way assess the likelihood that the complete chain of events takes place. This is a first step that should be taken in assessing plausible future scenarios. Once this is done, it is important to consider what the probability is that a disease actually emerges under this scenario. This can be done using existing techniques, for instance through the assessment of the reproduction number of a disease.

### **3. Assessment of the results, contribution to the future direction of the field, outcome**

The horizon scanning approach set out to the participants was novel and innovative and drew from the use of “cut-up techniques” by music artists to write song lyrics. In the “cut-up” technique multiple texts are cut up into smaller portions at random and rearranged to create a new text. According to Wikipedia the synthesised work often results in surprisingly innovative new phrases. In the “fold-in” technique, two different sheets of linear text, and cut in half and combined with the other. The resulting text is often a blend of two themes, somewhat difficult to read. In the workshop, the participants were given the tasks of creating the texts, and then randomly combining the texts to give a series of pathways, called spidergrams. The texts were lists of factors, events and changes that may (directly or indirectly) affect the risk of disease transmission.

#### **3.1 Development of a prototype database of factors (under eight header categories)**

The participants were asked (as a group) to propose eight header categories for the various factors which could affect disease emergence. That process was facilitated by a brain storming in which the group was asked to think up specific factors affecting disease with discussion on which header category they should fall under. The results of the brain-storming are set out in Appendix 1. The eight header categories were:-

1. Human demographics and behaviour/biology
2. Socio-economic

3. Non-human biology
4. Habitat use
5. Environmental factors/Climate change
6. Political
7. Technology/Medical Care/Medicine
8. Farming practice.

Eight flip charts were then set up, one with each of the above headers, and the participants randomly broke out into groups of 4/5 and visited each flip chart in turn filling in as many examples as they could think of under the header. The break-out process lasted for 30 minutes. The results are set out in Appendix 2.

### **3.2 Generating spidergrams**

The convenors then set out how factors from the different categories could be combined. By systematically taking one factor from each category and combining with one factor from another category and so on, thousands of complex scenarios could be generated. An illustration of how this could work was presented by the convenors (Figure 1). While most could be meaningless, some could give insights. This was illustrated using the example of decreasing vultures and increasing dogs. The resulting spidergram is shown in Figure 2, with combinations of factors shown as branches. The participants were then asked to form groups of 4/5 for the next break-out session. In the interests of time, a “seed virus” was used for each of the five groups of participants. Each group had at least one expert on the selected virus. The five viruses chosen were avian influenza virus, nipah virus, hepatitis E virus, an arbovirus (Dengue fever) and a hantavirus. It was proposed that each group should start with an anthropogenic or environmental factor (e.g. temperature). The factors should then be linked into a spidergram.

The spidergram for Nipah virus is shown in Figure 3. Temperature may in theory affect all the other factors (shown in Figure 3), leading to desertification, migration, poverty and affecting the level of pig biosecurity. Host behaviour in Figure 3 could include people eating bats (as bush meat) given a collapse in livestock after a disease such as Rift Valley fever initiated through changes in climatic conditions (Ref. Prof Koopmans’s presentation). Nipah virus (and its ability for person-to-person spread) was high on the list of viruses of concern according to Prof. Koopmans. The conclusion of Figure 3 that climate could affect emergence of Nipah virus is of interest and has not been documented.

- **Zoological**
  - Increase in rodents
  - Increase in insectivorous birds
  - Decline in amphibians
  - Increase in mosquitoes
  - Fall in wildlife biodiversity
  - Fall in dragonfly abundance
  - Increase in ectoparasites (ticks)
  - Increase in insects
  - **Collapse of a scavenger species**
- **Farming practice and husbandry**
  - Change in breeds
  - Intensity of farming
  - Expansion of livestock farming into new habitats
  - Mixing of sheep and cattle
  - **Failure of livestock carcass disposal**
- **Sustainability**
  - More households with livestock
  - Wood taken from corpses for burning
  - More allotments
- **Environmental and climatic**
  - Flooding
  - Warmer soil temperature
- **Land use**
  - Loss of ponds and marshes
  - Fragmentation of landscapes
  - Deforestation
- **Ecological**
  - Increase in feral dogs
  - Increase in vector breeding sites
  - Exposure of pigs to bat
- **Anthropogenic/ Socio-economic**
  - Generation of stagnant water bodies (swimming pools, poor plumbing, temporary water storage)
  - Increase in wind turbines
  - **Veterinary drugs and pesticides**
  - Increased globalisation and transport
  - Failure of drinking water treatment and sewage treatment
  - Failure of power supplies
  - Property maintenance
  - Eating more vegetables

Figure 1 : Linking of factors from different category groups – example used by convenors

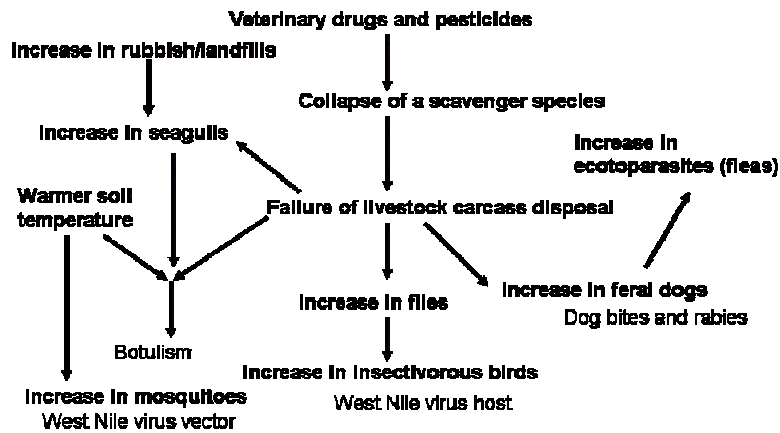


Figure 2 : Spidergram approach as presented by convenors

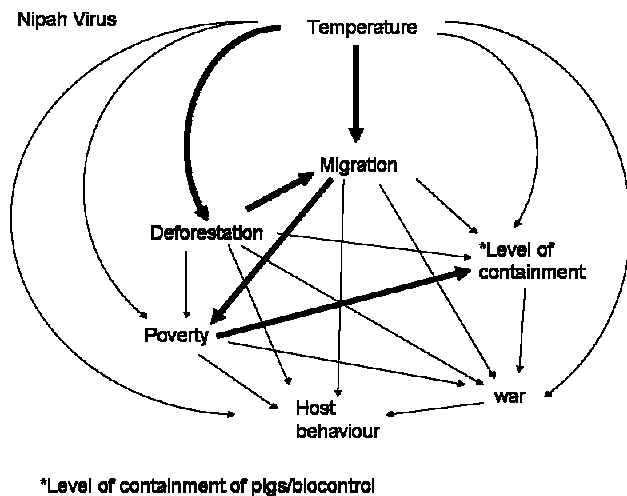


Figure 3: Spidergram generated by participants for Nipah virus

One approach that was developed in the workshop was the use of a table to compare pair-wise each combination of factors. This would allow an assessment of the rationality of paired linkages with respect to the virus under consideration. This is set out in Table 1 for Nipah virus. Paired linkages which are irrational would break a chain.

**Table 1 : Effect of pairwise linkages with respect to Nipah virus. For each pair the factor listed in the left hand column is the primary driver in the linkage, and the factor in top row is the factor that may be affected.**

Secondary	Migration	Level of containment	Temp	War	Host behaviour	Poverty	Deforestation
Primary							
Migration		+	NA	+?	+	+	+
Level of containment	NA		NA	NA	+	↓	NA
Temperature	+	+		+	+	+	+
War	+	+	NA		+	+	+
Host behaviour	NA	+	NA	NA+		+	NA
Poverty	+	+	NA	+	+		+
Deforestation	+	+	+	+	+	+	

For hantavirus, increased seroprevalence is observed in elderly people. The spidergram for hantavirus is set out in Figure 4 and identifies a number of factors which could result in greater exposure or greater susceptibility of the elderly to the disease. The spidergram produced for avian influenza virus (Figure 5) focussed on the link between organic food production, meat consumptions and farm and poultry density and on the generation time of the virus. In the case of hepatitis E virus (Figure 6) the group started by discussing what was known about the virus. Then factors were added in to the spidergram. For example, extreme events such as flooding could cause pig slurries to spread over fields and into water courses and also may affect movement, transport and mixing of pigs. Poverty/wealth affects the consumption of meat and the exposure through living in small farms close to livestock or going into woods. Reforestation may affect the distribution of wild boar. Liver transplants and also xenotransplantation from pigs were added in together with pregnant women who are at risk of death if infected with hepatitis E virus. The spidergram for dengue fever virus (Figure 7) focussed on travel, education and policy in the socio-economic category.



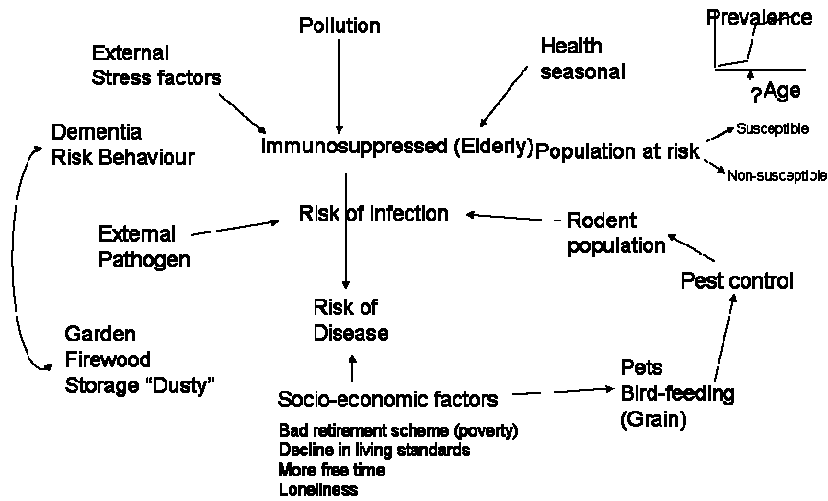


Figure 4: Spidergram generated by participants for hantavirus

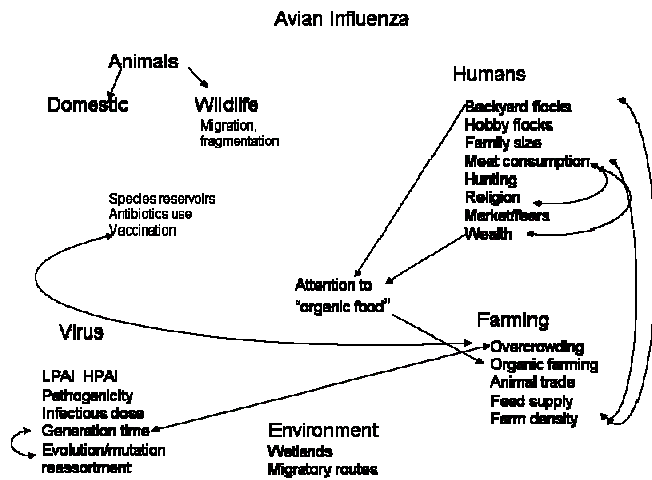


Figure 5: Spidergram generated by participants for avian influenza virus

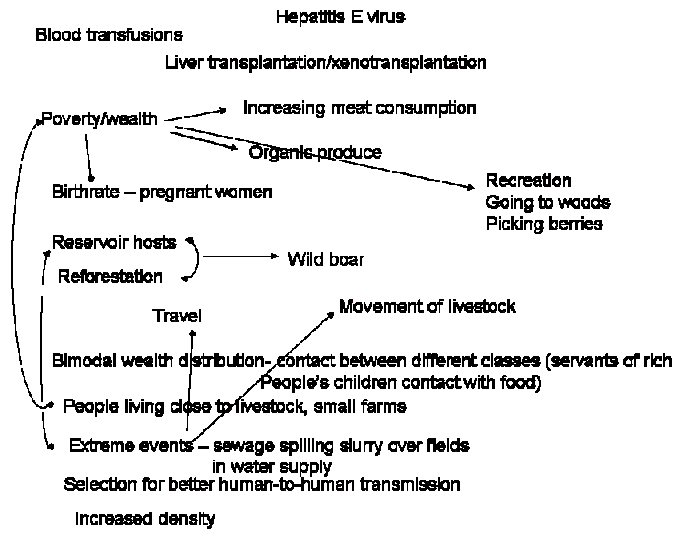


Figure 6: Spidergram generated by participants for hepatitis E virus

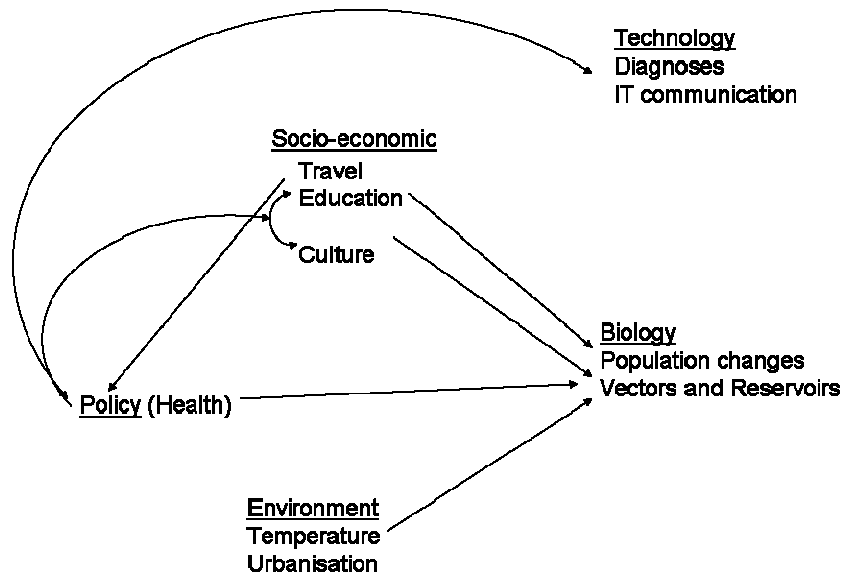


Figure 7: Spidergram generated by participants for dengue fever virus (Arbovirus)

### 3.3 Mathematical approaches

A strategic mathematic approach to model the impact of temperature on Nipah virus (Figure 3) was based on the household models developed for avian influenza virus (AIV) (Dr Michiel van Boven's presentation). This is set out in Figure 8. Person-to-person contact within households and between households through schools could be modelled as for AIV. Stochastic rates of contacts between humans and pigs could be used (e.g. humans frequently visit pig pens with 5- 10 pigs per pen). Temperature could increase the airflow in the pig house, is a driver for bat abundance and would affect environmental transmission of the paramyxovirus. Temperature could also affect the contact rates between pigs and bats.

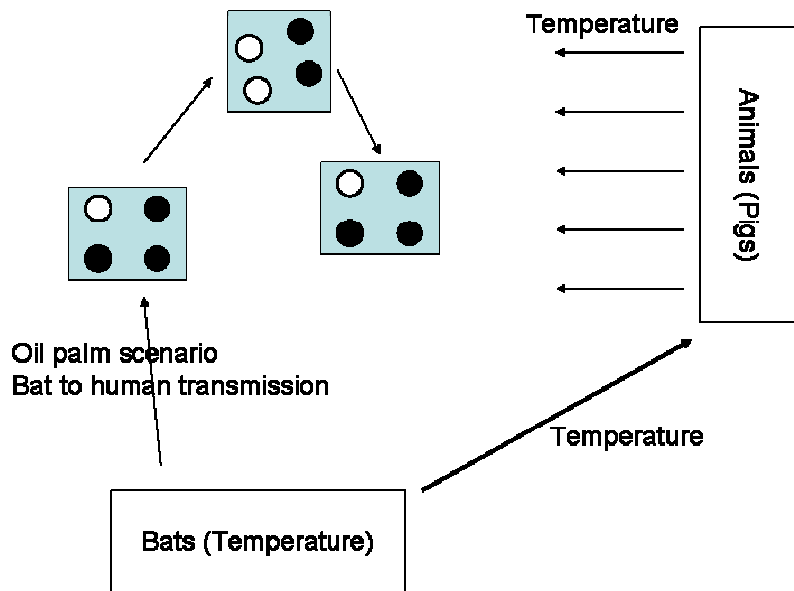
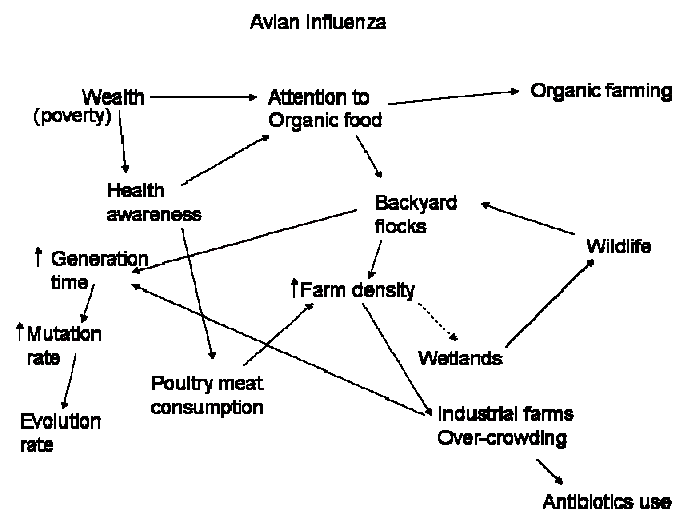


Figure 8: Framework for strategic household model for Nipah virus. Blue squares represent households and circles individual persons; filled infected, white susceptible.

In the case of hantavirus it is not clear why sero-prevalence increases in the elderly. The spidergram for hantavirus is set out in Figure 4 and identifies a number of factors which could result in greater exposure or greater susceptibility of the elderly to the disease. Designing a questionnaire is complicated by the fact that there are so many potential routes, many of which may be unknown at present. The spidergram approach, however, could help formulate previously unconsidered routes. In a slightly different approach, the group on hantavirus proposed using the spidergram to rationalise and develop the questionnaire in a case control study. This would aid data gathering. Furthermore the spidergram could then be improved from the risk factor analysis giving a feedback.



### **Figure 9: Pathways for avian influenza virus – the possibility of feedback loops would give non-linear dynamics**

The mathematical approach for avian influenza focussed on identification of potential feedback loops (Figure 9). These would give non-linear dynamics. Other parameters (e.g. proportion of wetlands and distribution of wealth) are constant input parameters. A critical feedback loop could involve risk perception during an AI outbreak which affects poultry meat consumption and health awareness which feeds back into industry structure and backyard flocks.

### **3.3 Contribution to the future direction of the field**

The approach to horizon scanning for viruses developed in the workshop is exploratory and novel. In terms of future direction it was felt by many of the participants that more work was needed before it could be taken forward into a Research Networking Programme (under ESF). It was agreed that the convenors would write and publish an opinion (or paper) to take the approach forward.

Overall the participants were very positive about the proposed approach which provided a means of brain-dumping and tracing all the elements of an invasive pathway. The approach provides a framework of how different factors could interact, irrespective of the disease. This could be generic in the first instance, and then the disease is slotted in. Work which could be taken forward would be to look at a whole series of pathogens and develop a universal set of terms. This would in effect build on the eight categories developed in the workshop producing a completed set of data terms. A structured approach could then be applied to generating the complex scenarios. Future work could include pattern recognition and recognition of the impact of small changes. The various factors may be collapsed down as some factors are seen to become redundant and tenuous connections are strengthened through identification of another factor. The approach may enable a database of disease patterns to be generated which could help to identify new combinations and routes, and in particular, what is connectable, for example car tyres and mosquito eggs. There may be role for neural nets to identify patterns.

At the very least the horizon scanning approach presented here could be applied to current emerging pathogens and developed to identify new pathways from tenuous links. This would give a framework of how the various factors overlap. The spidergrams could also be used to identify potential feedback loops which give non-linear dynamics and are important for perfect storm scenarios. Moreover the spidergram approach could be used in designing questionnaires for case-control studies as set out here for hantavirus where many of the reasons and routes are unknown. The concept is set out here and can be applied. Indeed in the convenors' opinions, this approach could be set up as a web forum where participants add to a universal set of factors and upload their spidergrams for other researchers to build on or use. This was not discussed at the workshop but could be taken forward with ESF.

## 4. Final programme

### 6<sup>th</sup> July (Tuesday, 06) 2010

- 09:30-10:30 Registration and *Coffee / Tea*
- 10:30-10:45 **Welcome and introduction by convenors**  
**Dr Paul Gale and Prof Vincent Jansen** (VLA, Addlestone, UK and RHUL, Egham, UK)
- 10:45-11:00 **European Science Foundation**  
**Dr Paul Gale on behalf of ESF** (RHUL, Egham, UK)
- 11:00-12:15 Morning Session:**
- Factors affecting emergence of diseases with consideration of whether their emergence could have been predicted**
- 11:00-11:30 **A view on viruses in food and the environment**  
**Prof Marion Koopmans** (National institute for public health and the environment, Bilthoven, Erasmus Medical Centre, Rotterdam, The Netherlands)
- 11:30-11:45 **A view on globalisation and socio-economic factors – could chikungunya in Italy have been predicted?**  
**Dr Stefano Pongolini** (Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia-Romagna, Brescia, Italy)
- 11:45-12:00 **A view on rodent-borne viruses**  
**Dr Rainer Ulrich** (Friedrich-Loeffler-Institut, Institute for Novel and Emerging Infectious Diseases, Greifswald - Insel Riems, Germany)
- 12:00-12:15 **Emerging viral infections in swine husbandry: introduction and transmission**  
**Prof Mart de Jong** (Wageningen UR, Netherlands)
- 12:15 – 13:00 *Lunch*
- 13:00-17:45 Afternoon Session:**
- How could those factors change in the future?**
- 13:00-13:15 **A view on wildlife biodiversity and zoonoses**  
**Dr Kate Jones** (Zoological Society of London, London, UK)
- 13:15-13:30 **A view on vector-borne diseases**  
**Dr Guy Hendrickx** (Avia-GIS Belgium)
- 13:30-13:45 **A view on flaviviruses**  
**Prof Norbert Nowotny** (University of Veterinary Medicine, Vienna, Austria)
- 5 minute break*
- 13:50 – 14:30 **Open Discussion to list main categories of factors, events and changes that may (directly or indirectly) affect the risk of disease transmission**  
**Dr Paul Gale** (Veterinary Laboratories Agency, Addlestone, UK) and **Prof Vincent Jansen** (RHUL, Egham, UK)

- 14:30 -14:50 **A Spidergrams: What they are and what is expected?**  
**Dr Paul Gale** (Veterinary Laboratories Agency, Addlestone, UK)
- 14:50-17:00 **Break Out Groups** – tea and coffee available throughout  
**New approaches for identifying complex pathways:** Horizon scanning – identifying and development of complex scenario pathways for ‘plausible futures’ and developing ‘spidergrams’
- 17:00-17:50 **Reporting back from break out groups**
- 19:15 *Workshop dinner*

## 7<sup>th</sup> July (Wednesday, 07) 2010

- 09:00-13.00 **Morning Session:**  
**The role for mathematical models in the development of ‘plausible futures’**
- 09:00-09:15 **Introduction**  
**Prof Vincent Jansen** (RHUL, Egham, UK)
- 09:15-09:30 **Network models**  
**Dr Rowland Kao** (University of Glasgow, Glasgow, UK)
- 09:30-09:45 **Neural networks**  
**Dr Ole Lund** (Technical University of Denmark, Denmark)
- 09:45-10:00 **How to use natural seasons in disease management**  
**Dr Gabriela Gomes** (Institute Gulbenkian, Portugal)
- 10:00-10:15 **Household models as a tool to detect emerging human transmissibility of novel pathogens**  
**Dr Michiel van Boven** (National Institute for Public Health and the Environment, Bilthoven, The Netherlands)
- 10:15-10:30 **Multi-type branching process approaches to the emergence of new infectious diseases**  
**Dr Roland Regoes** (Theoretical Biology, ETH Zurich, Switzerland)
- 5 minute break*
- 10:35-12:30 **Break Out Groups** – tea and coffee available throughout  
**Identifying current and novel mathematical and computerised modelling methodologies that are applicable to the area of horizon scanning**
- 12:30-13:00 **Reporting back from Day 2 break out groups**
- 13:00-13:45 *Lunch*
- 13:45-15:00 Afternoon Session:**
- 13:45-14:45 **Facilitated open discussion including ideas for proposals**
- 14:45-15:00 **Round up: The way forward**  
**Prof Vincent Jansen and Dr Paul Gale** (RHUL, Egham, UK and VLA, Addlestone, UK)
- 15:00 *End of Workshop, Coffee / Tea and departure*

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\*Attended Tues 6 July



## 6. Statistical information on participants

Countries of origin

Netherlands 3

Germany 1

Italy 4

Switzerland 1

Austria 1

Denmark 1

France 1

UK 5

Portugal 4

Belgium 1

Gender repartition

Male 11, Female 11

**Appendix 1: Results of initial brainstorming by participants on factors and categories of factors which could affect disease emergence**

Interactions humans, wildlife, domesticated species
Demographics - change in density, age structure
Feed and food - biofuel vs food, change in diets, change in land use
Migration and movements - humans and animals
Restoration and conservation vs habitat loss fragmentation
Farming practice - protein production, change in genetics, selective breeding
Trade, local and international
Bush meat hunting
Pathogen related factors
Mutation, recombination and rearrangement
Pathogen evolution
Vaccination patterns
Medical/pest control
GMs
Invasive species
Aging, immunocompromisation
Poverty, wealth distribution
Cultural habits
Consumption
Policies/governance
Medical technology
Education (access to)
Environmental - climate change

**Appendix 2: Prototype database of factors, events and changes that may (directly or indirectly) affect the risk of disease transmission. Database produced in break-out group by participants. The eight category headers were agreed after an initial brainstorming (Appendix 1).**

<b>Human demographics and behaviour/biology</b>	<b>Socio-economic</b>	<b>Habitat Use</b>	<b>Non-human biology</b>
Aging	Aging	Bush meat	Vector/pathogen/host
Migration humans	Knowledge, attitudes, practices and beliefs	Deforestation	Population changes
Migration pets	Travel	Irrigation/Dams	Migration (animal)
Immuno-compromised	Recreational habits	Conservation practices	Invasion
Urbanisation	Poverty	Expansion of agricultural lands	Bottlenecks (Expansions)
Depopulation	Wealth	Reforestation	Biodiversity
International travel - tourism	Pest management	Changes in forest management	Genetic diversity
International travel - medical tourism	Consumption	Fragmentation	Evolution
New food habits	Access to sanitation	Recreational use of landscape	Host-vector co-evolution
Anti vaccination (and others) movements	Trade	Wildlife watching	Host-virus co-evolution
Sexual behaviour	Waste Management	Hunting	Vector-virus co-evolution
number of children/family size	War (political)	Commerce exotic species	Immunology of the vector
	Education	Pollution	Resistance to antibiotics/insecticides
	Urbanisation	Invasive/alien species	Co-infection/recombinations
	Religion	Expansion of cities	Host behaviour
	Governance	Mushroom and berry picking	Biology of the vector/specificity
	Internet/Information networks	Wildlife restocking/Introduction	Amplifying hosts
	Connectivity	Pest control	Generation time
	Medical care		Infectious dose
	Surveillance		Pathogenicity
	Housing/recreation - swimming pools		Reservoirs
			Co-feeding ticks
			Genetic resistance to pathogen
			Demography (vector/host)
			Management

<b>Farming Practice</b>	<b>Environmental Factors/Climate change</b>	<b>Political</b>	<b>Technology/Medical Care/Medicine</b>
Movement of infected or susceptible animals	Changes in rainfall	Political fragmentation	Drug treatment/resistance
Restricted gene pool	Changes in temperature	Wars	Diagnostic techniques
Culturing of new species	Extreme events (Fluctuations)	Instability	Vaccines
Overcrowding	Storms	Famine	Blood transfusion
Drug abuse - i.e. antibiotics	Floods	Governance	IT in health care
Feeding practices, i.e. BSE	Volcanoes	Culture/Religion	IT communication in health care
Genetic modification	Earthquake	Consumption	Treatment for chronic diseases (anti-cancer/HIV)
Level of containment	Solar activity	Migration	Transplantation
Veterinary care - level provided	Changes in humidity	Silvio Berlusconi (Italy PM)	
Contact with people/domestic animals/wildlife	Desertification	Carla Bruni (France)	
Chain management	Re/Deforestation - human driven	Poverty	
Education and knowledge of farm managers	Re/Deforestation - natural	Resources allocation	
Organic agriculture farming	Re/Deforestation - wetlands	Public Health Decision making - surveillance	
Mega farms	Glaciation effects	Public Health Decision making - medical care	
Habitat loss/gain	Pollution	Public Health Decision making - policies	
Multi-species farming	Increasing connectivity	Information dissemination	
Biosecurity	Wildlife protection	Education	
Short commercial chains	Urbanisation	Trade agreements	
Small backyard farms		Trade-transport networks	
Aqua-culture		Protectionism	