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Globalization and disease

Globalization plays a role in the ongoing geographic redistribution of pathogens, hosts and vectors, through increased trade and traffic volumes and international passenger travel. Related drivers are land-use and climate changes. Where a combination of drivers is at play, a complex, multifactorial process is likely to emerge, usually making it difficult to identify how each driver contributes to the overall disease dynamics. Where a single introduction event leads to successful establishment and wider spread, the causality chain is less difficult to clarify. A new disease agent may be identified phylogenetically and matched against the pathogen fingerprints prevailing in potential source areas. This may lead to the identification of the main risk factors involved: travel by humans; or trade in live animals, plants, primary agricultural products, processed food or other commodities. International trade is increasing significantly in the emerging and transition economies, particularly Brazil, Chi-

na, India, Indonesia, the Russian Federation and South Africa.

The international community should also direct its attention to the ease with which new pathogens spread around the world. The experience acquired from the SARS pandemic in 2003 (Braden *et al.*, 2013) and the pH1N1 influenza pandemic in 2009 suggests that a novel human-to-human transmissible virus causing mild to severe acute respiratory disease may spread around the world in a matter of weeks, in a pattern that follows the passenger flow through the network of international airports. Once a new disease starts to spread within a country, it may be too late to close international airports (Ferguson *et al.*, 2006; Hollingsworth, Ferguson and Anderson, 2006). The potential for rapid global spread is a concern because a novel influenza, corona or other respiratory virus of animal origin that is capable of human-to-human transmission may lead to very substantial damage.

The globalization of pathogenic agents poses threats to the health of humans, livestock, plants, fisheries, forestry and ecosystems (de La Rocque *et al.*, 2008; Pfeffer and Dobler, 2010; Randolph and Rogers, 2010). Recent examples

of each of these categories or health domains are easy to find. For instance, a major epizootic of Rift Valley fever (RVF) virus in the Arabian Peninsula in 2000–2001 was attributed to shipments involving live animals and mosquitoes from mainland Africa (Miller *et al.*, 2002). In 2003, the bacterium *Ralstonia (Pseudomonas) solanacearum* race 3 biovar 2 was transmitted from Kenya to greenhouses in the United States of America via imported geranium plants (Strange and Scott, 2005). The globalization of fisheries production and supply allowed white spot disease in shrimps to make its way from Asia to the Americas in the mid-1990s (Walker and Mohan, 2009).

Spread may result from passive shipment or active migration by wild species. A wide range of wild mammals, birds, fishes and arthropods are important from a public health, veterinary or ecohealth perspective. Biological invasion entails the introduction of entire microbial reservoirs into a new geographic area (Altizer, Bartel and Han, 2011). Migration of infected humans travelling from remote African villages to urban settlements presumably triggered Chikungunya virus epidemics (Chevillon *et al.*, 2008). A combination of factors, including bird migration and land-use and climate changes, probably plays a role in the progressive spread of Japanese encephalitis virus into expanding areas of rice farming (Tyler, 2009).

The globalization of livestock production and supply is reflected in the increased trade in poultry, swine and ruminants, feeds and livestock products. Industrial poultry production became prominent in the United States of America and Canada during the 1950s and 1960s. Europe followed during the late 1960s and 1970s, next came Latin America, mainly during the 1980s and 1990s, and Asia during the 1990s to 2010s. In Africa, industrial poultry production is currently on the rise, with major increases expected for the coming decades. The globalization of intensive poultry production has been a factor in the spread of multiple, poultry-associated pathogens. Trade in live birds (day-old chicks),

poultry meat and soiled eggs are the main risk factors. For example, H5N1 AI virus was detected in 2001 in frozen duck meat imported into the Republic of Korea (Lu *et al.*, 2003). Chicken meat may be contaminated with Enterobacteriaceae containing extended-spectrum β -lactamase (Overdevest *et al.*, 2011).

The international trade in pigs and pig meat also contributes to the spread of disease. A prime example is the ongoing international spread of ASF virus. The ASF transmission mode depends on the ASF virus genotype involved. ASF may be directly transmitted from pig to pig, involve a tick vector, or spread over long distances in contaminated pig meat products that are fed to pigs as food scraps. Starting in the 1950s, multiple introductions of ASF virus from Africa to Europe eventually resulted in endemic ASF in the Iberian Peninsula (eradicated in 1995), where virus transmission was sustained, in part, by a local tick species; and to Sardinia, Italy, where the virus still circulates in wild boar. The Americas also experienced several ASF virus introductions, mainly from Europe. At least three different ASF virus genotypes started to spread across sub-Saharan Africa in the 1990s, devastating village-level pig production. An introduction of ASF virus into Georgia in 2007 probably concerned contaminated food scraps, which arrived on a ship from a country in Southern Africa and were fed to pigs in the port of arrival (Rowlands *et al.*, 2008). Following rapid spread throughout Georgia, outbreaks were subsequently reported in Armenia, Azerbaijan, the Russian Federation and Ukraine, affecting domestic pigs and wild boar (FAO, 2008a). Belarus reported ASF in 2013. The pig meat trade was found to be a major risk factor in the spread of this specific genotype, along with swill feeding, low biosecurity, free roaming of pigs and the presence of wild boar (FAO, 2012a). A gradual, progressive spread of this ASF virus to neighbouring countries with high densities of smallholder pig farmers is likely; most countries in Eastern and Central Europe are believed to be at direct risk.

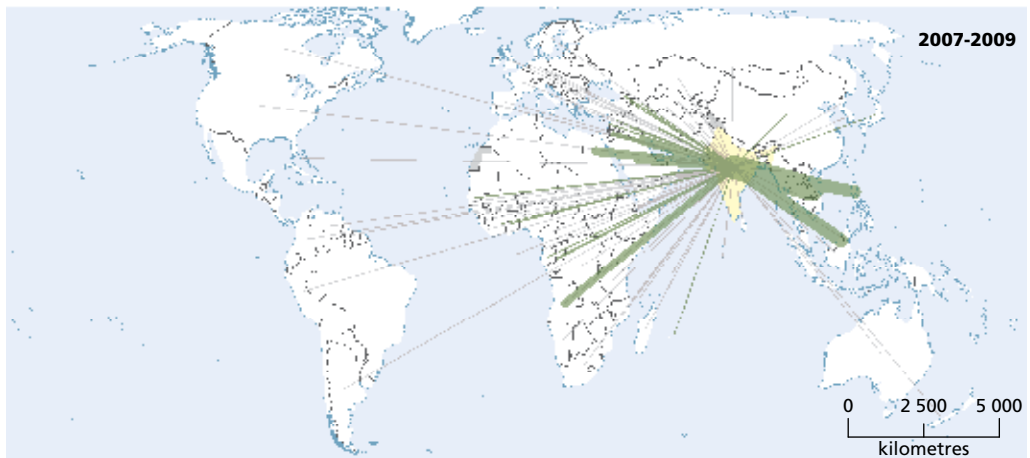
More distant introductions of ASF virus into the EU, Asia (including China) and the Americas cannot be excluded.

The global trade in live ruminants involves sheep, goats, cattle and buffaloes. Disease spreads with the trade of live animals as well as with the meat and milk trade. For example, illegal imports of FMD-contaminated food items combined with swill feeding to pigs presumably explain the FMD epizootic that occurred in 2001 in the United Kingdom of Great Britain and Northern Ireland (Hartnett *et al.*, 2007). FMD is the most contagious livestock disease known, spreading through direct animal-to-animal transmission, virus dispersal by wind, contaminated fomites or in food items, including frozen meat. Food items may be growing in importance as a risk factor; according to FAO-STAT, bovine meat exports from India, where FMD is endemic, increased by 800 percent from the late 1980s to the late 2000s, involving 87 importing countries, up from 38 (Figure 25). India (along with Brazil) tops the list of beef exporting countries worldwide.

The Greater Horn of Africa supplies increasing numbers of live ruminants to the Arabian Peninsula and North Africa. The Sudano-Saharan agro-ecological zone supplies cattle to the coastal markets of West Africa and countries in North Africa. South Africa, which has FMD-free status, exports growing numbers of live cattle to countries outside Africa (Figure 26).

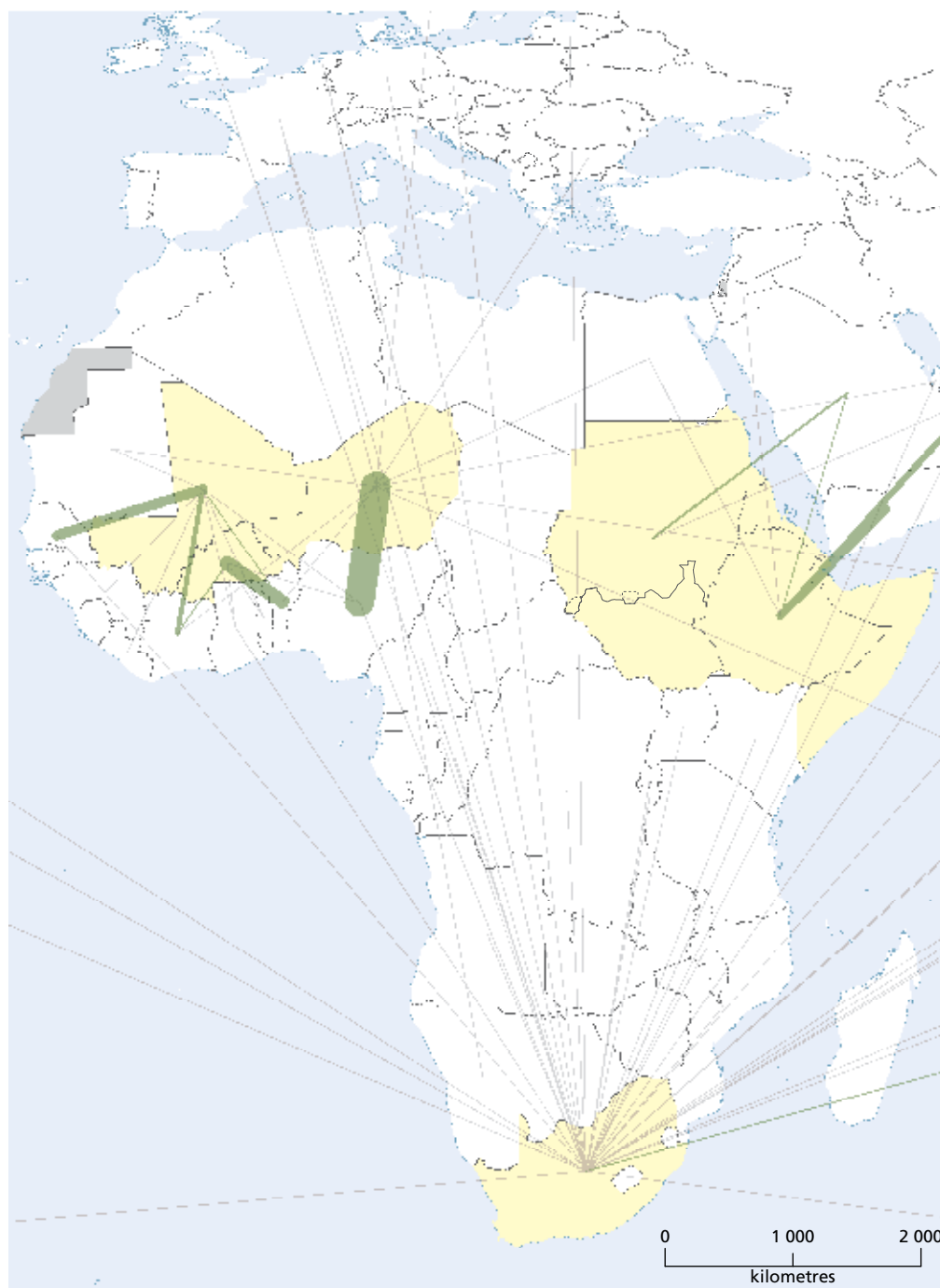
The global trade in small ruminants is dominated by sheep exports from Australia, the Horn of Africa and Central Asia, to the Near East and North Africa regions. When exchanges within the EU are excluded, the trade of sheep and goats to the Near East and North Africa accounts for 80 percent of global small ruminant trade (Figure 27). Australia is free from major infectious livestock diseases, although Australian ruminants carry a variety of potentially relevant arboviruses; a study carried out during the 1980s in sentinel livestock in northern Australia revealed 27 separate arboviruses belonging to the bluetongue, epizootic haemorrhagic disease, Palyam, Simbu, bovine ephemeral fever, tibrogargan and alpha virus groups (Gard *et al.*, 1988).

25 EXPORTS OF BOVINE MEAT FROM INDIA (2007–2009)



Source: FAO-STAT.

26 EXPORTS OF LIVE CATTLE WITHIN AFRICA AND TO OTHER COUNTRIES (2007–2009)



Cattle $\times 10^3$ per year

— <math>< 3</math>

— 3

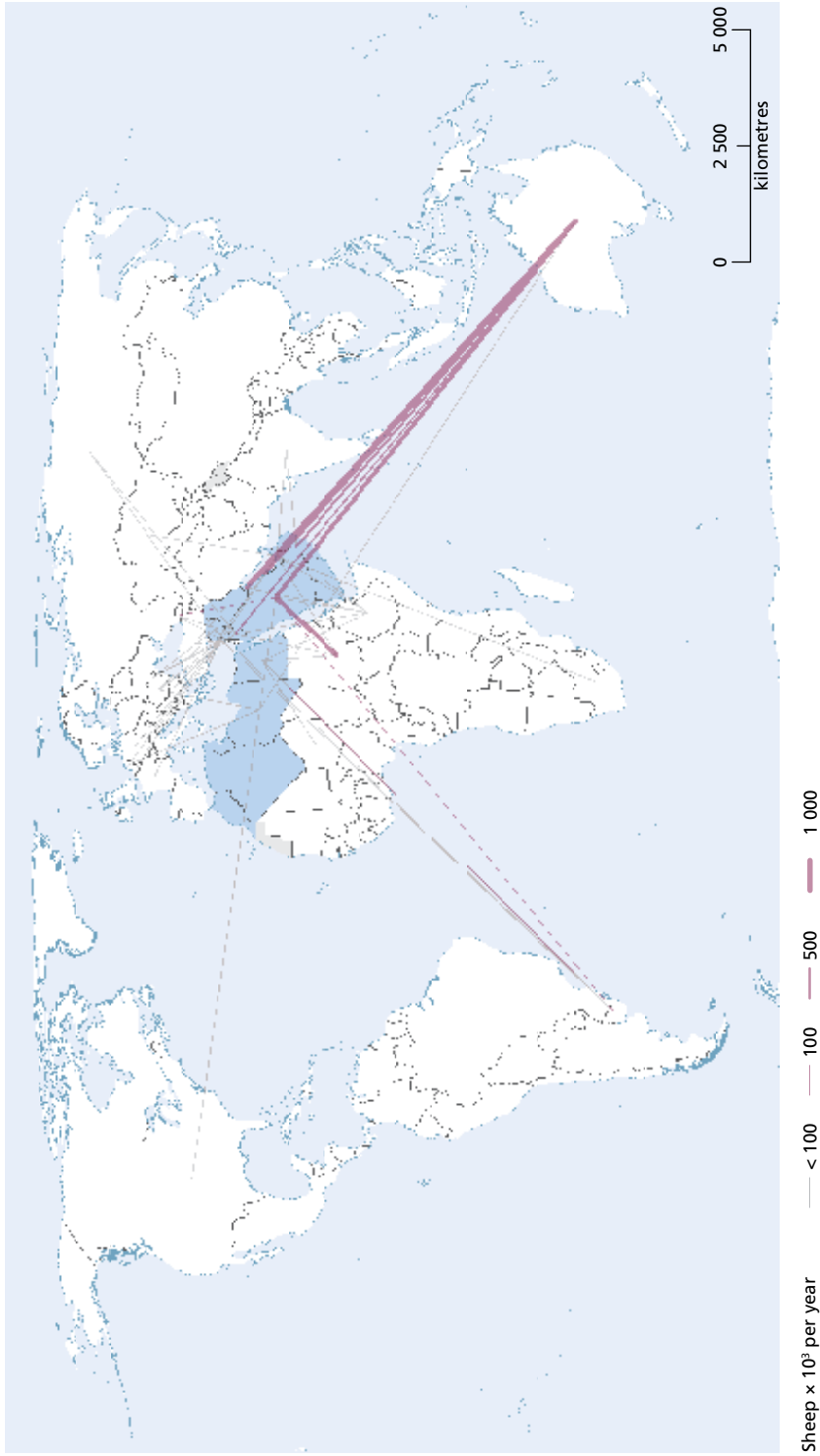
— 10

— 50

— 100

Source: FAOSTAT.

27 IMPORTS OF LIVE SHEEP BY COUNTRIES IN WESTERN ASIA AND NORTH AFRICA



Source: FAOSTAT.

Ruminants imported from the Horn of Africa to the Arabian Peninsula may carry the viruses of RVF, bluetongue, peste des petits ruminants and/or FMD.

A combination of factors, including climate change, may be responsible for the apparent increase in the incidence of arthropod-borne viral diseases in the eastern Mediterranean basin, which is posing a risk to the temperate climate zones of Asia and Europe. The emergence of bluetongue virus-8 in 2006 and Schmallenberg

virus in 2011 in northern Europe are examples (Beer, Conraths and van der Poel, 2012; Maclachlan, 2010). *Aedes albopictus*, the mosquito vector of dengue and Chikungunya viruses, was first detected in Europe during the 1970s in Albania (Adhami and Reiter, 1998), where it may have arrived from China, the chief trading partner of Albania at the time. In China and the Korean Peninsula, *A. albopictus* has spread northwards to higher latitudes, as far as Beijing. A similar development may be taking place in Europe.



Climate change and disease

As one of a set of factors that are modulating disease landscapes worldwide, climate change directly and indirectly influences disease emergence, spread and persistence. Climate change impacts operate in tandem with increased trade, traffic and travel by humans, to drive changes in the geographic ranges and occupancy patterns of disease complexes and pest agents. As discussed in the previous chapter, it is notoriously difficult to single out the role of climate change in situations where the disease dynamics result from several drivers operating simultaneously. A further complication is that climate change may influence the ecology of the host, vector abundance *and* the pattern of disease transmission. However, climate change has undeniable effects on the incidence of disease, as illustrated by its effects on the free-living pathogen stage: climate change has direct impacts on the environmental survival rate of disease agents and, therefore, on the success of disease transmission.

For example, the influenza viruses that cause common flu in humans survive well in cold and humid conditions during winter, and are transmitted via handshakes, infected aerosol particles or doorknobs (Lowen *et al.*, 2007). The ancestral influenza A virus circulates in mallard ducks – the foremost wildlife host – through faecal-oral transmission based on the ingestion of water. Viruses deposited by migratory waterfowl in and around water bodies during summer breeding in subarctic zones may be stored in near permafrost conditions and survive for extended periods (Zhang *et al.*, 2006). Climate change in the form of a gradual rise of ambient temperature may cause the meltdown of virus-contaminated ice (López-Bueno *et al.*, 2009). Environmental pathogen loads are important in the transmission of all food- and water-borne disease complexes. Food poisoning usually entails faecal contamination of food items or water. Environmental survival matters for gastrointestinal roundworms in ruminants because, on pasture, nematode larvae survive for weeks outside the host. The anaerobe bacterium *Bacillus anthracis* survives for many decades as spores in the soil (Dragon and Rennie, 1995). Climate

change may alter the frequency of flooding and drought events, which may lead to the congregation of animals in unusual places, enhancing the risk of exposure to anthrax spores.

Vector-borne diseases transmitted by arthropods are a distinct category. The transmission of a broad variety of viruses, bacteria, protozoa and blood parasites is facilitated by a range of arthropods, comprising midges, mosquitoes, fleas, flies and ticks. For example, soft ticks (*Ornithodoros moubata*) feeding on warthogs are vectors for the ASF virus, which survives for up to eight years in the tick. The sturdiness of the virus is an important feature in the natural, sylvatic cycle of ASF virus (Kleiboeker and Scoles, 2001). Environmental robustness has become important for ASF virus transmission in domestic pig and wild boar populations in Europe, with survival in contaminated meat products or in wild boar carcasses, at least during winter and at higher latitudes. Climate change is, therefore, likely to play a role in the dynamics of ASF virus in this part of the world.

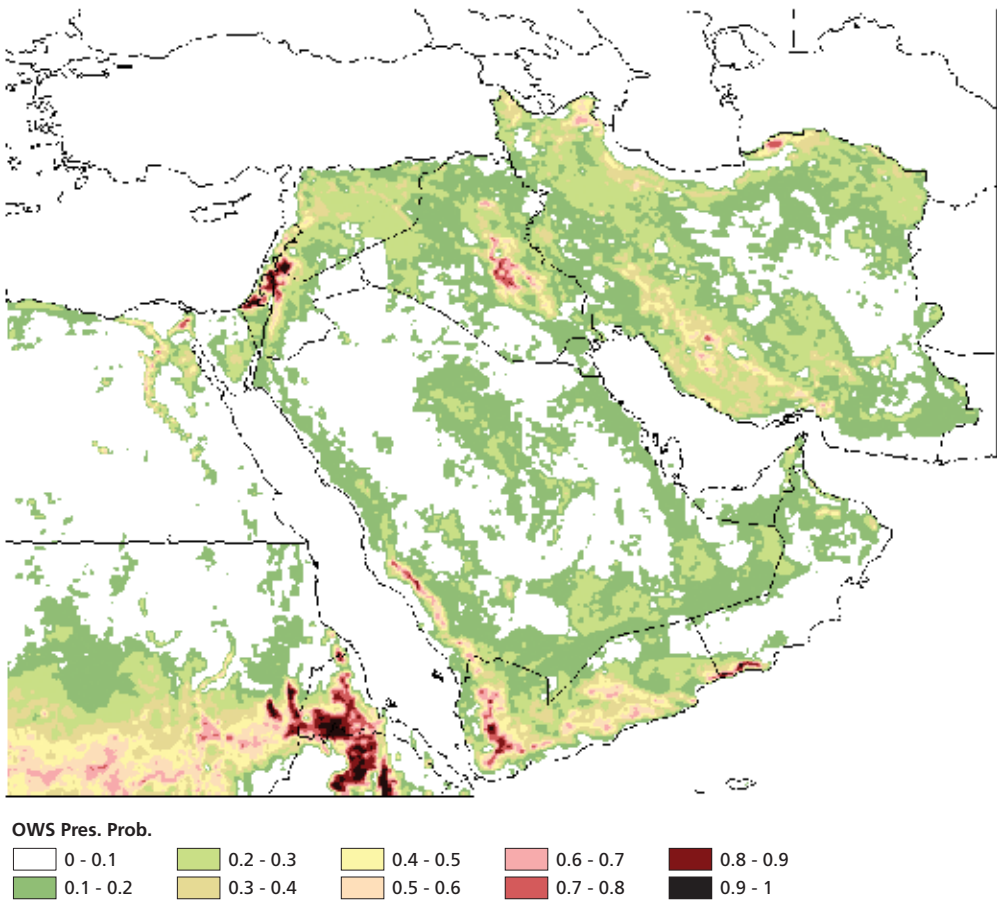
Midges and mosquitoes may also support a dormant pathogen stage outside the host body. RVF virus may survive for decades in mosquito eggs deposited in swampy areas, until a prolonged, heavy rainfall facilitates the hatching of countless *Aedes* mosquitoes. Once these mosquitoes start feeding on ruminants, a new RVF outbreak starts up (Anyamba *et al.*, 2009; Mondet *et al.*, 2005). When infected ruminants arrive at irrigation schemes with abundant mosquitoes, ruminants and people, *Culex* mosquitoes also take part in the transmission, and large numbers of people may be infected. Climate anomalies associated with El Niño Southern Oscillation modulate rainfall, and therefore RVF risk, in much of Africa.

Midges may spread disease when carried by wind across wide geographic areas. This is probably what happened when bluetongue virus-8 was introduced into the United Kingdom of Great Britain and Northern Ireland in summer 2006, having first spread from the southern tip of the Netherlands westwards across Bel-

gium (Gloster *et al.*, 2008). The introduction of Schmallenberg virus into the United Kingdom of Great Britain and Northern Ireland in early 2012 may also have resulted from wind carrying midges from mainland Europe (Gibbens, 2012). It could be speculated that a climate change-driven increase in temperature in the temperate climate zone of the Northern Hemisphere will trigger a northwards spread of vector-borne diseases, starting with the disease complexes that spread with greatest ease – midge-borne viral diseases – followed by diseases that spread via mosquitoes, then via ticks and flies.

There is growing evidence that at least some of the demographics and distributions of flies of veterinary and/or medical importance are influenced by climatic and weather conditions. For example, the flies from both Old World screwworm (OWS) and New World screwworm (NWS), (*Chrysomya bezziana* and *Cochliomyia hominivorax*, respectively) feature a free-living larval and an adult fly stage. The female deposits eggs in the open wounds of warm-blooded hosts, enabling the first larval stage to feed on live tissue (Spradbery, 1991). More than 200 larvae may result from a single egg batch, causing an ever-expanding wound that attracts additional screwworm flies. Larvae leaving the wound drop to the ground and bury 2 cm into soil to become pupae. The pupal stage lasts for about a week, depending on the soil temperature, after which an adult fly emerges from the pupa shell. The risk of screwworm fly may be mapped based on the fly's life cycle, using satellite-derived proxies for soil temperature and vegetation cover (Figure 28) (FAO, 2008b). From this somewhat simplified risk map, it would appear that substantial areas of the Arabian Peninsula and the Greater Horn of Africa currently provide suitable conditions for the survival and persistence of OWS. However, there are additional risk factors. The extensive trade in live ruminants typical of the Arabian Peninsula supports dispersion or "seeding" of OWS into novel territories, including where local conditions are or are becoming favourable for year-round OWS per-

28 AREAS WHERE THE RISK OF OWS IS RELATIVELY HIGH



Source: FAO, (2008b).

sistence. OWS in livestock and humans has been reported in the Gulf countries since the 1980s, starting with relatively small foci becoming established respectively in Oman, Saudi Arabia and the Islamic Republic of Iran. OWS myiasis did not pose a serious problem to livestock production until a major epidemic suddenly started in 1996 in the Mesopotamia valley in Iraq. Parts of Yemen have also become OWS-endemic since the 2000s. Climate change may have been one of several factors influencing spread of the screwworm fly and screwworm myiasis. In Uruguay, at the southernmost distribution limit of the

NWS fly, climate change has been identified as a main driver of the expansion in range of these flies (Pinto *et al.*, 2008).

The effects of climate change on the abundance and distribution of the tsetse fly – the vector of human and animal African trypanosomosis – are rather different from the effects on the screwworm fly, despite some remarkable life history similarities: tsetse flies also feature a pupa development stage in the soil. However, whereas a single batch of screwworm fly eggs yields more than 200 larvae, the female tsetse fly deposits one larva every nine days, and gener-

ates a mere six to eight larvae during its lifespan (Ford, 1971). While screwworm flies disperse over hundreds of kilometres within a few weeks, the tsetse fly rests on a tree stem for most of the daytime, waiting for a host to show up; tsetse fly activity is restricted to a mere 15 to 20 minutes a day. These and many other differences mean that the effects of climate change on the abun-

dance, distribution and disease transmission of the two types of fly cannot really be compared. The savannah-type tsetse fly from southwestern Ethiopia invaded the country's central highland plateau only very gradually, reportedly starting in the 1960s (Slingenbergh, 1992), whereas OWS fly abruptly colonized new areas of the Arabian Peninsula (Siddig *et al.*, 2005).



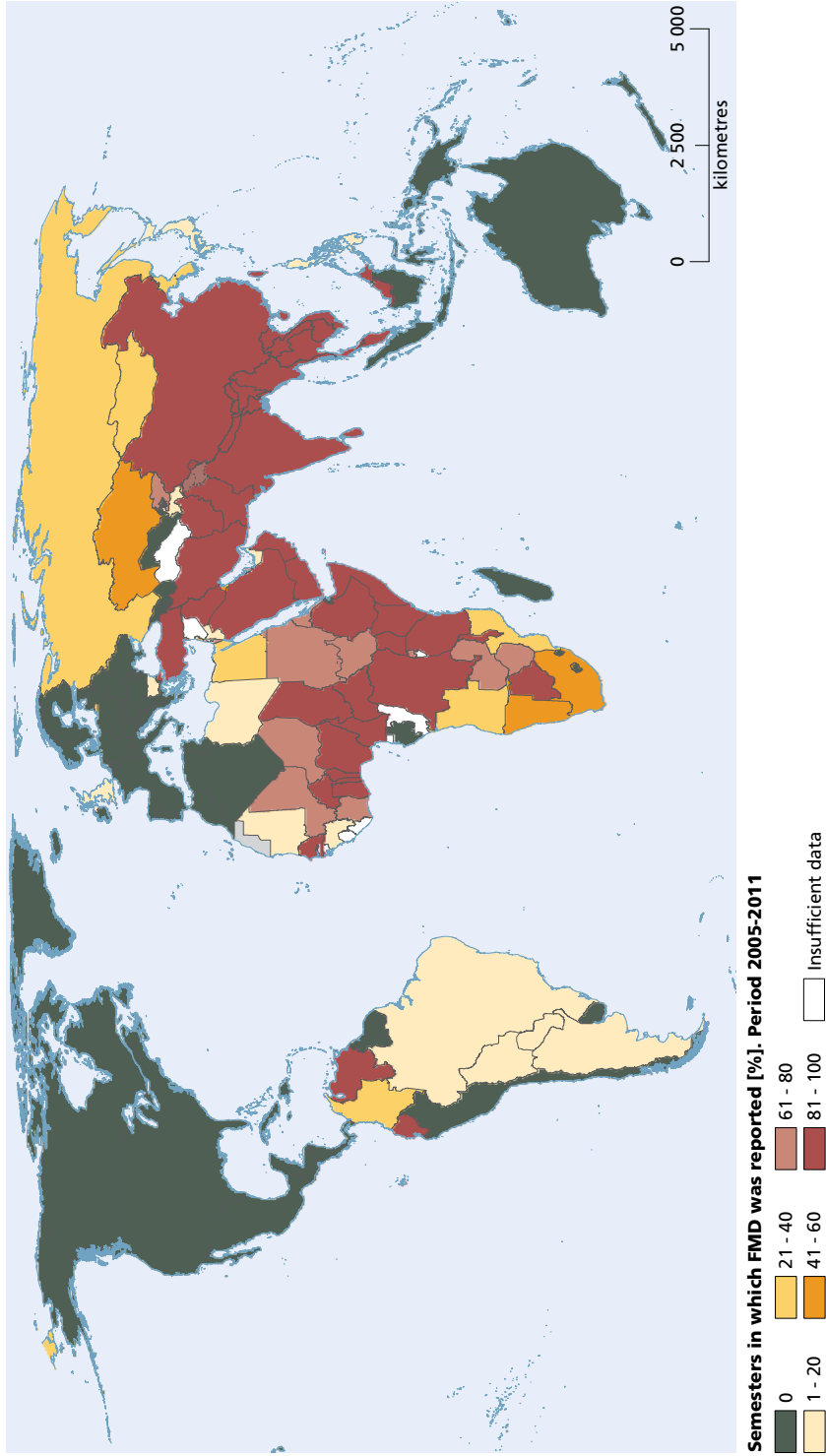
Livestock productivity, animal health inputs and disease

Developing countries feature relatively high burdens of disease in humans and animals. Among the endemic diseases affecting these countries, tropical diseases are prominent, comprising a variety of often vector-borne parasitic, protozoan and infectious diseases. As well as climate, a combination of other factors plays a role. In livestock, the high disease burden goes hand-in-hand with low productivity levels. Farmers tend to invest in animal health up to the point beyond which further investment would no longer be profitable, and the law of diminishing returns also applies to any disease campaigns orchestrated by public veterinary services. Where the livestock industry is important to the national economy, there is an incentive to invest in pro-

gressive disease control and prevention. In contrast, low-input, low-output systems generate a vicious circle in which disease lowers productivity while low productivity presents an obstacle to investments in animal health.

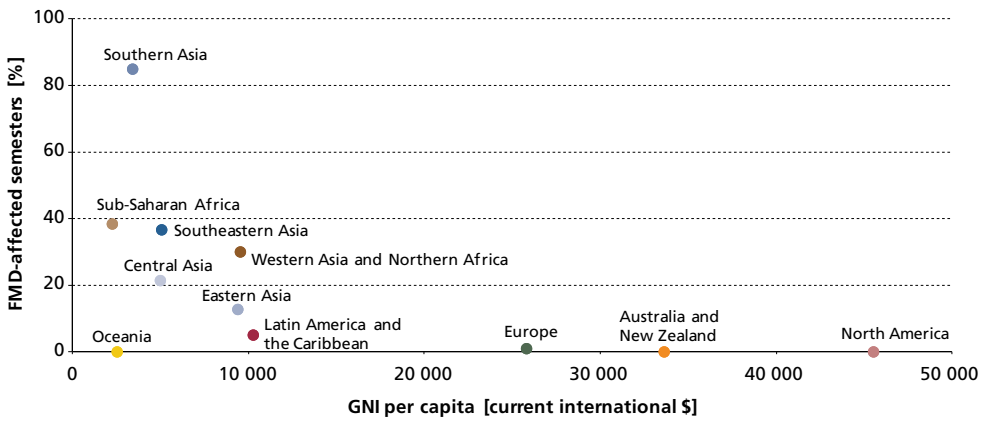
The relationships among livestock productivity, animal health investment and presence of disease may be illustrated using OIE data on FMD in domestic ruminants and pigs and on Newcastle disease in poultry. Historically, both of these high-impact diseases occurred ubiquitously. Figure 29 shows the FMD presence worldwide for the semesters of 2005–2011, including all FMD serotypes. The results suggest that FMD is endemic in Africa and Asia, while Latin America and the Caribbean is relatively FMD-free, and the developed world is mainly FMD-free, with a few exceptions. In Figure 30, the FMD scores from Figure 29 are used to calculate regional averages, which are matched against the corresponding per capita income levels. The results suggest that there may be a critical point beyond which the economic viability of FMD control increases rapidly. Recently, major success has been achieved with the elimination of FMD from the Philippines and countries

29 OCCURRENCE OF FMD (ALL SEROTYPES) IN LIVESTOCK REPORTED TO OIE (2005–2011)



Source: Adapted from OIE World Animal Health Information Database: http://www.oie.int/wahis_2/public/wahid.php (accessed 22 October 2013; information cited 3 October 2012)

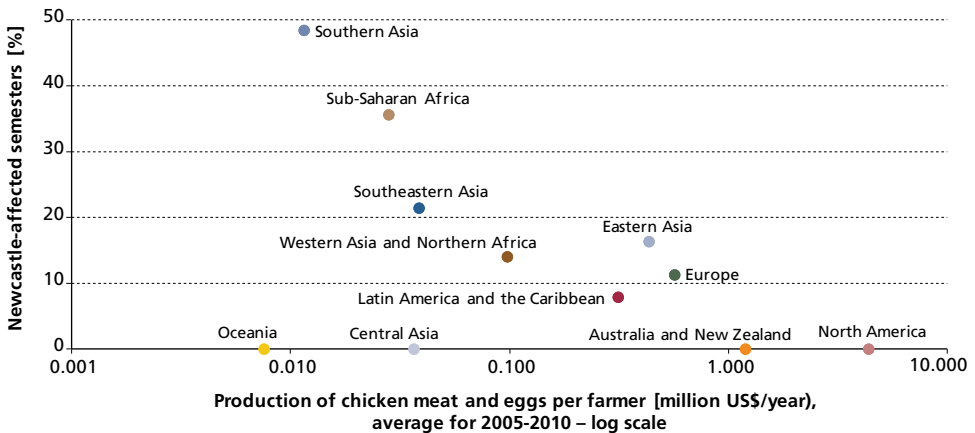
30 RELATIONSHIP BETWEEN REGIONAL INCOME PER CAPITA AND OCCURRENCE OF FMD



The FMD presence by region is based on the average country score, the number of semesters in 2005–2011 with FMD presence, as reported officially to OIE. Gross national income (GNI) per capita for the same period is calculated from the collective GNI generated by the regional population.

Sources: Adapted from OIE World Animal Health Information Database: http://www.oie.int/wahis_2/public/wahid.php (accessed 22 October 2013; information cited 3 October 2012); World Bank.

31 RELATIONSHIP BETWEEN REGIONAL POULTRY-RELATED FARMER INCOME AND OCCURRENCE OF NEWCASTLE DISEASE



Source: Adapted from OIE World Animal Health Information Database: http://www.oie.int/wahis_2/public/wahid.php; FAOSTAT.

in Latin America and the Arabian Peninsula. The Small Island States of Oceania appear to enjoy a relatively disease-free status, presumably because of their geographic isolation. The rather

high FMD score for the Near East and North Africa possibly relates to the large imports of live ruminants from FMD-endemic areas in sub-Saharan Africa and Central/South Asia. Disease

underreporting may have been an issue in some countries.

Figure 31 shows the relationship between the presence of Newcastle disease in poultry and the level of poultry-related income (log scale) in different geographic regions. The figure suggests that Newcastle disease is endemic in South Asia and sub-Saharan Africa, where smallholder poultry predominates, while recurrent epidemics occur in regions with a mix of intensive and extensive poultry production. The industrial poultry industries of Australasia and North America maintained Newcastle disease-free status, as did the Small Island States of Oceania, unless underreporting played a role – as was most likely the case for Central Asia.

Given the recent increase in livestock production in emerging economies, and also in a grow-

ing number of developing countries, it is likely that the harsh realities illustrated in Figures 29 to 31 will not apply in the future. The increased demand for animal-source food provides an incentive for farmers to upgrade domestic livestock production, and may also help smallholders with livestock. In countries where higher animal-source food consumption translates into an increased demand for livestock products, animal health investments become more profitable. Farmers, food industries and public veterinary services are encouraged to collaborate in progressive disease control, because animal health is a prerequisite for higher productivity. Investment in animal husbandry, whether in nutrition, animal genetics or housing, may become profitable provided the risk of high-impact livestock disease has first been contained.



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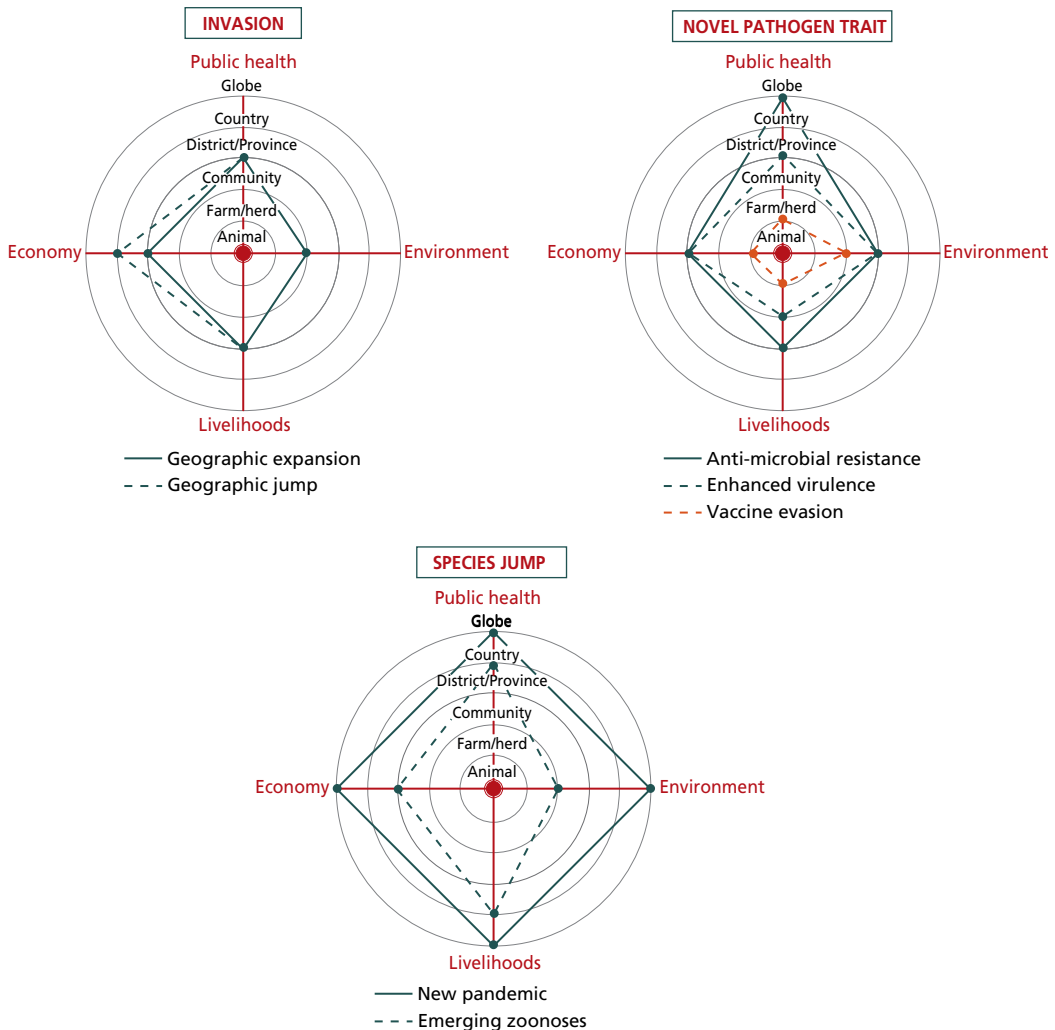
Interacting disease drivers, dynamics and impacts

In the event of a livestock disease outbreak, the direct impact is routinely measured in terms of morbidity and mortality, which helps to define the disease in clinical terms, and the extent of economic loss. Before considering the full array of actual and potential impacts, health professionals require adequate technical details, including information on the precise identity of the pathogen, the mechanisms of contagion, and the pattern and direction of disease spread. These details are needed to decide on the most appropriate disease control and prevention measures. The immediate priority is always to prevent further negative impacts by disrupting transmission through “firefighting”. Early detection, early warning and early response are key ingredients of the disease responses of modern animal health services.

Once the immediate challenges have been addressed, health professionals – along with livestock producers and other stakeholders – may consider the circumstances that led to the outbreak event. This stage may result in the identification of measures that could have prevented the outbreak in the first place, or at least might have dampened it. Such an exercise requires joint consideration of the disease drivers, dynamics and impacts. Developing an overall picture of a disease event is a notoriously difficult challenge and is not yet a routine part of the risk assessment exercise.

Previous sections have highlighted the common causes of disease emergence, spread and persistence. Global drivers of disease emergence and spread are rapid livestock development, high pressure on the natural resource base, globalization through increased travel and trade, climate change, and lagging socio-economic development and malfunctioning health systems. Preventive measures may involve the enhancement of socio-economic development, safe practices in food and agriculture, safe trade and travel, improved resource management and/or climate change mitigation. By acting on the drivers of

32 EXAMPLES OF TENTATIVE IMPACT PROFILES FOR DIFFERENT EMERGING DISEASE DYNAMICS



disease, health protection becomes an integral part of wider sustainable development efforts and, therefore, a cross-sectoral task.

Impact assessment is complicated by the inextricable links among poverty, disease burdens and food insecurity, making it necessary to consider the full set of livelihood-related concerns. Disease impact profiles should also be drawn up on a case-by-case basis, depending on the agricultural and socio-economic development set-

tings, specific disease ecologies, and prevailing perceptions and priorities of concerned communities and other stakeholders. Experiences acquired from the fight against animal and pandemic influenza have shown that although the international community may perceive tackling pandemic threats as an important public good, poor people prioritize more mundane day-to-day livelihood concerns. There is therefore need to consider the various disease threats in

the context of overall development and to apply these findings when looking for incentives that may involve collective action.

Environmental issues also need to be considered. The environment is affected by disease directly and indirectly and in various ways. Biodiversity may be directly affected when an emerging disease provokes high mortality and the (local) extinction of wildlife species (Dobson and Hudson, 1986). Biodiversity losses may bring disease, and diseases may bring biodiversity loss (Keesing *et al.*, 2010). An important *indirect* effect of livestock disease on the environment results from the decreased efficiency of production: lower feed conversion has a negative environmental impact on livestock. The result is increased demand on the natural resource base.

Livestock disease also has important effects on the national economy, but these are difficult to establish in quantitative terms. The collective expenditures of livestock producers, veterinary services, food safety authorities and public health agencies add to the costs of livestock diseases. A disease may indirectly influence the pace and nature of the agricultural or rural development process. For instance, horses, mules and donkeys are precluded from the tsetse-infested areas of sub-Saharan Africa because of the risk posed by AAT. Livestock keepers in tropical climate zones face a myriad of disease-related challenges. International disease outbreaks can lead to sudden, major economic shocks for farmers, com-

munities, businesses, organizations and even the global economy. Of even greater concern are the pathogens that jump host from animals to humans. In an internal report, the World Bank estimated that a severe influenza pandemic would cost more than US\$3 trillion and hit the poor the hardest. Current international initiatives, therefore, seek increasingly to establish more equitable allocation and sharing mechanisms for therapeutic resources, public health interventions and other broad-based support in the event of a pandemic in developing countries (Ong *et al.*, 2008).

Adding to the complexities of disease drivers and impacts are the disease dynamics themselves. This is illustrated in Figure 32, which provides tentative impact profiles for three distinct disease emergence scenarios in which a pathogen:

1. becomes established in a new area, adjacent to or located across a geographic barrier;
2. displays a novel trait, in the form of antimicrobial resistance, hyper-virulence and/or vaccine evasion;
3. performs a host species jump from animals to humans, causing a severe pandemic.

Figure 32 highlights the complexity of impact profiling and the difficulty of comparing different disease dynamics. However, everyday health policies tend to be defined on the basis of vague assumptions regarding the impact profile, so even a modest improvement in this regard may provide useful support to health policy decision-making.