Emerging Diseases: Causes, Conditions and Controls

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Summary

There is no doubt of the increasing risk from new and emerging diseases and that such diseases have the potential for profound implications for all sectors of society. The emergence of entirely new diseases such as SARS is usually the result of changes in the way that we do things and is often difficult to predict. The increasing emergence and spread of more traditional diseases may be due not only to evolution of the causative agent but also to the impact that we, as humans, have on our environment. Whatever the cause, the risk is increasing and threatens as much those striving to emerge from poverty as the more developed groups in our society. Understanding better the conditions that drive these changes, recognising emerging diseases earlier than we currently do and having in place more effective mechanisms for responding to each threat will be critical. Increasingly though, such diseases are emerging from complex interactions between humans, animals and environment and an effective national animal disease surveillance program is an essential component of enhanced preparedness. Unfortunately for many developing countries resources are not available for such systems, the risks remain unmanaged and the opportunities brought by the livestock revolution could abruptly disappear. Importantly many of the new diagnostic and surveillance tools being developed for use in Australia will be applicable to poorer regions of the world and could assist in the better management of risk due to new and emerging infectious diseases.

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The emerging and new diseases

That traditional diseases are evolving and new ones arising are indisputable facts. In the seventeenth century, the emergence of bubonic plague in epidemic proportions illustrated dramatically the emergence of a traditional infection of rats to one that infected and killed many hundreds of thousands of humans. Since that time, numerous pathogenic organisms have evolved causing infections that have changed both in terms of host range and severity of disease. The classic example is that of influenza. In 1918 this disease killed some 40 million people globally, and the likelihood of a pandemic influenza virus occurring again is high. The arrival of severe acute respiratory syndrome (SARS) is the most recent example of an apparently new virus infection (Rota *et al.* 2003), but there are many other examples in recent times ranging from those with profound global implications such as AIDS and BSE to those with more local effects such as Nipah virus (Chua *et al.* 2000) or Hendra virus (Murray *et al.* 1995) infections (Table 1).

For the remainder of this paper, examples chosen of new and emerging diseases will be those that

have a more direct bearing on rural livestock producers in developing countries, although this is just a subset of diseases that could be cited. Furthermore, the focus will be on the natural occurrence of such diseases and not on the risk posed by bioterrorism, although in many cases managing the risks will have considerable parallels.

Whenever a new disease appears, inevitable questions arise. How new is this disease and/or the causative agent? Even if considered new, is it related to other known diseases or causative agents? When did the disease actually appear and are there unknown reservoir hosts? A disease that illustrates this well is bovine spongiform encephalopathy (BSE). The appearance of BSE and the subsequent development of the concept of transmissible spongiform encephalopathies (TSE) recognises the similarities not only between BSE and the more traditional and older disease scrapie, but also between BSE and some of the newer forms of prion-mediated disease that have emerged.

Table 1. Examples of new and emerging virus infections 1988–2003

Year	Virus	Syndrome	Location
2003	SARS corona virus	SARS	Asia, Canada
2001	Metapneumovirus	Respiratory Illness	Worldwide
1998	Menangle virus	Systemic febrile illness	Australia
1998	Nipah virus	Encephalitis	Malaysia
1997	Influenza H5NI	Influenza	Hong Kong
1996	Australian bat lyssa virus	Rabies-like	Australia
1995	Hendra virus	Pneumonia, encephalitis	Australia
1993	Sin Nombre virus	Haemorrhagic pulmonary syndrome	US
1990	HHV8	Karposi sarcoma	Worldwide
1990	HHV7	Fever, roseola-like rash	Worldwide
1989	Hepatitis C virus	Hepatitis	Worldwide
1988	Barmah Forest virus	Ras, arthritis, fever	Australia

Even in this case we have been forced to recognise a difference between an older, well-known disease in humans called Creutzfeld-Jacob disease (CJD) and a new version, new variant CJD (Will *et al.* 1996). An enormous amount of work has been undertaken on BSE to try to determine its first appearance. This has profound implications in terms of control and trade in livestock and livestock products, and it is now mostly accepted that this indeed is a new disease that is closely related to other previously recognised prion infections.

The implications of this for livestock producers in the developing world is interesting, as it has now become incumbent on developing countries to demonstrate freedom from BSE although it is highly unlikely that the factors that predisposed to the emergence of this new infection could have occurred in such locations. The need to demonstrate freedom from infection has, of course, more to do with the risk of importation of contaminated material of bovine origin.

Another interesting 'new' disease is SARS. That this has emerged as a new disease in humans is not contended and no evidence has yet been found of anyone showing antibodies to the SARS virus prior to the outbreaks of this disease. What remains to be determined is whether this new coronavirus has been circulating unnoticed amongst a restricted group of animals for some time. On the basis of nucleotide sequence data, the SARS coronavirus certainly sits alone in the coronavirus family. The key question, however, is whether the virus that caused SARS in humans is identical to that found in its wildlife reservoir in China, or did a chance mutation or recombination event lead to a change in cell tropism and an ability to infect humans? The virus isolated from humans has certainly caused a new disease in humans but is it an old virus, from either humans or animals, that has changed and learnt 'new tricks'? This is a question beyond the academic, and goes to the heart of control and management of new and emerging diseases.

But not all evolving diseases have widespread, regional or global implications. Take the example of 'ormilo'. This is a disease that has only recently been recognised by the Maasai tribesman in eastern Africa (Bourn 2002). The Maasai focus wholly on rearing livestock; they revere livestock above themselves and they understand their livestock and the diseases that affect them as well as any farmer in the world. Some 20 years ago they recognised this new disease that now claims some 90% of

zebu cattle in any one herd. The Maasai lack the sophisticated microbial understanding and equipment to characterise the causative agent, but they recognised that it was new. It is now known that the causative agent is *Theileria tauratragi,* although why this usually benign pathogen has switched to cause a new, severe disease is unknown. Today ormilo is ranked by pastoralist communities of northern Tanzania as their greatest constraint to increased livestock production. Nearly three-quarters of pastoralist households in the Ngorongoro Conservation area in northern Tanzania now have insufficient livestock herds to ensure food security or escape from poverty.

Two livestock diseases that continue to have profound implications for livestock producers in developing countries are rinderpest and foot-and-mouth disease. Both these diseases have been known since the turn of the twentieth century, have been managed, and in the case of rinderpest, eliminated from the developed world: but are they evolving? The simple answer is yes. Examining rinderpest first, it became clear around three years ago that a new clinical entity, a mild form of rinderpest, was being recognised in east Africa. This has serious repercussions in terms of global eradication of rinderpest as the eradication process was based on recognition of severe clinical disease characterised by discharge, diarrhoea and death. Molecular studies soon showed that three lineages of rinderpest have emerged globally, one of which, lineage two, is characterised by mild disease. Although some debate exists as to whether mild rinderpest has been around for over half a century, the fact remains that this has severe implications for global eradication. What drove this evolution is unknown, but it is interesting to note that the only remaining foci of rinderpest in the world today are in the region of east Africa where mild rinderpest is recognised.

Foot-and-mouth disease (FMD) virus, like other RNA viruses, mutates readily, and this has lead to the appearance of an evolving complex of diseases caused by seven different FMD serotypes. For many years it has been assumed that whilst the virus was subject to change in terms of its surface antigens, the concepts of disease control and eradication remained consistent and straightforward. The paradigm was: virus will change, vaccines cannot keep pace with the antigenic alterations, carrier animals will always be generated and control must be based on slaughtering of susceptible animals until the virus is unable to find any susceptible hosts in which to replicate. What were not understood, perhaps, were the implications of an evolving virus in terms of host specificity, expression of disease, susceptible populations and movement of livestock products. The catastrophic outbreak of FMD in the UK in 2001 was not so much due to the *appearance* of a new virus variant but rather due to the *factors* that allowed the virus to spread. The outbreak in the UK was caused by a novel FMD virus strain that had evolved to have distinct characteristics, but the magnitude of the impact was more to do with factors other than those attributable to the virus or the disease itself.

Prior to the outbreak of FMDV in Europe there were many who considered that FMD was a disease of trade and that the impact of this disease was minimal for rural livestock producers in developing countries. Whilst in some of the Least Developed Countries (LDCs) this might be the case, a number of excellent studies by ILRI (Berry *et al.* 2003) have clearly shown the considerable losses that accrue due to endemic FMD. In a number of recent rankings of important livestock disease, FMD has been at the top for both developed and developing countries, yet how well do we understand the evolution of FMD viruses? We do have systems in place that attempt, at least, to map the global movement of the seven serotypes and related subtypes, but our understanding of what drives these movements, and what creates change in the virus and the associated disease manifestation, is extremely limited.

The final example of an emerging disease is that of bluetongue. Although there are 24 recognised serotypes of this virus and no new serotypes have been discovered in the past decade, the disease has constantly changed location based on both the movement of infected animals and the virus vector, a number of *Culicoides* species. In the past two years, bluetongue has made incursions into previously uninfected areas of Eastern Europe and has now moved as far north as Bulgaria. This is attributable both to changes in vector competence (new species of *Culicoides* that now can transmit the virus) and relocation of traditional vector species of *Culicoides* due to climatic changes. Whether the virus has changed to accommodate the vector, or it is a change in the vector itself, is not known. Whatever the case, the emergence of this disease in new areas of the world has profound implications for livestock producers and trade in livestock.

The causes

The development of a new disease or the evolution of an existing disease to a new level of virulence or host range will be driven by a range of factors. In terms of viruses — the simplest of disease-causing agents and ones which, in the case of the simplest viruses, we are now able to fully reconstruct — we still have very limited knowledge of what causes disease and what governs host range. We do know that single amino-acid changes can dramatically alter the virulence of a virus but, with most viruses, we have little appreciation of factors that govern tropism and we have been unable to widely use our molecular knowledge to generate new genetically engineered viral vaccines to protect against virulent viruses. However, we do understand some of the factors that drive change in causative agents and the diseases they cause.

Conditions that drive change

From a Darwinian perspective it is recognised that whilst viruses mutate, reassort and recombine depending on the nature of their genome, it is external factors that permit a particular mutant, reassortant or recombinant to dominate a population of genetic variants. Survival is driven not by the intrinsic rate of mutation, but rather by the ability of the mutant or variant to gain advantage in the external environment. However, a mutation is a chance genetic event and any organism that exhibits a higher rate of mutation creates more opportunities to create successful mutations and, thereby, an enhanced chance of survival. Given the high mutation rate of viruses, especially viruses with RNA genomes, it is not surprising that viruses cause many of the new and emerging diseases.

Evolving viruses

Spontaneous mutation and recombination is a characteristic of most viruses, although this will vary significantly depending on whether the virus contains single or double-stranded DNA or RNA. A popular concept in virology that has added much to our understanding of virus evolution and disease emergence is that of 'quasi-species' (Holland *et al.* 1992; Duarte *et al*. 1994) where viruses are regarded, not as populations of identical particles, but as heterogeneous populations containing viruses that differ from each other genetically and less frequently, antigenically. Viruses constantly undergo dynamic population changes, depending on external factors, especially when they move into new ecological niches. Thus external factors govern the emergence of disease, not the presence *per se* of a virulent member of a virus population. This concept has profound implications for our current classification of countries or zones free of disease for trade purposes, as it indicates an ignorance of the fact that a virulent organism capable of causing disease could exist in such a country or zone, but that circumstances have not permitted the overt expression of disease! Recent studies with Newcastle disease virus infections in poultry may well change the basis on which we currently classify countries free of disease: a move towards identifying the presence of virulent virus is logical.

In summary, selective pressure from the host, the environment or — in situations where viruses are transmitted between susceptible hosts by a second species in which the virus replicates — the vector, will lead the evolution of new virus populations that may have increased virulence and host range. Understanding and manipulating these pressures is critical to disease risk management strategies.

Changed host/pathogen interactions

Perhaps the most alarming factor associated with the emergence of new diseases is the perceived change in host specificity displayed by the causative agent. There are many examples of infectious agents existing in symbiotic, subclinical relationships with natural hosts that 'spill over' into new susceptible hosts and create disease. One such example is Russian spring-summer encephalitis or tick-borne encephalitis virus, which circulates in the forests of Russia and Eastern Europe without causing disease in its natural hosts, predominantly rodents and small mammals. Man became infected either through the bite of infected ticks or by eating unpasteurised cheese made from the milk of virus-infected livestock. Tick-borne encephalitis became an accepted disease syndrome in this part of the world. In this case there is no clear evidence that the virus itself evolved to infect man, but that the opportunity to invade a new host arose through simple contact of virus-infected ticks with man and his livestock.

Other examples highlight the relationship between genetic alterations and the capacity to replicate in new hosts. Canine parvoviruses first appeared in the late 1970s and spread rapidly around the world. Evidence strongly suggests that several point mutations in the genome of feline panleukopenia virus, a virus which does not replicate in canine cells, increased virus host range and led to the ensuing major pandemic in dogs (Parrish 1999). An intrigu-

ing hypothesis, along similar lines, has been suggested to explain the 'jump' of the SARS cornavirus from an animal reservoir to humans. A comparison of the sequence of the virus isolated from civets with that of the vast majority of SARS viruses isolated from human cases indicated that the latter had a 26-nucleotide deletion in a region of the genome that coded for membrane-associated proteins. It is of interest that one of the earliest isolates of SARS from humans maintained the 26-nucleotide insertion compared with subsequent isolates. Did the loss of 26 nucleotides, with the concomitant alteration in viral membrane proteins, permit the virus to attach to human cells and spread from human to human? Has the new 'human' virus lost the capacity to infect animals? Will it remain in the human population? Much research will be required to answer these and other questions on the evolution of SARS cornavirus, but current evidence suggest strongly that handling of wildlife species infected with a SARS-like virus was the critical factor. The implication of this for livestock producers remains unclear, although no evidence has been found of SARS-like virus in any farmed species, nor indeed has the SARS virus been shown to infect such species.

Climate changes

Infectious agents can be transmitted by direct contact, by dispersion in the environment and by vectors. In the latter two cases, climatic conditions can have a profound influence on the spread of the disease and on the ability of the causative agent to survive and spread into new areas.

Numerous examples exist of the effects of climate on the maintenance and spread of disease, but perhaps more important today are the effects of changing weather patterns on the emergence of disease. Whilst El Nino is a well-recognised global weather pattern, increasing examples link this phenomenon to outbreaks of disease such as the recent occurrences of Rift Valley fever along the east coast of Africa. Perhaps more subtle is the ability of FMD virus to survive in humid and cool conditions, and thus the concept of wind-borne spread of the virus is more applicable to the wet conditions in northern Europe than to the arid hot conditions of much of Australia. In this context, can global warming be seen as a factor that may potentially limit the spread of FMDV in certain regions of the world? Complicating this whole area will be the ability of viruses to change in response to weather patterns and create the potential for new diseases and/or altered occurrence of traditional diseases.

Increased movement (of livestock and people)

Globalisation is having a profound effect on the occurrence and pattern of diseases of both livestock and people. The ability to move around the world is not new, but the rate of movement of humans, livestock and livestock products has considerable implications in terms of disease spread. The recent understanding of the SARS epidemic is a tribute to our acceptance and management of the risks associated with travel. Without doubt the limitations that were imposed on global travellers following the outbreaks of SARS in China, Hong Kong, Canada and latterly Taiwan were critical to bringing the disease under control. But the issue of globalisation goes further than this. Any new or emerging disease focus has the ability, given the right circumstances, to spread across the world to entirely new populations of humans or animals with different susceptibilities and immunities. Thus we need to be globally vigilant in detecting and responding to the emergence of new disease pathogens.

The Office International des Epizooties (OIE) was the first international organisation set up in the early 1900s in recognition of the fact that trade in livestock and livestock products carries a risk of spread of disease. Managing that risk is the *raison d'etre* of the OIE, but as globalisation progresses this risk becomes far more difficult to manage. The whole tenet of the global livestock revolution is that it offers opportunities for rural livestock producers in developing countries to escape the poverty trap. As such countries demand that their rural livestock keepers participate in the global livestock trade, it becomes increasingly important to understand and manage risks associated with such participation. Livestock producers from the developing world who wish to avail themselves of the benefits of international trade will need to demonstrate management of disease risks associated with this trade. It is already apparent that technical barriers associated with this process will be an enormous problem to be overcome if they are to effectively participate and realistically benefit from the global livestock revolution.

The threats

Threats to livestock producers in the developed world

Livestock production in the developed world is undergoing profound change, most significantly through the ever-increasing influence of the consumer and consumer protection groups. Whilst consumers are continually requesting more of the end product in terms of quality and safety, they are now turning their attention to the production process, euphemistically described as from 'farm to fork'. Issues of animal welfare, of antibiotic use and of environmental impacts now face the producer, beyond the traditional ones of cost and output. Complicating the market place is the issue of variable subsidies whether they be tax incentives, product bonuses or direct payments, all providing for a 'variable playing field' in the global marketplace.

It is recognised that in the competitive marketplace for livestock products (meat, dairy, wool, hides etc.) profit margins are thin and production diseases have to be managed in a manner that geographically limits the impact of the disease while maintaining international trade in disease-free areas of the world. For the past 20–30 years, producers in the developed world have been able to operate, by and large, in the absence of the main livestock epizootics or so-called OIE List A diseases (rinderpest, contagious bovine pleuropneumonia, tuberculosis, FMD, etc). A number of recent disease events, however, have profoundly altered the way we look at the impact of disease on livestock production in the developed world.

BSE and FMD have highlighted, more than others, the significant threat that livestock diseases can pose. This threat goes beyond the individual producer and has the potential to go the very heart of a nation. In terms of disease and threat to human life, BSE is of relatively minor significance. In terms of the consumer and their perceptions, BSE has had an enormous influence. One only has to look at the cost of the recent discovery of a single case of BSE in an adult cow in Canada to recognise the grave threat this poses to livestock producers.

The recent outbreaks of FMD in Europe underscore another set of issues for livestock producers, with equally devastating effects. Firstly, the virus came not from a neighbour but from across the other side of the globe. Secondly, changes in market practices had enormously increased the risks of spread of FMDV in the UK. Thirdly, the management strategies in place to deal with an outbreak of FMD had not taken account of a range of matters relating to mass slaughter. Fourthly, there was no real appreciation of the potential impact of such an outbreak on others areas of the economy such as tourism. Much has been written about the cost of FMD to the UK; the consensus figure would seem to be around $30 billion Australian. Whatever the cost, it has awakened Governments and veterinary services throughout the world to the possibility that a disease of livestock — that does not even infect humans — has the potential to economically devastate a country. Management of that threat is having profound effects on veterinary and related services in practically all developed countries. More resources are being made available, new approaches to surveillance and responsiveness are being developed and implemented, and — perhaps most importantly — a new appreciation of the role of livestock in the fabric of our society has emerged.

Threats to livestock producers in the developing world

Livestock producers in developing countries are beset by enormous risks to their enterprises, and managing that risk has been at the heart of the systems that have emerged. These risks are very different to those facing livestock producers in the developed world, and strategies to manage them have evolved over a considerable time. In many ways these producers are highly resistant to change, as their management strategies have, in the main, proved successful and the risks they face are so complex that the implications of change are difficult to evaluate. Over many years numerous research studies have identified ways of improving the productivity of farmers in developing countries. For the most part, uptake of these research findings has been dismal, quite simply because the farmer cannot afford to take risks. His very survival and that of his family or village relies on his productivity and he knows that his current practices work! He might well have too many lean and unproductive cattle, but if half of them die he still has the other half. This is not so if he has one highly productive Fresian cow that is as susceptible or more susceptible to disease as his local cattle breeds.

Where he is most amenable to change is in the management of a major epizootic. When a life-threatening disease strikes his animals he will respond. He will use a new vaccine, try a different

treatment or move his animals away from the risk. In addition, his proximity to and familiarity with the animals in his herd provide surveillance information in real time. Unlike the producer in the developed world, the subsistence farmer is usually closer to his livestock, more aware of their health status and will more rapidly spot a change in behaviour or conditions that marks the arrival of a new disease event. The biggest threat he faces is not failing to recognise the new, but being able to do anything about it. Almost certainly he will have limited access to veterinary help, to drugs or vaccines or even to methods to characterise the new disease. The greatest threat to his wellbeing is the lack of a supportive animal health infrastructure to assist in the management of a disease threat.

These comments highlight the plight of the developing country farmer and his approach to disease control within his traditional market place. The Livestock Revolution heralds new and growing markets both nationally and internationally, but many will argue that rural livestock keepers can expect no more than new national markets that arise predominantly as a result of increased local urbanisation. Whatever the case, exploitation of these new opportunities will demand increased investment, increased specialisation and greater focus on the livestock enterprise, but will come with an accompanying increased risk. Without doubt, the risk of disease will increase and there will be an enhanced emphasis on product safety from urban consumers. In many countries these threats will have to be managed in the absence of an effective veterinary or public health service.

The role of animal surveillance

The key to managing the threat of new and emerging diseases or the changing pattern of an already-known infection relies on the capacity to detect them at an early stage. The focus is on detecting a change from the normal pattern of disease occurrence or disease-related events. A number of studies following the FMD outbreaks in the UK have looked at how this routine surveillance for changing patterns can best be operated. The conclusions suggest that having veterinarians routinely on farms is the critical component.

It is worthwhile reflecting on the veterinary support services that were available 10–15 years ago in most developed countries. Whilst routine disease diagnosis and treatment were carried out by local veterinary practitioners, unusual cases were investigated by veterinary investigation officers. Usually based at a local laboratory, these investigators would pursue the unknown, a process that often required weeks or months of laboratory work and was rarely funded by the farmer, but covered through Government support for veterinary services. We contend that this routine search for the new or unusual was an important component of disease surveillance programs. As privatisation took hold, Government services were diminished and many laboratories closed. In their place private laboratories emerged that required full cost recovery for any activity undertaken. Taxpayer's money has been saved at the expense of the eyes and ears of our surveillance system. It seems certain that, in part, the lack of such a system led to the failure to detect FMD in the UK for some 14 days, and this contributed significantly to the subsequent bill of $30 billion. We contend that a sum of this magnitude would easily cover the cost of maintaining the veterinary investigation service in the UK for many years.

What about the developing countries? In most cases no routine surveillance system exists, very few veterinarians are found in rural areas and a veterinary investigation laboratory probably does not exist. In Africa, very few countries have functioning regional laboratories and even those in capital cities struggle to survive. The cost of reagents, equipment and expertise limit all but the most basic work and, at the end of the day, few samples are submitted routinely from the field for differential diagnosis. This poses a threat not only to the detection of new and emerging diseases and their local impact on animal health, but it also limits trading opportunities because it becomes difficult to document freedom from specified diseases as required by the OIE and potential trading partners. Against this background, as indicated above, the farmers themselves are perhaps as good as any at recognising change and the emergence of new diseases. The challenge therefore in developing countries would seem to be how best to harness and use local expertise, and to bring this into an intelligence-gathering process that can recognise the unusual, and ultimately take appropriate action.

Can new science assist?

We have entered an era where global collection and dissemination of information is possible through sophisticated communication systems, and where nano-technology and biosensors offer us new possibilities to identify and track the movements of individual animals and remotely detect in

real time changes accompanying infection in animals. We also have the capacity to collect weather, moisture and vegetation data by satellite, and — with the help of geographical information systems — analyse complex relationships between human, livestock, wildlife, and vertebrate and invertebrate vectors of a range of new and emerging viral pathogens such as bluetongue, Japanese encephalitis, West Nile and Nipah viruses. Finally we have new systems of laboratory-based diagnosis that can detect multiple pathogens and differentiate them from non-pathogenic strains in a single test system. In addition, the new technologies permit simultaneous detection of antibodies to multiple pathogens in a single reaction. Much of this has been recognised by the Commonwealth Government in its support for the new Australian Biosecurity Cooperative Research Centre on Emerging Infectious Disease. But can this assist developing countries? We would like to think the answer is 'yes', but in a way that demands a new global perspective and not the usual preoccupation with nationalism and national preoccupation with self-sufficiency.

Already a global WHO network has been set up for influenza, and the FAO EMPRES program strives to achieve the same for livestock pathogens such FMD, rinderpest and Rift Valley fever. As new technologies comes on stream, would it not be prudent to take a global approach to seeking out new and emerging diseases? Using expensive but high-throughput machinery and utilising economies of scale, could we not establish specific centres that would screen samples from around the world for known diseases and unusual events? Of course this would require a new openness and transparency, but we have already learnt that new and emerging infectious disease threats are global, and that we must take a global approach to managing and mitigating such risks.

Managing the risks

In recent years the management of disease risk has increasingly become a preoccupation of veterinary services. From the early days of zero risk in trade, we have moved on to undertake a risk analysis under the auspices of OIE guidelines for any commodity that poses a threat to national livestock industries or consumers. The science of risk analysis is now firmly established and an everyday part of livestock trade negotiations. Despite this, the threat of new and emerging infectious diseases by definition remains significant, and the best approaches to managing these are still evolving. We have learnt some important lessons recently through disease events such as BSE and FMD, but clearly there is much to be done. Without doubt the single most critical impediment to the process is the 'don't want to know' attitude that can pervade sectors of the livestock industry. The recent outbreak of SARS highlighted this again, with livestock producers in a number of SARS-free countries opposing the inoculation of the SARS virus into production species under controlled conditions in case it was shown that they could be infected and thus be a potential source of infections for humans. This attitude does little to assist the management of risk from such diseases. Effective control or eradication is just not possible without a thorough knowledge of the causative agent, its host range and its ability to spread or survive in different species.

Critical therefore to managing the risk is a detailed knowledge of the epidemiology of a particular disease threat. This is recognised in the Australian Biosecurity CRC, where unknown but critically important interactions between specific exotic pathogens and potential hosts in Australia will be examined to better understand the biology of the host-pathogen interaction and to facilitate development of risk management strategies. Given that new and emerging diseases are chaotic events. such research is required to provide the managers with adequate information to manage risk. There is now a growing awareness that an effective research program undertaken in purpose-build laboratories and overseen by quality scientists will be fundamental to managing this threat. New high-security laboratories are being built or planned at considerable cost in a number of countries, although it is questionable whether existing facilities are being fully utilised. The USA has recognised the need for quality scientists to manage this research and there is a growing clamour for serious investment in this area (Anon. 2003).

One thing must be appreciated: such research and the capacity to undertake it will require considerable investment both in the immediate and longer term. The longer-term commitment should be fully recognised and agreed to if a difference is to be made.

All the above will not only assist the veterinary services and livestock producers in the developed world but also those in developing countries. The processes and tools will for the most part be applicable both globally and nationally. One thing is clear: the failure to tackle disease threats from the developing areas of the globe will provide a con-

stant threat to livestock producers in the developed world. Given the scant resource available to most disease management strategies, considerable investment will be required in the developing countries by richer nations to reduce the risk associated with new and emerging diseases. The problems are global, they will have a global impact, and the problem needs to be tackled on a global basis.

The recent global research initiative to develop a new generation of FMD vaccines and antivirals through a collaborative research venture involving the top high-security laboratories in the world is a good example of the way forward. The outputs from this research are aimed at providing new tools to deal with future outbreaks in areas free of the disease, as well as developing a new-generation vaccine that can effectively control and eventually eradicate the disease from areas currently infected.

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