Mapping the future dynamics of disease transmission: risk analysis in the United Kingdom Foresight Programme on the detection and identification of infectious diseases.

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This paper reflects on the qualitative risk analysis framework developed for a Foresight study on the Detection and Identification of Infectious Diseases, which was coordinated in 2005 by the United Kingdom (UK) under what is now the Government Office for Science, Department for Innovation, Universities and Skills. The risk assessment covered human, plant and animal diseases in the UK and Africa in the years 2015 and 2030. Through engaging a diverse pool of experts, we developed a model conceptualising disease spread as the outcome of interactions among sources, pathways and drivers. We then used this model to conduct a Delphi survey of experts. The factors perceived most likely to contribute to infectious disease spread in 2015 and 2030 included geographic extension of existing pathogens (partially due to climate change), over-use of antibiotics/antivirals/pesticides leading to drug resistance, and zoonoses. Our methodology provides a framework for those who need to integrate a wide range of perspectives and factors into their planning and analyses.

Table 1

Main categories of drivers associated with emergence and reemergence of human pathogens (reproduced from Woolhouse *et al.* (2005) [5])

Rank*	Driver
1	Changes in land use or agricultural practices
2	Changes in human demographics and society
3	Poor population health (e.g., HIV, malnutrition)
4	Hospitals and medical procedures
5	Pathogen evolution (e.g., antimicrobial drug resistance, increased virulence)
6	Contamination of food sources or water supplies
7	International travel
8	Failure of public health programs
9	International trade
10	Climate change

* Ranked by the number of pathogen species associated with them (most to least).

Introduction

It is by now well documented that a wide range of factors, including changes in land use and agricultural practices, changes in human demography, pathogen evolution, international travel and trade, climate change, and poor public health infrastructures can all trigger or exacerbate the spread of infectious diseases, determining how and where they will emerge in the future and the circumstances under which they could progress to epidemic or even pandemic proportions (Table 1) [1-5].

Less widely documented are methods for analysing these factors in ways that enable a better understanding of how they are interlinked and how to prioritise their importance. One of the key challenges is that relevant information, when available, is not consolidated in a few hands but spread across numerous institutions and disciplines. Anticipating the emergence or altered transmission of any disease is likely to require expertise in biology, epidemiology, animal and human medicine, demographics, economics, and even sociology and anthropology. Although the importance of cross-sectoral collaboration in disease control is increasingly recognised [6-8], there remains the need to develop new ways of ensuring that diverse and sometimes divergent perspectives are accounted for. Doing so is essential for developing multi-sectoral understanding and commitment – increasingly required for the pursuit of pubic health action in a rapidly changing world.

With a long-term vision in mind, the United Kingdom (UK), under what is now the Government Office for Science, Department for Innovation, Universities and Skills, conducted a Foresight project on Detection and Identification of Infectious Diseases (DIID) with the objective of supporting strategic investment in disease detection, identification and monitoring technologies and systems [9-12]. This paper reflects on the risk analysis component of the DIID project, describing a methodology that could be adapted to subsequent analyses.

Methodology

We analysed expert opinion on infectious disease risks in plants, animals and humans, in sub-Saharan Africa and the UK in 2015 and 2030 (comprehensive details on the methodology, workshop

and survey results are available at the Foresight website [12]). Potential changes in sources, pathways and drivers of disease risks were identified and assessed according to how the magnitude and nature of risks are evolving, as well as the range of plausible future risk patterns. Research questions focused on:

- Factors driving changes in infectious disease risks ('risk drivers') and how they might evolve;
- Future risks for infectious diseases and their importance;
- Uncertainty attached to future risks;
- Comparisons among plant, animal and human disease risks.

To answer these questions a preliminary scoping phase, which included an expert workshop, developed an understanding of important issues and their interactions and formulated the overall approach to the research. A Delphi survey was then carried out in order to assess a broad range of expert opinions on future risks in the UK and Africa.

Scoping phase

The scoping workshop brought together 22 UK infectious disease experts (recommended by the UK Foresight Scientific Advisory Group) to advise on the challenges presented by new and emerging infectious diseases. A disease systems model was developed (Figure 1), as well as an initial list of key factors ("drivers") likely to give rise to changes in disease patterns and emergence of new diseases, such as biological changes and socio-economic factors acting on disease sources and pathways of disease spread. The initial long list of drivers derived at the workshop was refined and clustered under the six main headings listed in Table 2.

Identification and selection of participants for the survey

The experts who took part in the Delphi survey were scientists selected to cover a broad range of expertise in plant, animal and human diseases, from epidemiological modelling, disease identification and disease pathology to disease control, regulation and policy making. They were selected upon the advice of approximately 30 senior advisers who took part in the DIID Foresight project, including members of the UK Foresight Scientific Advisory Group, the UK Foresight High Level Stakeholder Group and UK Health Protection Agency staff, to represent the best available informed judgement across our six areas of interest – the future development of plant, animal and human diseases in the UK and in sub-Saharan Africa.

African respondents from 20 countries in sub-Saharan Africa were invited on the basis of the best available expertise, rather than ensuring geographical equity. Francophone countries were under-represented as we did not have sufficient time within the project to translate questionnaires. This omission may have influenced the findings. There was, however, no evidence of any specific bias among the 55% respondents who completed the questionnaires, with relatively equal representation across the six survey areas (Table 3), and also across relevant areas of expertise (20 areas of expertise were mentioned in the questionnaire responses).

Questionnaire development

A two-stage questionnaire-based survey was sent to 145 experts in infectious diseases from the UK and sub-Saharan Africa. In the second stage of this Delphi-type process [13], respondents were given the results from the first phase and asked to re-assess their own responses. Where their opinions diverged from those of others they were asked to explain their reasons rather than being encouraged to reach a consensus.

The questionnaire was based on the disease systems model (Figure 1, Table 2), but slightly different versions were sent out depending on whether the participants were being asked about human, plant, or animal diseases. Nonetheless, the questionnaires were designed so as to be as comparable as possible. For example, question 3.2.4 in Table 2 was worded as "lack of availability of new vaccines or engineered resistance", broadening the scope of the question from vaccines (mainly relevant for humans and animals) to also include engineered resistance (mainly relevant for plants and animals). As another example, question 2.9 in Table 2 shows a question that was worded differentially depending on whether it was considering animal or human diseases; however, this question was not included in the plant diseases survey.

Each questionnaire asked about future changes in disease sources, pathways and drivers, leading to future disease outcomes. These terms were defined as follows:

- Sources: phenomena or biological events that give rise to potential new diseases, enable existing diseases to become more harmful, enable existing diseases to infect new hosts, or enable existing diseases to spread to new areas;

FIGURE

The disease systems model as a tool for assessing future infectious disease risks

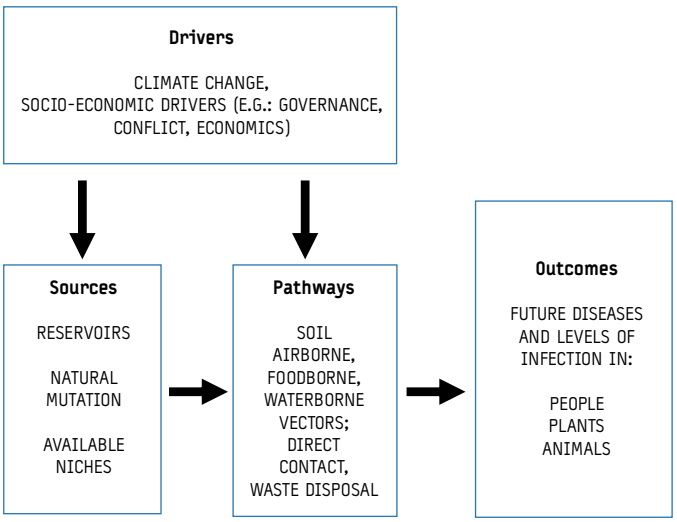

TABLE 3

Sample size, UK Foresight questionnaire, 2005

Questionnaire type	No. distributed	No. of responses (Round 1)	No. of responses (Round 2)
UK animals	20	10	6
UK humans	20	12	5
UK plants	24	13	5
Africa animals	29	18	11
Africa humans	27	13	9
Africa plants	25	14	6
Total	145	80	42

Table 2

Classification of factors influencing the spread of infectious disease, Foresight questionnaire, 2005

	Sources
1.1	New pathogens or new strains of existing pathogens arising through natural genetic change
1.2	Geographical expansion of pathogens
1.3	Emergence of new disease vectors
1.4	Failure of engineered resistance (e.g. vaccines, genetically manipulated animals/crops)
1.5	Increased number of accidental introductions of pathogens
1.6	Increased pathogen resistance (e.g. to microbicides, antivirals, pesticides)
1.7	Decreased immuno-competence of target populations
1.8	Emergence of new diseases from other species reservoirs, including wild species reservoirs
	Pathways
2.1	Increased role of soil-borne route for disease spread
2.2	Increased role of air-borne route for disease spread
2.3	Increased role of water-borne route for disease spread
2.4	Increased populations of disease vectors
2.5	Increased host-to-host transmission due to increased density of host populations
2.6	Increased role of food-borne (or feed-borne) route for disease spread (plant diseases excluded)
2.7	Increased role of food-borne (or feed-borne) route for disease spread (plant diseases excluded)
2.8	Increased spread of disease in veterinary hospitals and/or herding of animal for veterinary interventions (animal diseases) OR Increased spread of disease in hospitals (human diseases) (plant diseases excluded)
2.9	Increased spread of disease through mass veterinary interventions (e.g. campaign vaccinations with shared needles) (animal diseases) OR Increased spread of disease through blood/tissue (e.g. needle sharing, blood transfusions, transplantation) (human diseases) (plant diseases excluded)
2.10	Increased spread of disease due to sexual contact (human diseases only)
	Drivers
3.1	Legislation and government systems
3.1.1	Lack of adequate systems for disease control
3.1.2	Lack of adequate surveillance systems to detect and monitor diseases
3.1.3	Poor implementation of national legislation on disease surveillance and control
3.1.4	Poor implementation of international legislation on disease surveillance and control
3.1.5	Lack of or ineffective biosecurity legislation regarding disease surveillance and control
3.1.6	Low degree of inter-institutional cooperation
3.1.7	Failure of government bodies to accurately or honestly report disease incidences
3.2	Technology and innovation
3.2.1	Lack of innovation in relevant and rapid technologies for detection and identification of existing diseases
3.2.2	Lack of innovation in technologies for detection and identification of new diseases
3.2.3	Lack of innovation in information technology for disease surveillance and communication
3.2.4	Lack of availability of new vaccines or engineered resistance
3.2.5	Development of potential new pathogens for bioterrorism
3.2.6	Drug use leading to the emergence of drug-resistant disease organisms
3.2.7	Lack of new food preservation and decontamination technologies
3.2.8	Lack of new drugs (or pesticides for plants) to control disease
3.3	Conflict and war
3.3.1	Loss of effective detection and identification systems
3.3.2	Increased movement of people (e.g. refugees, armies) spreading disease
3.3.3	Damage to infrastructure (e.g. water, sewage, power supplies)
3.3.4	Increased bioterrorism, exploiting existing diseases
3.3.5	Increased use of wild species as alternative human food source (plant diseases excluded)
3.4	Economic factors
3.4.1	Decreased economic prosperity
3.4.2	Increased disparity between rich and poor
3.4.3	Increase in trade and transport of animals and crops
3.4.4	Decreased average education levels
3.4.5	Reduced quality of sanitation and water supplies
3.4.6	Increased movement of migrant workers, spreading disease
3.4.7	Increased number of disease-susceptible individuals in the population
3.5	Human activity and social pressures
3.5.1	Decrease in public willingness to change behaviour in order to help contain or prevent disease
3.5.2	Decrease in individuals' readiness to report disease incidences
3.5.3	Increase in illegal practices leading to spread of disease
3.5.4	Malnutrition/poor husbandry of animals/crops affecting resistance to disease
3.5.5	Increased travel related to tourism and international business, spreading disease
3.6	Climate change
3.6.1	Increase in mean temperature in the range of 0.5-2.0 °Celsius
3.6.2	Increase in frequency of heavy rainfall events and/or flooding
3.6.3	Increase in frequency of drought in arid and semi-arid areas

- Pathways: mechanisms or routes by which a disease-causing organism can be transferred from one host to another, within or between species;
- Drivers: social, economic, biological or environmental factors that affect disease outcomes, by changing the behaviour of disease sources or pathways;
- Outcomes: plants and animals at the individual, community and ecosystem, or farming system level, and humans at individual and societal levels, that are affected by infectious diseases.

'Drivers' operate in the infectious disease system through 'sources' of disease emergence and/or 'pathways' of disease transmission to determine the 'outcome' in terms of the emergence of future diseases and the levels of infection.

'Risk' was defined as the product of 'the future extent of a hazard' and 'the probability of occurrence of that hazard'. For each factor listed in Table 2, the respondents were asked to rate the extent and probability of different outcomes in the years 2015 and 2030, on a three-point scale. The survey thus provided a systematic method for gathering informed opinions on rankings of the impact of drivers on sources and pathways, as well as on the importance of changes in sources and pathways themselves.

The questionnaires also asked respondents for additional observations, including the phenomena or processes they thought were likely to decrease risk and what they expected to be future risks (for example, which classes of diseases or organisms were likely to represent the greatest risk).

Data analysis

Questionnaires generated qualitative scores for both the perceived extent of the hazard and the perceived probability of its occurrence (1, 2 or 3; low, medium or high). The risk associated with a particular factor for each source, pathway and driver was then calculated as the product of these two scores, giving a range of potential values: 1, 2, 3, 4, 6 or 9. , Thus we compared the perceived importance of sources, pathways and drivers in contributing to future disease outcomes for the six risk questionnaire categories (permutations of host and location: Africa-human (AH), UK-human (UKH), Africa-animal (AA), UK-animal (UKA), Africa-plant (AP), UK-plant (UKP)). We focused on factors that were consistently predicted to be of higher risk through a data filtering process - risk assessments were categorised as low, moderate or high as follows:

- Low risk: an overall score in the range 1-3, i.e. either hazard or probability were scored as low (1);
- Moderate risk: an overall score of 4, i.e. both hazard and probability were scored as moderate (2);
- High risk: an overall score of 6 or 9, i.e. either hazard or probability were scored as high (3) and the other was scored as moderate or high (2 or 3).

The first filter selected the cases for which more than 50% of the responses were in the moderate or high category (scores 4, 6 or 9). The second filter selected cases for which more than 50% of responses were in the high category (scores 6 or 9).

Survey results

Participants

The response rate in the first round of the survey was 55%, and 53% of the first round respondents contributed to the second round (Table 3). The respondents' self-reported areas of expertise were primarily: epidemiology (12%), virology (9%), pest and disease management (8%) and animal health and veterinary science (7%). This participation rate was more than sufficient to conduct the analysis, as breadth of expertise was deemed to have priority over absolute number of respondents. The declining number of respondents from the first and second round partially reflects those participants that did not feel that they needed to alter their responses.

Risk assessments

The complete survey results are available on the UK Foresight website [10]. Table 4 compares the factors which, for 2015 and 2030, passed the first and second filters of 50% or more of respondents.

The highest perceived risks (for 2030) related to:

- new pathogens or new strains of existing pathogens arising through natural genetic change;
- and geographical expansion of pathogens from within or outside the UK and Africa.

In five of the six categories there was a perceived high risk of:

- new diseases from other species reservoirs, including wild species reservoirs;
- drug use leading to the emergence of drug-resistant disease organisms;
- an increase in disease due to a mean temperature increase in the range 0.5-2 °C.

Changes in sources were seen as important in all six categories (plants, animals and humans; UK and Africa), and there was little difference between UK and Africa in perceived overall risks generated by changes in sources.

Changes in pathways were seen as less important generators of disease risks across all categories than were changes in sources, although there were marked differences between UK and Africa. Increased host-to-host transmission due to increased density of host populations was seen as important for animals, plants and humans in Africa, but not at all in the UK. Increased disease vector populations were seen as important for plants and animals in the UK and for plants in Africa.

Many more disease drivers were considered important in Africa than in UK. For Africa, intriguingly, many respondents predicted lower risks arising from 'Legislation and Systems of Government' and 'Conflict and War' in 2030 compared to 2015, which reflects optimism about the future.

Finally, the three elements of climate change that were examined (increased temperature, rainfall and drought) were all seen as important drivers for human disease risks in Africa; yet only drought was highlighted for animals, and only temperature and rainfall was highlighted for plants.

In the UK, drivers seen as generating high levels of risk for human diseases were: drug use leading to the emergence of drug-resistant disease organisms and climate change, specifically rising temperatures. For UK plant diseases, the emergence of pesticide-resistant disease strains and the lack of new pesticides, increased trade and transport of crops and higher ambient temperatures, were seen as important risk drivers. For UK animal diseases, lack of adequate systems for disease control, poor implementation of international systems of disease surveillance and control, increased ability to engineer new diseases or to exploit existing diseases for bio-terrorism, emergence of drug resistance and the lack of new drugs, increased trade in animals, increase in illegal practices

Table 4

Responses for the years 2015 and 2030 that passed the first filter (moderate and high > 50%) and the second filter (high >50%), Foresight questionnaire 2005

	Africa animals		UK animals		Africa plants		UK plants		Africa humans		UK humans	
Year	2015	2030	2015	2030	2015	2030	2015	2030	2015	2030	2015	2030
Source												
1.1												
1.2												
1.3												
1.4												
1.5												
1.6												
1.7												
1.8												
Pathway												
2.1												
2.2												
2.3												
2.4												
2.5												
2.6												
2.7					n/a	n/a	n/a	n/a				
2.8					n/a	n/a	n/a	n/a				
2.9					n/a	n/a	n/a	n/a				
2.10					n/a	n/a	n/a	n/a				
2.11	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a				
Driver: Legislation & government												
3.1.1												
3.1.2												
3.1.3												
3.1.4												
3.1.5												
3.1.6												
3.1.7												
Driver: Technology & innovation												
3.2.1												
3.2.2												
3.2.3												
3.2.4												
3.2.5												
3.2.6												
3.2.7												
3.2.8												
Driver: Conflict & war												
3.3.1												
3.3.2												
3.3.3												
3.3.4												
3.3.5	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a				
Driver: Economic factors												
3.4.1												
3.4.2												
3.4.3												
3.4.4												
3.4.5												
3.4.6												
3.4.7												
Driver: Human activity & social factors												
3.5.1												
3.5.2												
3.5.3												
3.5.4												
3.5.5												
3.5.6	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a				
Driver: Climate change												
3.6.1												
3.6.2												
3.6.3												

The numbers in the first column correspond to the variables listed in Table 2.
Black cells represent 'high risks' (factors passed the first and second filter); grey cells represent 'moderate risks' (factors that passed the first filter but not the second); empty cells represent 'low risks' (factors that passed neither filter).

leading to the spread of diseases and climate change, specifically increased temperatures, were highlighted as important.

High hazard, low probability responses

We also examined high hazard, low probability risks, which would be scored as a 3 (1 for probability multiplied by 3 for hazard) and therefore would not have passed through the data-filtering analysis. However, only 17 out of the total 636 possible responses were of this nature, and in each case only between two and four respondents had categorised the risk in this way.

Discussion: Employing Foresight to understand future disease outcomes

If it is clear that a wide range of factors influence the spread of infectious disease [1-3,14], then there is a need to better understand and prioritise them:

"The rate and scale of global change in agriculture, trade, demographics, species translocations and invasions, microbial adaptation, and other complex factors, have evidently outstripped our ability to understand and respond to EIDs [emerging infectious diseases], and exposed serious limitations of approaches that fail to engage with the wider contexts from which infectious diseases emerge." [15]

For each factor, it is important to: identify and quantify the relevant sources, pathways and drivers, model their relationships and interactions, and identify potential intervention points where synergistic interactions promoting disease emergence can be arrested. Quantitative analyses are ideally suited for this, yet in many instances crucial knowledge gaps exist, creating the need for complementary analyses to help guide decision-making and priority-setting until more hard evidence becomes available. Although some analysts have called for interaction across a very broad range of expertise [15-17], there has been little discussion about how this could be practically done.

Foresight projects, such as the UK DIID project, aim to develop scientific and technological priorities, integrate multi-disciplinary perspectives, co-ordinate research opportunities with economic and social needs, and stimulate communication and partnerships between researchers, research users and research funders [18,19]. Meanwhile, survey methodologies such as Delphi enable a systematic approach to eliciting, aggregating and synthesising expert opinions [20-22]. The approach we describe here begins to develop a framework for identifying, assessing and prioritising infectious disease spread by incorporating a wide range of perspectives and insights into the analysis. Through engaging a wide range of expertise, we identified and developed a preliminary prioritisation of the myriad factors relevant to plant, animal and human disease.

There are, of course, limitations to this approach. One is that in order to cover the broad geographic and disease range mandated by this project, it was inevitable that the disease systems model on which the research was based would be rather general; the predictions should be interpreted with this in mind.

One other limitation of our study, and perhaps of Foresight in general, is that the answers are not 'evidence-based' in the scientific sense of the word. In our study, the respondents' predictions are based on their experience and knowledge, and represent the respondents' expectations of future courses of events. Where little data exist (necessarily the case when mapping the future), or where these data are not easily comparable, we would suggest that demonstrating general agreement – or the lack thereof – on common themes across a broad range of disciplines and institutions can be an important starting point for framing and pursuing multi-agency action.

Finally, we are also aware that our disease systems approach has been unrealistically linear. For any specific disease, dynamic interactions and feedback loops among drivers, sources and pathways will amplify or diminish overall disease risks. However, it was not possible to include this level of sophistication in a general, meta-level model applicable to all the disease categories in this study. Future studies would be well advised to focus on specific classes of disease, or even on specific drivers, pathways or sources of disease.

Ultimately, the challenge is to identify the processes that influence the spread of new and emerging diseases before they become significant problems for national public health systems or public health emergencies of international concern. The approach described here, appropriately applied, could help facilitate this.

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