



Poster in the Sofia Airport, Bulgaria

Main animal disease threats in 2010: pathogen types, drivers and challenges

Infectious animal diseases can have a major impact on public health, national economies and livelihoods. Disease emergence is triggered by multiple, interrelated factors, which veterinary services need to take into account to ensure better control of diseases through incorporating other relevant disciplines such as economics and sociology. This article describes the main animal disease threats reported during 2010, their drivers and challenges (page 2).

FAO/EUFMD mission to Turkey concerning FMD outbreaks in Bulgaria

The Food and Agriculture Organization of the United Nations (FAO) and the European Commission for the Control of Foot-and-Mouth Disease (EUFMD) sent a team to the Demirkoy District of Kırklareli Province in Turkey to evaluate what would be the most likely immediate source if spread had been through local wild boar or livestock. The team visited villages close to the recent foot-and-mouth disease (FMD) detection locations in Bulgaria to conduct interviews and provide advice on surveillance (page 14).

AND...

FMD in Mongolia in 2010: FAO response (page 18)

PRRS: virulence jumps and persistent circulation in China and Southeast Asia (page 30)

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Mixing species, as in this backyard poultry farm, may lead to expansion of the host range of HPAI

H5N1 HPAI worldwide in 2010

Following three years of progressive retraction, geographic expansion of the H5N1 highly pathogenic avian influenza (HPAI) virus was again observed in 2010. It is interesting to note that in late 2010 clade 2.3.2 became the most common clade in the spread of H5N1 HPAI and its invasion into new territories (page 21).



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World free from rinderpest:

FAO and the World Organisation for Animal Health (OIE) are about to declare that rinderpest has been eradicated from the planet (page 36).



Main animal disease threats in 2010: pathogen types, drivers and challenges

Infectious animal diseases can have a major impact on public health (zoonoses), national economies (high-impact diseases), household livelihoods (enzootic diseases) and, in very serious cases, global societal stability and security (pandemics, bioterrorism). Disease emergence is triggered by multiple, interrelated factors: human and animal demographics, climate change, increased mobility and globalization, urbanization, land degradation, drug resistance, and mass animal rearing. The booming demand for animal-source protein has driven large increases in livestock production and trade during the past few decades. The resulting changes to host environments, and therefore to pathogen dynamics, can lead to adjustments such as expanding geographic range, jumping host species and/or shifts in virulence. The most common and least complicated pathogen adjustment concerns slight changes in virulence, usually following changes in susceptible host availability. Infectious diseases of animals and humans show some variability in virulence, thus accommodating local and seasonal fluctuations in susceptible host availability and consequent contact rates. For emerging disease pathogens there are three main pathways for pathogens to adjust host exploitation.

There are three main pathways for pathogens to adjust host exploitation

Pathogens as invaders into new territories

This scenario occurs when a pathogen finds access to new areas and host populations. These invasions are typically triggered by globalization, climate change and changes in land use. Invasion may take the form of a travelling wave, saltation or a mix of both. Vector-borne diseases are prominent in this group, as are pathogens that are food-borne or environmentally robust enough to be transported by fomites across wider areas. Invading pathogens may adapt to new arthropod vector species and/or different host types. More often, however, there are no dramatic changes in host range or in the infection process in the individual host but, rather, a modest change in the overall transmission pattern. The incursions of West Nile virus in North America, bluetongue in temperate climate zones of Europe, African swine fever (ASF) in the Caucasus and eastern Europe, Japanese encephalitis in southern Asia, and Rift Valley fever (RVF) in the Arabian Peninsula are among the more prominent invasions of pathogens into new locations in recent years.

Pathogens performing virulence jumps

This event typically associates with the mass rearing of host species, which first became evident during the green revolution in crop agriculture. More aggressive pest agents showed up in plant monocultures, requiring vast amounts of pesticides and triggering the development of pesticide resistance. This development was eventually contained when integrated pest management concepts were introduced. There is a parallel development in animal production; the livestock revolution translates into sharp increases in livestock numbers, particularly of poultry and pigs, with mass rearing in confined holdings. In situations where pathogens find access to rearing units



of tens of thousands of animals – most of which are of the same age and sex, genetically near-clones and often immuno-compromised – there is a fitness premium for pathogens that are capable of a virulence jump and of becoming more host-aggressive and transmitting faster than competing pathogens. In situations where traditional and industrial farming systems coincide, and share distribution and marketing channels, there is opportunity for virulent pathogens to exploit the mix of production settings. Highly pathogenic avian influenza (HPAI) viruses are an example of this phenomenon in the poultry sector. Other examples in poultry are hyper-virulent Gumboro disease or infectious bursal disease virus, velogenic Newcastle disease virus and infectious bronchitis viruses; in pigs, examples include the viruses causing porcine reproductive and respiratory syndrome (PRRS) (see article on p. 30). With the livestock revolution advancing from North to South and involving emerging economies in particular, the conditions are present for other hyper-virulent pathogens to evolve and emerge as serious production problems. The appearance of antimicrobial-resistant bacteria can also be classified within the virulence jump category. Multi-drug resistance is on the increase because of the massive scale and erroneous application of antibiotics for medical treatments, and the use of drugs as growth promoters. Although animal- and human-related drug resistances usually evolve separately, drug resistance genes may traverse the bacterium species barrier, opening the door for drug resistance to pass between animal- and human-related species.

Pathogens performing species jumps

Where there are changes in the host community composition and/or the inter-host contact rate, pathogens capable of a species jump may be selected for. Many of today's human diseases passed from newly domesticated animals to humans during the early days of the agriculture revolution, starting about 10 000 years ago. A similar event started during the second half of the twentieth century, with the still ongoing livestock revolution. Increases in the animal-human contact rate and the pathogen exposure of humans also result from the bushmeat and exotic wildlife offered for sale in wet markets, while recreational activities and tourism bring humans into contact with pathogens circulating in forest and game reserves. The human immunodeficiency virus (HIV) emerged in humans following increases in the consumption of chimpanzee and other bushmeat. The severe acute respiratory syndrome (SARS) coronavirus found its way to the human host via people's encounters with civet cats on sale for consumption in wet markets. Influenza A viruses, abundant in wild water bird reservoirs, increasingly find their way into pig and poultry production systems, occasionally followed by animal-to-human spill-over or species jumps. Of the total of about 4 600 mammal species found on the planet, 43 percent are rodent and 24 percent bat species. Rodent-borne emerging zoonoses include hantaviruses, arenaviruses, plague, Lyme disease, scrub typhus and a number of rickettsial diseases. Bats harbour SARS-like viruses, Hendra, Nipah, lyssavirus (ra-



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Collection of a bat trapped in a net placed in the Yoko Forest, Democratic Republic of the Congo



The One Health approach outlines a collaborative, international, cross-sectoral, multidisciplinary mode of addressing threats and reducing risks of infectious diseases

bies), Ebola and other less well characterized ribonucleic acid (RNA) viruses. Wildlife and natural ecosystem health form part of responsible health management. The interfaces between wildlife and livestock and between animal-source food and humans are receiving increasing attention.

A new approach is needed for disease prevention and control

Current approaches to animal disease prevention and control are based on the disruption of disease transmission (through stamping out, vaccination, quarantine and other veterinary sanitary measures). While these have proved effective in both short- and long-term disease control programmes, such as national responses to foot-and-mouth disease (FMD) outbreaks and global rinderpest eradication, they have been less successful in some instances, as shown by the current persistence of H5N1 HPAI, despite significant national and international efforts. This is because most current approaches apply strong veterinary science and medicine disciplines in isolation from other relevant disciplines, such as economics, sociology, anthropology, communication, and ecology and land management. Such straightforward veterinary approaches do not confront the root causes of disease emergence at the animal-human-environment interface. Beyond core laboratory and epidemiological surveillance functions, veterinary services now need to expand into an agro-ecological approach to control diseases better. This means focusing on identification of the drivers of disease flare-ups, depicting disease behaviour in the context of host availability and farming landscape dynamics, and investigating the role of ecosystem dynamics and wildlife as the source of pathogens infecting domestic animals and humans. The international community is increasingly converging on such a multi-sectoral, multidisciplinary approach to addressing the increasing disease threats. This approach, termed "One Health", outlines a collaborative, international, cross-sectoral, multidisciplinary mode of addressing threats and reducing risks of infectious diseases at the animal-human-ecosystem interface, including the wildlife component.

Global animal disease situation

The following sections describe the main animal disease threats reported during 2010, by geographic region.

■ Africa

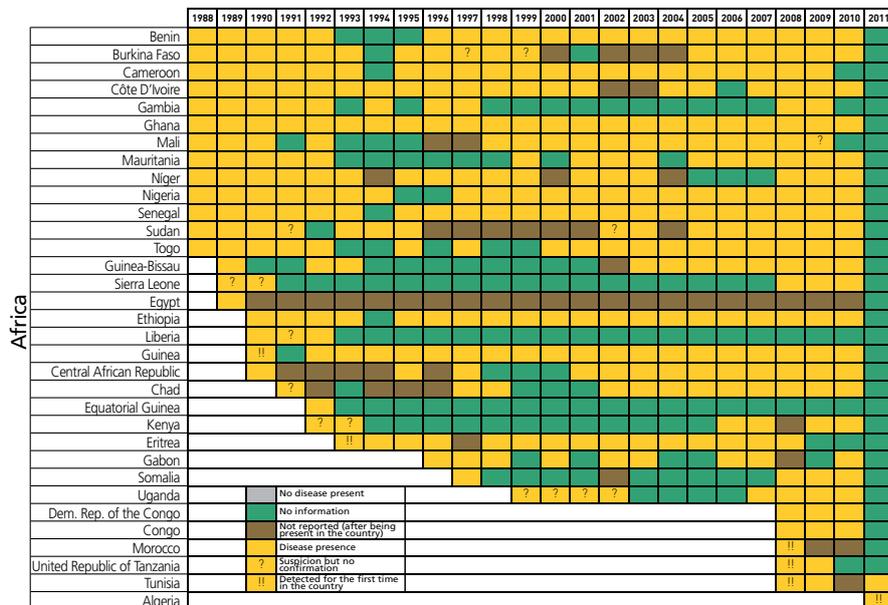
Emerging zoonotic diseases caused by viruses circulating in non-human primates, bats and rodents in sub-Saharan Africa are becoming the centre of attention in the region, particularly because of their pandemic potential. The fauna-livestock interface is also of growing importance, as pathogens that used to circulate in large game have gained a foothold in domestic ruminants, which have generally been present in greater numbers since the twentieth century. This has implications for animal and human health, and for general rural development. One example is African trypanosomiasis and the impact where livestock have become infected with *Trypanosoma brucei rhodesiense*. Where the pathogen was once dependent on a tsetse fly-wildlife-human cycle there is now a



tsetse-livestock-human cycle that greatly increases human exposure and the incidence of disease. Interaction of domestic livestock and wildlife is also important in the epidemiology of some animal diseases, such as FMD.

Peste des petits ruminants (PPR) distribution in Africa traditionally included the sub-Saharan countries that lie between the Atlantic Ocean and the Red Sea, where the disease has been recorded in almost every country. In recent years, PPR is rapidly expanding beyond its traditional boundaries and now poses a major threat to northern and southern Africa and Europe. On its spread south, PPR has already become endemic over recent years, first in Kenya and then in the United Republic of Tanzania, sometimes without the presence of overt disease. An incursion of PPR in 2008/2009 in Morocco was successfully contained through rigorous blanket vaccination of the entire national small ruminant flock, suggesting that PPR control presents a viable technical target. These incursions into northern Africa have been followed by the very recent finding of PPR sero-positive animals in Algeria in early 2011. Trade, transport, tourism and migration of PPR-susceptible animals may all contribute to the spread of the disease. Basic questions about the epidemiology of the disease remain unanswered, such as why the virus seems suddenly to invade and spread across PPR-free regions, sometimes in an apparently subclinical way. It is not known what modulates the virus virulence that seems to allow it to switch from virulent to non-virulent and back. The exact roles

Figure 1: Historical distribution and spread of PPR



Sources: Adapted from Sanz-Alvarez et al., 2008; Food and Agriculture Organization of the United Nations (FAO) registry; World Organisation for Animal Health (OIE) animal health data, 1988 to 1995; OIE World Animal Health Database, 2005 to 2011.



of wildlife, cattle and camels in the epidemiology of PPR also remain unknown. Some cattle herds show high rates of sero-conversion but no clinical signs, and uncertainty remains as to whether they are dead-end hosts or have ever shed the virus. PPR virus is closely related to the now extinct rinderpest. Both diseases shared similar clinical signs, and their geographic distribution was identical. For this reason, clinical surveillance often confused the two diseases, to the extent that the full global distribution of PPR has been unclear. With the last known outbreak of rinderpest reported in 2001, the world stands at the threshold of eradication of this disease. To some extent, PPR has become more apparent in the absence of rinderpest, with which it may often have been confused in sheep and goats. After the hugely successful Global Rinderpest Eradication Programme (GREP), perhaps the international community should move on to PPR as the next target disease for control/eradication. Such an initiative could build on the infrastructure, lessons learned and momentum created by GREP.

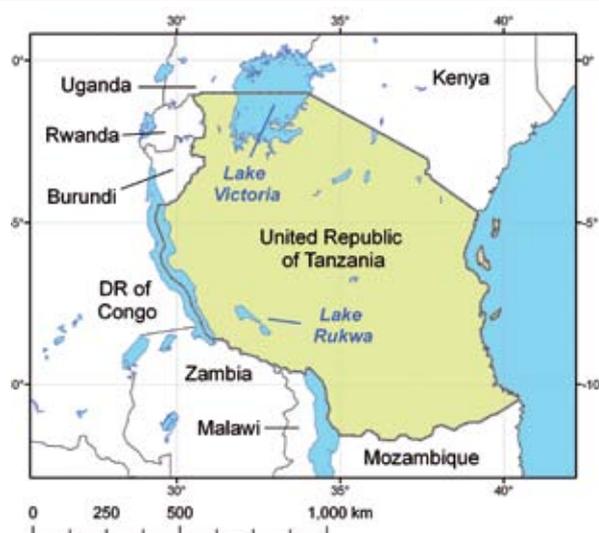
RVF is unique in that its emergence is closely linked to climate events

Rift Valley fever (RVF) is unique in that its emergence is closely linked to climate events. This allows the use of forecasting models that combine near-real-time measurements of sea surface temperatures, precipitation and vegetation cover to predict when and where an outbreak might occur. However, there are still unexpected events, such as the recent outbreak in northern Mauritania that affected camels, small ruminants and humans. In September to October 2010, unprecedented rainfall created large ponds of water in the oases of the Saharan region of Adrar, northern Mauritania. These ponds were rapidly colonized by high densities of several species of mosquito, including competent vectors for major arboviruses. A few weeks after the rains, these areas experienced severe outbreaks of malaria and RVF. For RVF alone, a total of 63 human cases, including 13 deaths, were officially reported at the end of December 2010. RVF also caused severe abortion storms in small ruminants and high rates of mortality in camels. The current hypothesis is that the virus was probably introduced rapidly through viraemic animals from RVF-endemic regions, which were transported by truck to take advantage of grazing opportunities.

As an example of changing agricultural practices influencing disease distribution, eastern and southern African ruminant populations are no longer disconnected. Important pathways for the spread of mainly ruminant diseases have opened up, facilitated by the movement of people and their stock from areas of high land pressure, such as the Lake Victoria basin, towards the agriculturally productive southern highlands, traversing the inhabitable tsetse belt that used to form a barrier for livestock and, with it, the spread of disease. The Sukuma tribe, the largest ethnic group in the United Republic of Tanzania, with an estimated population of 5.5 million people (16 percent of the country's total), traditionally lived on the southern shores of Lake Victoria in northwestern United Republic of Tanzania, but Sukuma families and their livestock have now migrated southwards into the Lake Rukwa area. This may explain the recent southwards spread of PPR to southern United Republic of Tanzania and of FMD type O to the Zambia border area. There has also been a northwards spread of contagious bovine pleuropneumonia (CBPP) and ASF, again facilitated by livestock trade or exchange along these movement pathways.



Figure 2: Migrations of the Sukuma tribe in the United Republic of Tanzania



Source: FAO.

■ Eastern and southeastern Asia

Eastern and southeastern Asia is the geographic setting for a relatively high number of transboundary animal diseases (TADs) in ruminants, poultry and pigs. Demographic processes, including strong economic growth and a rising demand for animal protein products, are the basis of a rapid intensification of the livestock sector, particularly poultry and pigs, in a farming landscape where traditional systems continue to play a major role in food production for the rural population. The mix of smallholder farming and intensive production results in increased vulnerability to livestock disease epidemics in eastern Asia, and poses a risk to agriculture's sustainability, environmental protection and public health. Geographic and trade corridors linking different livestock subpopulations pose increasing epidemiological challenges, and explain how highly virulent PRRS and other diseases, including FMD and classical swine fever (CSF), spread in eastern Asia.

H5N1 highly pathogenic avian influenza (HPAI) perhaps best illustrates the complexity of the factors involved in the local, national, regional and even global spread of a newly emerged animal pathogen. H5N1 HPAI has demonstrated what happens when a new virus enters a new host population (chickens) from where it can jump to further species (human infections, illustrating how the virulence of an agent can vary), and what happens when a new virus can spread across very large distances to new susceptible populations.

H5N1 HPAI persists in areas with rice-duck agriculture, causes outbreaks in both industrial and backyard poultry, infects humans in live-bird markets, and can spread over short and long distances through wild birds and by poultry trade. During the recent fight against HPAI, it became clear that animal disease management has to be viewed in the broader context of sustainable agriculture and rural development, natural resource



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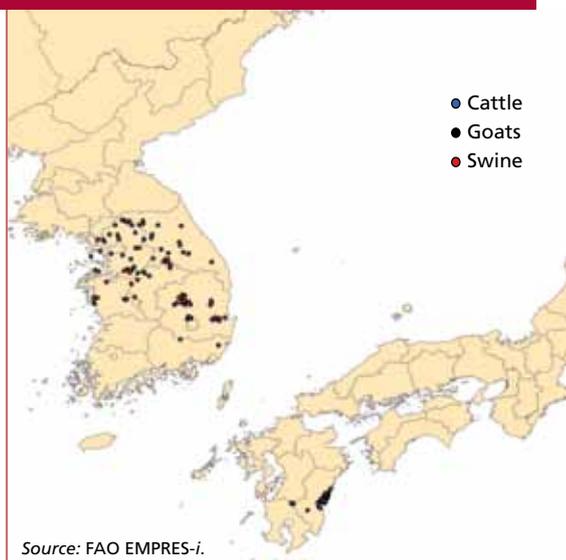
Ducks on a motobike in Hanoi market, Viet Nam

management and socio-economic development. Eastern Asia provides the setting for the mixing of poultry, pig and human influenza A viruses, which together constitute an expanding gene pool of diverse virus subtypes, clades and lineages circulating in the avian, swine and human host reservoirs, and thus representing a grave risk of emergence of new highly pathogenic transmissible viruses through recombination. The progressive control of avian influenza in eastern Asia and elsewhere continues to pose a formidable challenge. It is also recognized that H5N1 HPAI represents a threat for the rest of the world outside eastern and southeastern Asia, as demonstrated by the endemic situations in Egypt and Bangladesh, and the incursions into southern Asian and eastern European countries.

Foot-and-mouth disease (FMD) is regarded as endemic in most mainland countries in eastern and southeastern Asia, but a pattern of increased movement of viruses emerged in 2010. The drivers for this greater penetration of the FMD virus (FMDV) in the region are not clear; they may relate to the virus or they may be related more to human activity such as trade or smuggling. Since the beginning of 2010, confirmed FMD outbreaks have been reported in seven eastern Asian countries. FMD serotypes O and A were identified in these outbreaks, with serotype O predominating: Taiwan Province of China (FMDV O in February 2010), the People's Republic of China (FMDV A in January 2010, and FMDV O in February and March 2010), China, Hong Kong Special Administrative Region (SAR) (FMDV O in March 2010), Japan (FMDV O in April 2010, the first outbreak since 2000), Mongolia (FMDV O in May 2010), the Republic of Korea (FMDV A in January 2010, FMDV O in March 2010, and FMDV O in November 2010, the first outbreaks since 2002), Viet Nam and the Democratic People's Republic of Korea (FMDV O in December 2010, the first outbreak since 2002). This suggests that there is continued movement of viruses across international borders in Asia, and highlights the persistent threat posed by FMD as a TAD in the region. Livestock movements (both formal and informal) play an important role in the epidemiology of FMD worldwide and in mainland eastern and southeastern Asia. Livestock trade in this region is dynamic and can show marked seasonal variations, but it is predominantly driven by demand for meat and the price differentials this generates for livestock and livestock products. Of great concern has been the incursion of FMD into the Republic of Korea and Japan, where strict quarantine regulations govern animal imports. Both countries are continuing to investigate the route of introduction (possibly through contaminated fomites) and to review their risk management procedures. The occurrence of FMD in Mongolia, where ruminants and Mongolian gazelle populations were affected, also suggests a regional spread, most likely through livestock movements. It also shows an additional dimension of the disease: susceptible wild animals and their still unclear epidemiological role. (See article on p. 18 for more about FMD in Mongolia.) Increased coordination and sharing of data on FMD surveillance among countries in the various Asian agro-ecological zones are urgently required to identify transboundary transmission routes and ensure that suitable vaccines are available for protection against the disease (Sumption *et al.*, 2010).



Figure 3: Outbreaks of FMD type O, by species, in eastern Asia since January 2010



Porcine reproductive and respiratory syndrome (PRRS): Starting in 2006, the pig sector of China, Viet Nam, the Philippines and Thailand has been continuously hit by atypical highly virulent strains of PRRS virus. During 2010, the disease affected additional countries in Southeast Asia, including Lao People's Democratic Republic and Cambodia, while causing a higher than expected epidemic wave in Thailand. These developments are described in greater detail in the article on p. 30.

Other pathogens: This region has also seen a number of viruses emerge and jump species, with serious consequences for animal and human health. In general, these outbreaks have been related to viruses crossing the interface between wildlife (especially bats) and livestock and/or humans. The known examples are SARS, Hendra and Nipah viruses and, more recently, the Reston Ebola virus. Given the structure of the livestock sector and the increasing incursions of humans into wildlife habitats, additional pathogens may follow.

■ Southern Asia

Southern Asia faces particular challenges because of the huge populations of small and large ruminants, the human population's great dependence on milk and meat as a food source, the trade that takes place across the region, and the presence of important livestock diseases. India has the largest ruminant population and the second largest dairy production in the world. Losses due to infectious ruminant diseases are of such magnitude that progressive control presents a viable economic target, provided activities are coordinated with neighbouring countries. Many additional challenges remain, however. With rapid growing urban agglomerations and poor sanitation, India faces major veteri-



nary public health challenges, including rabies and a high prevalence of food- and water-borne diseases. HPAI is a significant threat in the region, and emerging zoonotic diseases that flared up during 2010 in southern Asia were Japanese encephalitis virus (JEV) and Chikungunya virus. India, Bhutan, Nepal, Pakistan and Bangladesh have very porous country boundaries, facilitating important exchange of trade commodities, including live animals. Livestock pathogens are shared in the process. The progressive control of TADs such as FMD and PPR across the Indian subcontinent, on an area-wide basis, is long overdue given the high density of livestock-based incomes, generated mostly by smallholder producers. India has requested FAO to contribute by facilitating a cohesive approach.

Anthrax is a somewhat neglected zoonotic disease

Anthrax is a somewhat neglected zoonotic disease. Control tools are available, but anthrax presents a challenge owing to the longevity of the spores in the soil in endemic areas. During 2010, FAO responded to a request from the Government of Bangladesh to review a flare-up of anthrax in ruminant livestock that led to human infections. Within a few weeks from mid-August 2010, Bangladesh had reported more than 500 human cases suffering from the cutaneous form of anthrax, in 11 out of 64 districts. The source of infection in most of the cases was infected cattle, which had been slaughtered, processed and sold without being inspected by a veterinary inspection authority. Anthrax is endemic in Bangladesh and outbreaks in livestock are reported every year. A large outbreak affected both livestock and humans in 2009. The Bangladesh public veterinary service is experiencing increasing difficulties in addressing a growing list of high-impact livestock and zoonotic diseases. The country is endemic for H5N1 HPAI, and confronts recurrent FMD outbreaks, PPR, brucellosis and haemorrhagic septicaemia.

Other pathogens: During 2010, in Pakistan, FAO focused mainly on the flood impact on rural livelihoods. In conjunction with this, the FAO Crisis Management Centre – Animal Health (CMC-AH) fielded a mission to draw up a strategy against *FMD*. The FMD virus strains found in Pakistan have much in common with viruses encountered in central Asia and the Near East, and are distinct from those circulating in India. At the time of the floods, Pakistan also experienced unusual episodes of *Crimean Congo haemorrhagic fever* (CCHF) and requested the World Health Organization (WHO) and FAO to investigate. A tick-borne arbovirus, CCHF virus may flare up in areas where there is unusual movement of people and animals.

■ **Latin America**

In Latin America, although the progressive control of FMD is becoming a viable target, major international animal health challenges remain, some of which are not yet adequately addressed. These include the upsurges of mainly bat-transmitted rabies in many countries, the rise of porcine cysticercosis in rural areas of central and South America, and the flare-up of mosquito-borne viruses such as bluetongue, West Nile fever, vesicular stomatitis, equine encephalitis (Venezuelan, Eastern and Western) and New World screwworm. Higher susceptibility to insect vector-borne disease incursions is a global phenomenon, triggered by the greater mobility of people, increases in trade and traf-



fic, climate change and land utilization patterns. The control of vector-borne diseases requires contributions from experts in multiple disciplines, including meteorologists, epidemiologists, biologists and ecologists, and from local communities. Global warming trends predicted in the 2007 Intergovernmental Panel on Climatic Change (IPCC) report for South America are likely to change the temporal and geographical distribution of infectious diseases, including those that are vector-borne. Changes in distribution will be partially modulated by El Niño Southern Oscillation events, which will become more frequent and lead to more drought and flood events (Pinto *et al.*, 2008).

West Nile fever is a zoonotic vector-borne disease that was detected for the first time in the Western hemisphere in New York in 1999, and subsequently spread throughout the United States of America to central and parts of South America; it continues to spread. The status of the disease in some countries of South America remains uncertain, because animal disease surveillance systems and vector surveillance are deficient in most of these countries. Wild birds are known to be reservoirs, serve as amplifying hosts and can spread the virus when migrating. The migration of birds is driven in part by seasonal climatic factors, and any change in climatic conditions may modify the direction and intensity of the spread of diseases (Pinto *et al.*, 2008).

Porcine teschovirus (PTV): Since February 2009, Haiti veterinary services have been confronting PTV encephalomyelitis, a lethal pig disease in smallholder pig holdings that has spread progressively in the country. Infection with the causative PTV serotype 1 results in an acute disease that affects swine of all ages and is characterized by nervous clinical signs and mortality. Viral circulation and spread are facilitated through movement of infected pigs and contaminated fomites, such as transport vehicles, feed or people. Smallholder pig production is important in Haiti, for food and income security and the livelihood of, particularly, the lower strata of society. However, scavenging pigs are associated with waste disposal and sanitation challenges, so pig disease control and prevention forms part of a broader development equation requiring a coherent approach. The presence of highly transmissible PTV is also affecting the control efforts for other diseases, and the CSF vaccination campaign had to be postponed to avoid the spreading of PTV by vaccination teams (Pinto *et al.*, 2010). Circoviruses and PRRS virus also co-circulate with PTV in Haiti pig populations today, adding to the disease burden; CSF and ASF have brought severe losses in the past.

Backyard pigs in Haiti



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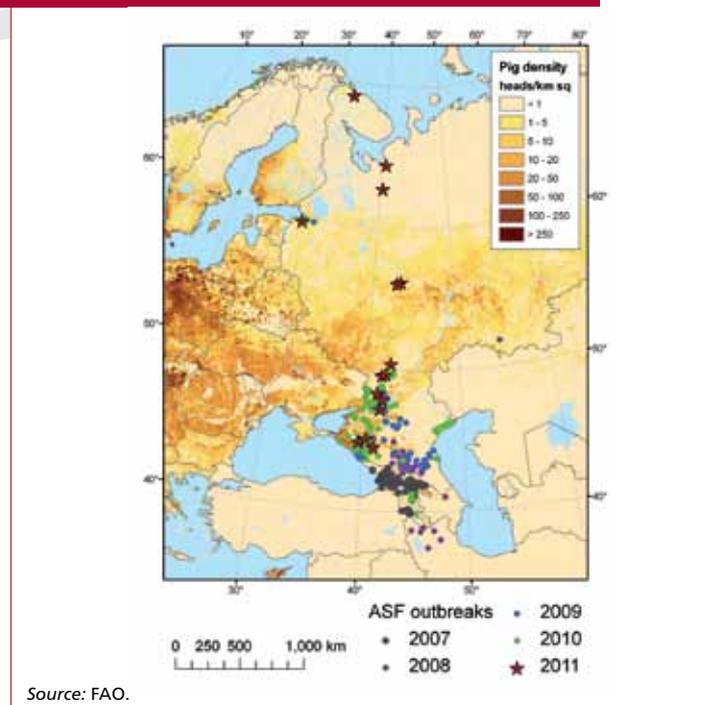
■ Eastern Europe

African swine fever (ASF) entered Georgia in 2007, presumably arriving in the Black Sea coastal port of Poti with a shipment from southeastern Africa. This represented a significant geographic leap for a virus that has a wildlife reservoir and for which infection of domestic pigs is a species jump. As is the case for many large shifts of animal viruses, this was probably the result of some form of illegal activity, in this case swill feeding of ship waste without any previous thermal treatment. As the veterinary services of Georgia were

ill-prepared, ASF spread freely, affecting mainly backyard pigs along the main trade routes, and moved to Armenia, Azerbaijan and the Islamic Republic of Iran (wild boar). By the end of 2007, ASF had crossed to the Russian Federation and continued to spread uncontrolled, arriving just a few kilometres from the Ukraine border. The disease also circulates in areas where civil strife and military action complicate its containment. Spread is linked mainly to the movement of infected pork products, where the virus can resist for long periods.

The disease has jumped thousands of kilometres on several occasions, with repeated introductions into Leningrad Oblast (close to the Estonian and Finnish borders), Orenburg Oblast (close to northern Kazakhstan), Nizhniy Novgorod Oblast and, most recently, Murmansk Oblast (north of the Arctic Circle) and Arkhangelsk Oblast. Most of these jumps have been related to military premises, suggesting that military food supply chains play a prominent role in disease spread in the Russian Federation. The exact epidemiological role of wild boar, which have been extensively affected, and the presence of *Ornithodoros* soft ticks in the region will need to be carefully addressed in the design of ASF prevention and control plans. FAO assistance started in 2007, and has concentrated on the options available not only to halt the progressive spread of the disease, but also to address virus amplification at source. The main prospects for effective prevention and control are strengthening the first line of defence at the village level, through the engagement of pig keepers, private veterinarians, wild boar hunters, butchers, animal traders and other intermediaries. In the presence of weakened official veterinary services, empower-

Figure 4: Spread of ASF in the Caucasus and the Russian Federation, 2007 to September 2010





ing these stakeholders to take preventive and control measures against the disease may be the only viable short to medium-term solution. Again, the complexity of the situation demonstrates that disease control and prevention cannot be viewed in isolation, but need to be part of a broader sustainable agriculture and rural development agenda (Beltrán-Alcrudo, Khomenko and Dietze, 2010).

Other pathogens: The upsurge of ASF in the Caucasus and eastern Europe is only one of the many disease challenges in this region. Countries of the former Soviet Union feature the collapse, or at least weakening, of their veterinary services, together with national shifts from vertical command systems to less efficient sub-national disease management structures. At the same time, there has been an exodus of young people, particularly into the cities. Land abandonment triggers the regrowth of undergrowth, favouring rodents and other forms of wildlife, which in turn attract wild carnivores and influence the pathogens associated with rodent-wild carnivore cycles. Disease dynamics respond to changes in land use, agricultural policies and access to public services. Progressive rabies flare-up is now seen in many former Soviet Union countries, with red foxes playing a key role. Disease emergences at the animal-human-environment interface also include tick-borne encephalitis, hanta viruses, CCHF, Lyme disease and alveolar echinococcosis, in addition to the existing TADs: brucellosis, anthrax, CSF, FMD, avian influenza and sheep and goat pox. Progressive control pathways in the form of regional roadmaps are to be pursued for FMD and brucellosis.

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Foot-and-mouth disease

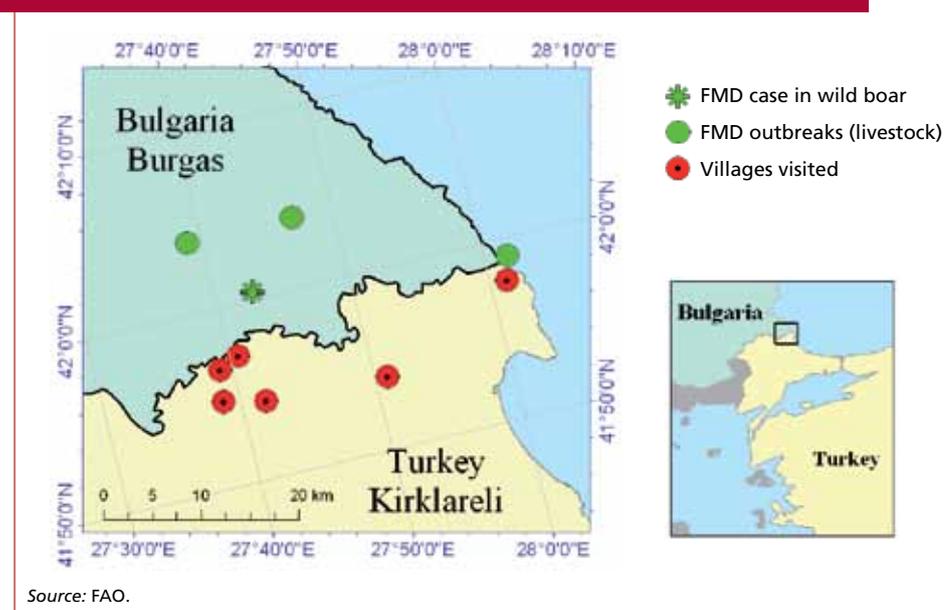
FAO/European Commission for the Control of Foot-and-Mouth Disease mission to Turkey concerning foot-and-mouth-disease outbreaks in Bulgaria

Background and itinerary

Molecular epidemiological evidence indicated that the foot-and-mouth disease (FMD) virus isolated in Bulgaria early this year had most likely come from Turkey (Valdazo-Gonzalez *et al.*, 2011). The immediate question was whether there was any evidence of FMD virus (FMDV) circulating across the border in Turkey, in either domestic animals or wildlife. The involvement of wild boar in the Bulgaria outbreak suggested that this species could have been the means by which the virus crossed to Bulgaria, so this needed to be investigated. If this species was implicated, the further question was whether the incursion was from spread through the wild boar (*Sus scrofa*) population alone or if domestic species were also involved.

FAO and the European Commission for the Control of Foot-and-Mouth Disease (EUFMD) sent a team to the Demirkoy District of Kırklareli Province, which lies right across the border from the sites of the outbreaks in Bulgaria and would be the most likely immediate source if spread had been through local wild boar or livestock. The team visited the six villages closest to the recent FMD detection locations in Bulgaria (Figure 1). Villagers and community leaders (*mukhtars*) were interviewed regarding

Figure 1: Villages visited in Demirkoy District (Kırklareli Province, Turkey), in relation to the location of recent FMD outbreaks (December 2010 to January 2011) in Bulgaria





numbers of livestock, husbandry practices, disease awareness, whether signs of FMD had been seen in livestock or wild boar, wild boar abundance and hunting. In the six villages, a total of 4 647 domestic animals are kept, of which 45.4 percent are sheep, 29.1 percent cattle, 17.0 percent goats, and 0.6 percent water buffaloes. According to Turkish veterinary authorities, all livestock in this area is vaccinated against FMD once or twice a year (depending on the species).

Epidemiological observations relevant to livestock

In all six villages, the villagers were familiar with the clinical signs of FMD and reported that there had been no sign of the disease in their animals in the past months. No sick or lame wild boar had been seen in any of the villages, and the head of the Demirkoy Hunters' Club also said that no sick or lame wild boar had been reported in Demirkoy District. Domestic livestock are not normally grazed in the forests and are not left out unattended overnight. Cattle had crossed over the river into Bulgaria five or six times in the previous few years, but this is a rare event. Small ruminants have human attendants when out grazing, so do not cross the river. Twenty-four water buffaloes had crossed recently into Bulgaria (water buffaloes sometimes leave the river on the wrong side), and this had been a relatively common occurrence in the previous few months. In summer the river is easy to cross, but in winter it is crossable only on some days. Numerous tracks lead down to the river on the Turkish side, and crossing by foot is possible in several places, and by vehicle in a few. The river is not a barrier to the movement of wild boar, and it is possible that crossing might be an escape route during the hunting season (see following section).

The Turkish authorities made available the raw results from the extensive non-structured protein (NSP) sero-surveillance conducted in Turkish Thrace in autumn 2010; these showed no evidence of circulating FMD virus. Several precautionary measures had been undertaken in the Thrace region as a result of the outbreaks in Bulgaria; these included closing all livestock markets, stopping all livestock movements and confining all livestock. In the areas defined as risk areas, including the villages close to the Bulgarian border, supplementary vaccination had been initiated for all susceptible animals over two months of age. Active clinical surveillance was being carried out in the villages of Demirkoy District, with frequent examinations of animals by the district veterinary service. No clinical signs had been detected.

In addition to this active surveillance, the Turkish FMD Institute had prepared a proposal for sero-surveillance of domestic species in villages in or adjacent to the forest areas of Turkish Thrace. The mission reviewed the survey design and proposed revisions to the methodology to achieve the desired confidence of detection and to bias the sample further towards the areas closest to the outbreaks detected in Bulgaria. Biasing towards high-risk populations or populations of interest is desirable and common for detection samples such as these, in contrast to samples aimed at estimating prevalence or incidence.



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*Forest-farmland interface
in Demirkoy District,
Kırklareli Province, Turkey*



© FAO/SERGEI KHOMENKO

*Interview with local farmers
in Demirkoy District,
Kırklareli Province, Turkey*

The high price of meat in Turkey this year means that animals are worth more in Turkey than in Bulgaria (possibly up to twice as much), so there is no financial incentive for moving animals illegally from Turkey to Bulgaria. For many years, the festival of Kurban Bayram in Turkey has been identified as a period of high risk of spread of FMDV owing to the large number of animal movements. The last Kurban Bayram was in mid-November 2010, but because of the risk of FMD spread and the high price of meat in Turkey, animals were imported to Turkish Thrace from Greece, Bulgaria and other FMD-free European countries for slaughter. This would have decreased risky movements from other parts of Turkey where FMD is endemic and should have decreased the risk of virus being reintroduced into Turkish Thrace, as has happened before. In addition, a supplemental vaccination campaign was carried out for all animals being moved out of Turkish Thrace in October and November 2010, and a ban on any of these animals returning was put in place and checked by visits after the festival.

Wild boar hunting and proposed emergency surveillance scheme for FMD

The Turkish Ministry of Environment and Forestry estimates the total wild boar population of Demirkoy District to be between 2 000 and 2 500 animals (with three head per square kilometre in forest habitats, or a maximum of 2.6 head per square kilometre across the whole district). According to the head of the district hunting club, its 103 members annually harvest a total of about 500 animals from the forests of Demirkoy District during the official hunting season for wild boar (September to late February). In addition, the estimated 85 hunters living in the six villages visited harvest about 160 wild boars a year. The remaining ten villages in the district do not seem to be as suitably located for wild boar hunting habitats, but assuming that together they probably account for twice as many harvested wild boars as the six villages visited, the annual wild boar hunting bag for club members and village hunters in Demirkoy District can probably be estimated to be in the range of 900 to 1 200 animals. This represents nearly half of the estimated population, which is the moderately high hunting pressure normally reported

from elsewhere in Europe. Over the last ten years, there does not seem to have been any apparent increase in the area's wild boar population or any remarkable increase of group size. From interviews, it appears that hunters had never observed any dead wild boars (or any other wild animals).

Both driven hunts (involving people and dogs) and individual hunting take place in the period from September to late February (the best months are January and February, particularly when there is snow cover). Hunts are usually carried out at distances of 5 to 10 km (and up to 15 km) from the village, in the surrounding forest. Up to four animals can be shot at a time, and up to 20 people are involved in the driven hunt. Shot animals are left in the forest, as pig meat is not consumed or otherwise utilized anywhere in Turkey. Hunters' dogs may eat the meat right after the hunt, or return later to scavenge on the carcass. It is also permitted to shoot wild boars on private



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Goat farm in one of the villages visited in Turkey

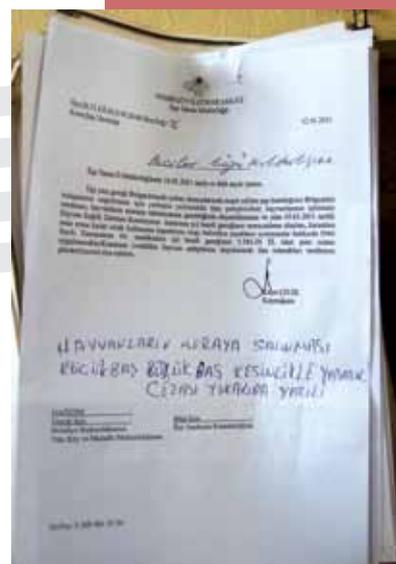


land during the summer, particularly when they cause damage to crops, but this rarely happens in the villages visited, where few crops are grown. Direct contacts between domestic animals and wild boars were also reported to be rare.

As part of emergency surveillance, local hunters in villages close to the Bulgarian border – Begendik, Yesilce, Karacadag, Yigltbasi, Boztas, Sislioba and Avclar – had been requested to shoot five to ten animals per village, and to collect blood samples for serological testing. This was to provide a total sample of 30 to 60 animals, which is sufficient for detecting FMD, if present in the population at prevalence of 50 per cent. It was also to ensure that the surveillance effort covered at least some of the wild boar herds inhabiting the area in immediate proximity to the FMD outbreaks in Bulgaria (Kosti and Rezovo Villages). In the absence of reliable data on herds' average home ranges in the Demirkoy area, it was assumed that animals shot more than 5 km apart from each other would almost certainly belong to different groups (i.e., that the maximum monthly home range did not exceed 20 km²). In addition to these efforts, the Turkish General Directorate of Protection and Control (GDPC) planned to initiate similar sampling activities in other forested districts of Turkish Thrace, closer to Istanbul (approximately 25 blood samples) and in the southwest (approximately 25 blood samples).

The mission examined the possible negative impacts on the wild boar population that might arise as a result of the emergency surveillance. It was advised that extensive driven hunts were being avoided (individual or small group hunting was preferred), to prevent potential dispersal of the animals. Hunting pressure can increase the home ranges of both wild boar herds and individual boars, although its effect has been shown to vary strongly, depending on local conditions. When possible, hunters seek to change their hunting areas, to avoid the continuous harassment of animals, particularly when well-trained dogs are used. The shooting of adult females is also avoided, as herds without leading sows are likely to disperse and join other herds, thus potentially spreading the FMD further, if present in the original group. Juvenile and sub-adult animals were viewed as being more appropriate targets for surveillance because, being smaller, they are easier to handle and dispose of (if needed) than full-grown boar. For the surveillance, the location of each animal shot had to be identified as precisely as possible, preferably with geographic coordinates using a Global Positioning System (GPS). Hunters had also been requested to record the sex and age of each animal shot (and, if possible, to photograph it). Any suspicious clinical signs of FMD (and other diseases) found during external examination were to be photographed. Additional useful epidemiological information would be gained if hunters provided the number of animals in the group to which the sampled individual belonged.

Concerns were raised about biosecurity when hunting and sampling potentially FMD-infected wild boar, and about the need to prevent spread through inanimate objects (fomites) or from boar carcasses. Recommendations were made to minimize such risks. The disposal of carcasses in forest regions is particularly challenging, as burning is



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Administrative circular highlighting the importance of increased surveillance in relation to the FMD outbreak occurring in January 2011 in Bulgaria

not safe and the soil is often shallow, so it can be difficult to dig pits of sufficient depth. While moving a potentially infected carcass to a village for disposal may increase the risk of virus transmission, it was considered that the risk to livestock from shot carcasses left at hunting sites was low, owing to the absence of domestic pigs in Turkish Thrace, although scavenging by wild boar was possible. The low risk of transmission through this route could be mitigated further by covering carcasses with quicklime, to inactivate any virus in exposed body fluids and deter scavenging from the carcass.

Reference

Valdazo-González, B., Knowles, N.J., Wadsworth, J., King, D.P., Hammond, J.M., Özyörük, F., Fırat-Saraç, M., Parlak, U., Polyhronova, L. & Georgiev, G.K. 2011. Foot-and-mouth disease in Bulgaria. *Veterinary Record*, 168(9): 247.

Contributors: Sergei Khomenko (FAO), Nick Honhold

Foot-and-mouth disease in Mongolia in 2010: FAO response Background

Foot-and-mouth disease (FMD) causes significant economic losses from its high morbidity and through its impact on animal health and production, the cost of control programmes and the trade restrictions imposed on infected countries. It is the most contagious transboundary animal disease affecting cloven-hoofed animals, both domestic and wild, and is found in various parts of Africa, Asia and South America.

FMD has been present in Mongolia in the past. It occurred as sporadic outbreaks in the periods 1931 to 1935, 1941 to 1948 and 1963 to 1974. After 26 years of FMD freedom, the disease was reported in Mongolia in April 2000, February to May 2001, July 2002, February 2004, August 2005 and June 2006, when the last cases were seen. Since then, no additional FMD events had been reported until April 2010.

An FMD (type O) outbreak started in April 2010 with FMD cases in Dornod Province in eastern Mongolia. As of 24 November 2010, the Government of Mongolia had reported more than 20 other outbreaks to the World Organisation for Animal Health (OIE). The outbreaks occurred in five eastern provinces.

Livestock production is considered to be an important part of Mongolia's economy and cultural heritage; it accounts for more than 87 percent of the country's gross agricultural product, which in turn contributes about 30 percent of gross domestic product. There are roughly 43 million head of livestock in Mongolia, and essentially five types are raised: goats, sheep, cattle, horses and camels.

In Mongolia, FMD-susceptible species include cattle, sheep, goats, camels, yaks and Mongolian gazelles (*Procapra gutturosa*). Domestic animal production is chiefly nomadic on the open steppes, and wild gazelles also graze widely, in herds of up to several thousand.

Yaks grazing near Gobi
Sumber in Mongolia
winter 2011



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Figure 1: FMD outbreak locations in Mongolia in 2010



FMD situation in Mongolia

The Government of Mongolia responded quickly to the 2010 FMD outbreaks in the east of the country, coordinating a large-scale disease eradication effort.

Following the government's request of 18 October 2010, the Food and Agriculture Organization of the United Nations (FAO) Crisis Management Centre – Animal Health (CMC-AH) provided an expert team to review and document the current situation of the FMD outbreak in Mongolia; assist in disease investigation and evaluation of the risk of FMD spreading; advise on preparedness, response and contingency plans, including appropriate risk reduction measures; and develop options for an action plan to support prevention and control of the disease.

The mission team noted that laboratory capacity was advanced and diagnosis was rapid. There was obvious commitment from all those involved in addressing the outbreak, and this was supported by clear chains of command and lines of communication, established among a number of agencies at the national, provincial and local levels. The authorities demonstrated considerable concern for the well-being of affected herders and made the recovery and sustenance of affected people a clear priority. There are generally good relationships and communication among the authorities, herders and veterinarians.

There is apparent success with eradication in the eastern provinces where the disease was first diagnosed, and it seems likely that this success will be repeated in the more recently infected areas. The key to this success seems to have been the use of vaccination and biosecurity measures. Mongolia will need to maintain surveillance for FMD in the long term, and this surveillance should be heightened in the period immediately following the end of this outbreak.

Sheep grazing near
Gobi Sumer in Mongolia
winter 2011



The data available suggest that FMD has not previously persisted in the long term in Mongolia, with different virus types occurring in different years. Physical conditions and demographics provide some unique challenges for disease control authorities, but also some possible advantages. The nomadic nature of herding means that different animal groups intermingle, and opportunities for disease spread occur. Disease controllers therefore need to consider the epidemiological units of nomadic groups, rather than farms or pieces of land where animals are raised, and good local knowledge of individual herders is essential for understanding the contacts among groups.

Long and severe winter conditions have created significant problems in recent years, with large stock losses due to heavy snow falls and icy conditions (*Dzuds*) when temperatures below -40°C have lasted for more than a month. In winter, animals are kept in places where the cold is less severe and are not moved about as much as during the rest of the year. Although animal-to-animal contact is close in these wintering places, groups tend not to mix during this period, and wider virus spread seems less likely to occur.

Vaccination is a crucial part of Mongolia's FMD control programme. While the maintenance of vaccines at consistently cold temperatures is a challenge in many countries, in Mongolia the vaccines must be prevented from freezing. However, in achieving this, it is also important that they are not kept too warm. Similarly, most disinfectants work in the liquid phase, and this is difficult to ensure when outdoor temperatures are below zero.

Numbers of Mongolian gazelles showed clinical signs of FMD in 2010, resulting in their death or the need for their destruction for reasons of animal welfare. The role of these gazelles in disease maintenance and spread is difficult to assess from the evidence available to date. While they may have been involved in some instances, it may be that they have only an occasional impact and that the disappearance of the virus from domestic herds and flocks will result in its disappearance also from gazelles. This appears to have been the case in the past, and is discussed by Nyamsuren *et al.* (2006).

FMD represents an ongoing challenge in the East Asia region, and FAO recognizes the disease as one that requires a regional and progressive control approach. It is truly transboundary in its behaviour and is a serious disease risk shared by many countries in the region, as evidenced by recent FMD outbreak events.

Reference

Nyamsuren, D., Joly, D.O., Enkhtuvshin, S., Odonkhuu, D., Olson, K.A., Draisma, M. & Karesh, W.B. 2006. Exposure of Mongolian gazelles (*Procapra gutturosa*) to foot and mouth disease virus. *Journal of Wildlife Diseases*, 42(1): 154–158.

Contributor: Ian Douglas (FAO-CMC)



Highly pathogenic avian influenza

H5N1 highly pathogenic avian influenza worldwide in 2010

Introduction

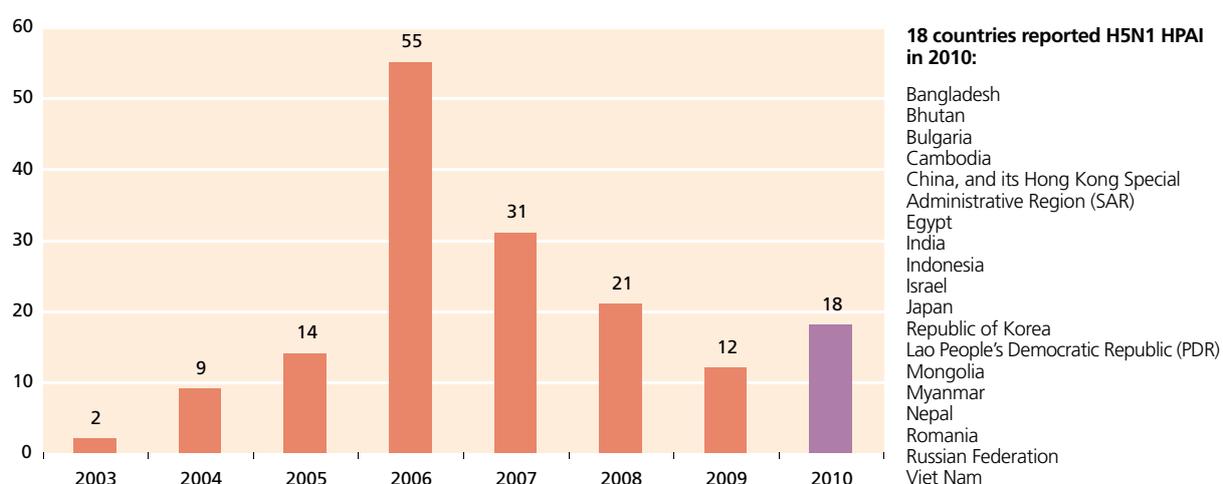
A total of 63 countries/territories in Asia, Europe and Africa have been affected by H5N1 highly pathogenic avian influenza (HPAI) since the beginning of the epizootic in poultry in 2003. Following three years of progressive retraction, geographic expansion of the virus was again noted in 2010, with 18 countries affected (14 in Asia, three in Europe, and one in Africa), compared with only 12 countries in 2009 (Table 1 and Figure 1). However, H5N1 HPAI outbreaks still occurred predominantly in Asia, as was also the case in the previous three years. The peak of disease activity was once again seen during the months of January to March (as in Bangladesh, shown in Figure 3). At the country level, the numbers of outbreaks generally decreased or remained at the same level, with the exception of those in Egypt (Table 1), where the number of reported outbreaks has increased, following a change in the disease reporting system. The activities of the Community Animal Health Outreach (CAHO) project, initiated in December 2008, were expanded in February 2009, following an apparent enhancement of outbreak notification. Bhutan was newly infected in 2010, reporting H5N1 HPAI outbreaks in February and March for the first time. Bulgaria, Israel, Japan, Myanmar, the Republic of Korea and Romania had not reported outbreaks of H5N1 HPAI in 2009; the disease



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Mixing species, as in this backyard poultry farm, may lead to expansion of the host range of HPAI, and increase the risks of recombination of influenza viruses

Figure 1: Numbers of H5N1 HPAI-infected countries over time

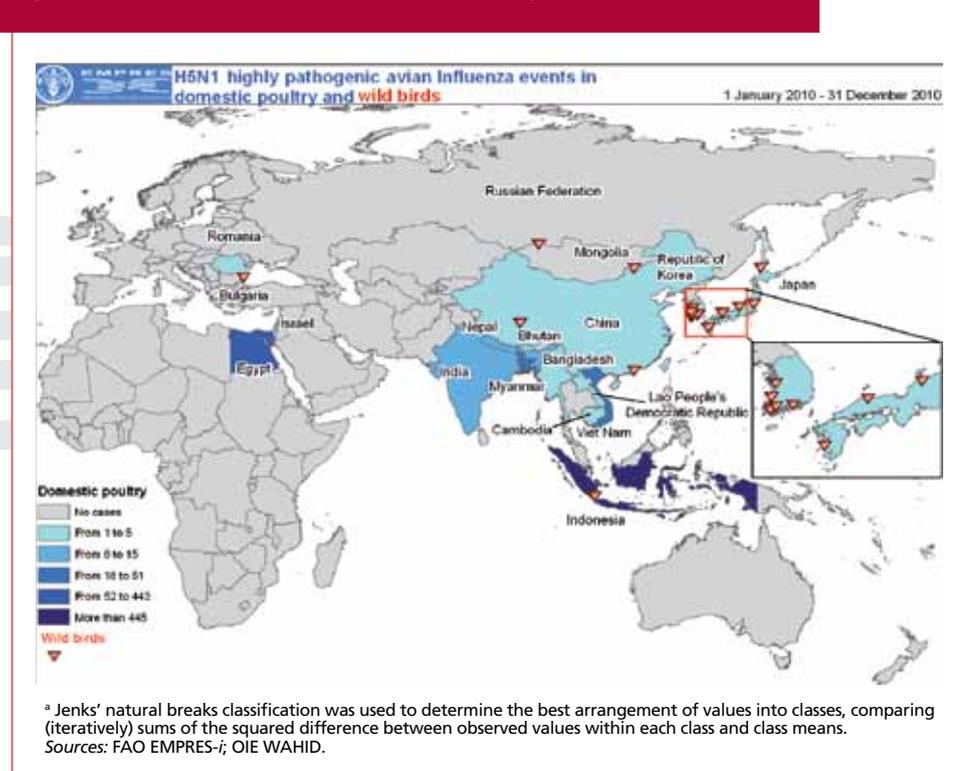


Sources: FAO EMPRES-i; OIE WAHID.

Table 1: Numbers of outbreaks, 2009 and 2010

	Bangladesh	Bhutan	Bulgaria	Cambodia	China / Hong Kong SAR	Egypt	Germany	India	Indonesia	Israel	Japan	Republic of Korea	Lao PDR	Mongolia	Myanmar	Nepal	Romania	Russian Federation	Viet Nam
2009	32	0	0	1	4 / 19	176	1	10	1502	0	0	0	5	2	0	2	0	2	56
2010	31	5	1	2	1 / 2	443	0	15	1212	2	5	8	1	1	3	8	2	1	48

Sources: FAO EMPRES-i; OIE WAHID.

Figure 2: H5N1 HPAI events in domestic poultry and wild birds, 2010^a


was reintroduced into these countries (or reoccurred) in 2010. The reported outbreaks in Romania in March 2010 were the first H5N1 HPAI poultry outbreaks in Europe since October 2008, when the H5N1 virus was detected during routine surveillance in a poultry flock in Germany. It is evident that the threat from H5N1 HPAI remains, including the risk of human infection. In 2010, the World Health Organization (WHO) reported 48 human cases of H5N1 infection – of which 24 were fatal – in five countries: Egypt (29 cases, including 13 fatalities), Indonesia (nine cases, including seven fatalities), Viet Nam (seven cases, including two fatalities), China (two cases, including



one fatality) and Cambodia (one fatality). The same countries also reported human cases in 2009. The incidence of the disease in humans decreased in 2010, except for in Viet Nam, where it increased from five to seven cases.

Four high-burden countries remain enzootic

As was also the case in 2009, in 2010 the great majority of H5N1 HPAI outbreaks in animals occurred in four high-burden countries, where the disease is deeply entrenched: Bangladesh (2 percent of total cases), Egypt (25 percent), Indonesia (68 percent) and Viet Nam (3 percent) (Table 1). Progressive control of avian influenza (AI) in these settings poses a formidable challenge, and elimination remains the long-term goal. In eastern Asia, the mixing of poultry, pig and human influenza A viruses gives rise to an ever-expanding gene pool of virus subtypes, clades and lineages.

Bangladesh: During 2010, there were 31 H5N1 HPAI poultry outbreaks reported in Bangladesh (Figure 3), with the majority on commercial farms (29) and just two in backyard holdings. Approximately 175 000 birds were culled. In 2009, there were 32 outbreaks reported, with a high proportion of events observed between January and April in both years. Although no outbreak was observed between June and December 2010, the country is still believed to remain endemic, with active circulation of the virus (clade 2.2). In particular, 2010 virus isolates grouped in sublineage 3 and clustered with sequences of viruses from Bangladesh isolated in 2007 to 2009. This suggests that the virus is maintained in unnoticed reservoirs within the country, possibly domestic ducks. Bangladesh recorded fresh H5N1 HPAI outbreaks in January and February 2011. In total, 49 out of 64 districts recorded outbreaks both on commercial farms and in backyard holdings.

Figure 3: H5N1 HPAI outbreaks in Bangladesh, 2009 and 2010

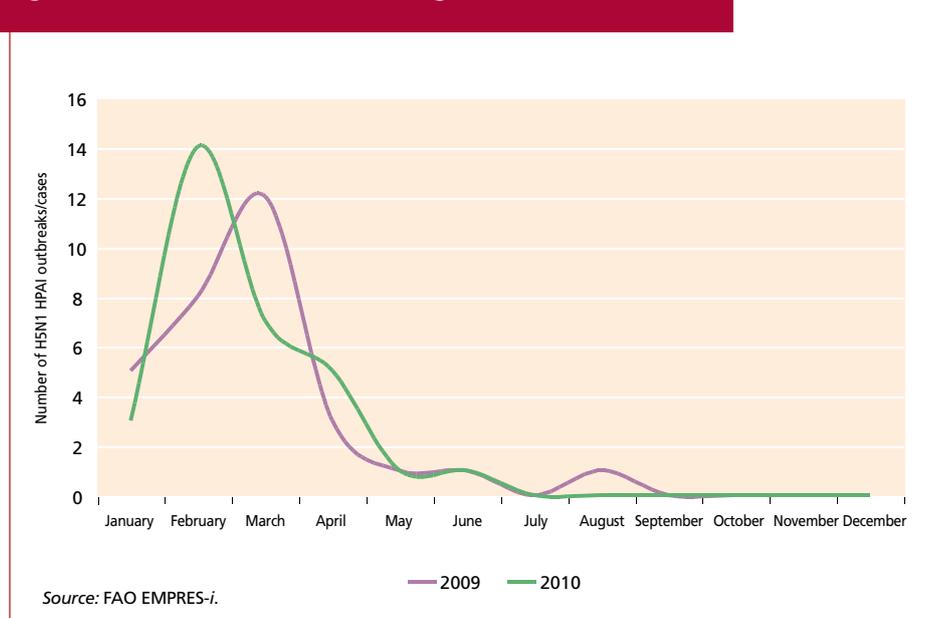
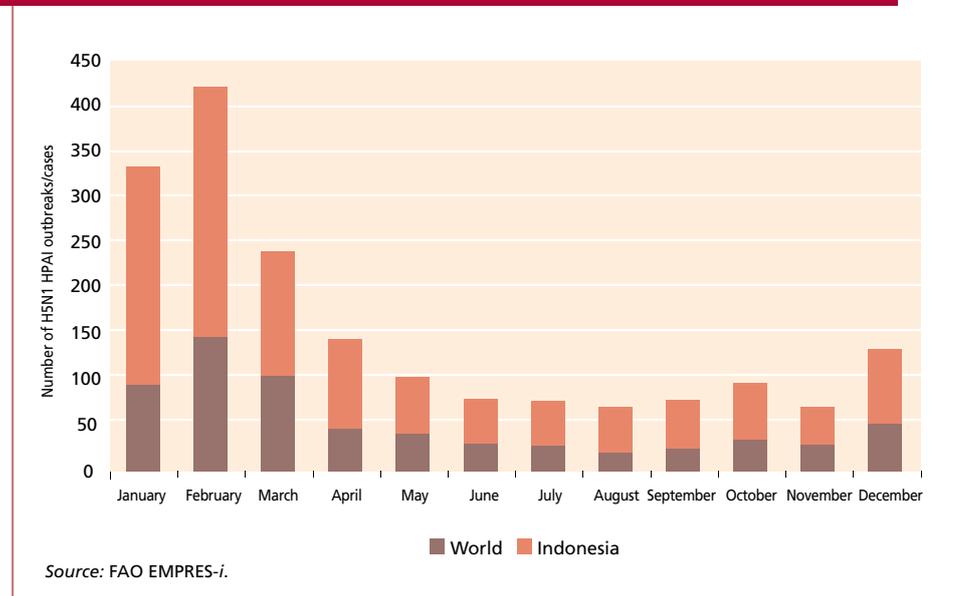


Figure 4: Indonesia compared with the rest of the world, outbreaks in 2010


Indonesia continued to report a high number of H5N1 HPAI outbreaks in poultry, as it has done for the past four years. More outbreaks were reported in this country than in the rest of the world combined (Figure 4). H5N1 HPAI is endemic on Java, Sumatra and Sulawesi, with sporadic outbreaks reported elsewhere. High-incidence areas are recognized at both the provincial and district levels on Java (especially Yogyakarta) and in the south of Sumatra (Lampung). The high number of reports stems in part from the Participatory Disease Surveillance and Response (PDSR) programme (established and supported by FAO), which targets village poultry production systems (mainly backyard) and reports outbreaks at the village level. Only two of Indonesia's 33 provinces (Maluku and North Maluku) have never reported H5N1 HPAI.

Viet Nam in 2010 reported 48 H5N1 HPAI outbreaks in 20 of its 63 provinces (32 per cent), mostly on duck farms (83 per cent) and in the small-scale commercial sector: 61 per cent of outbreaks were in flocks of 50 to 1 000 birds. Approximately 45 000 birds were culled. A total of 56 outbreaks had been reported in 2009. Active virus circulation surveillance was carried out in eight target provinces and cities. Prevalences of influenza type A and H5N1 avian viruses were 0.94 and 0.67 per cent, respectively, in ducks, and 0.54 and 0 per cent in chickens. There was no evidence of AI virus persistence in Muscovy ducks. In 2010 three virus clades were isolated: i) haemagglutinin (HA) clade 1, predominantly in southern Viet Nam and also in Cambodia; ii) HA clade 2.3.4, predominantly in northern Viet Nam during the first half of 2010, and also circulating in China; and iii) HA clade 2.3.2, detected for the first time in late 2009, with four cases detected in the first half of 2010, and others – predominantly in northern Viet Nam, but also isolated in the south – since September 2010.



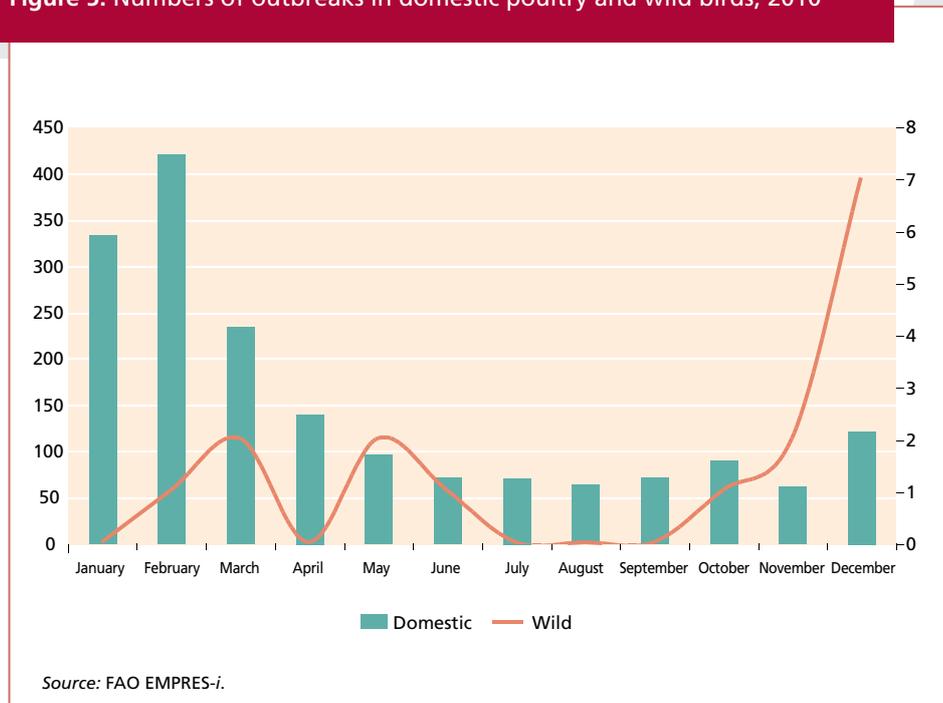
Egypt, which reported its first H5N1 HPAI outbreak in February 2006, is considered endemic, regularly reporting outbreaks from almost all of its 29 governorates. During 2010, 443 outbreaks were observed, mainly in backyard systems, against 176 in 2009. However, detection has probably improved because of implementation of the PDSR-like CAHO programme in ten governorates (Bani-Seuif, Behera, Dakahlia, Fayoum, Gharbia, Kafr el Shiekh, Menia, Menufia, Qalubia and Sharkia). Viruses isolated during 2010 were genetically similar to those isolated in 2009.

Some knowledge gaps remain in the role of wild birds

During 2010, H5N1 AI events in wild birds continued, with a slight increase from 2009, when 12 were reported. There were 16 events reported in 2010, with Bulgaria, China, its Hong Kong SAR, Indonesia, Mongolia and the Russian Federation each reporting one, Japan reporting four, and the Republic of Korea reporting six (Figure 5). None of the events in 2010 were on the scale of thousands of wild birds dying within weeks, as was the case in 2005 in China and the Russian Federation. The current H5N1 HPAI viruses may be less deadly to wild birds.

The wild bird species infected in 2010 were mallard, hooded crane, tundra swan, mute swan, eagle owl, great crested grebe, goosander, grey heron, gadwall, Eurasian spoonbill, red-billed chough, bar-headed goose, brown-headed gull, whooper swan, greylag goose, common buzzard and barn swallow. Since the beginning of the epizootic, more than 100 species from 13 orders of birds have been found to be infected with H5N1 AI virus.

Figure 5: Numbers of outbreaks in domestic poultry and wild birds, 2010





H5 HPAI outbreaks worldwide are caused, by viruses in clades 1, 2.1, 2.2 and 2.3

Wild bird H5N1 AI outbreaks in 2010 were reported in single birds found during routine surveillance in China, Hong Kong SAR, Indonesia, Bulgaria, Japan and the Republic of Korea. However, this was not the case for events in Mongolia (n = 26) and China (n = 170) in May 2010, the Russian Federation (n = 367) in June 2010, and the Republic of Korea (n = 20) in December 2010, where larger numbers of wild birds were found dead. For both Mongolia and the Russian Federation, similar temporal and spatial patterns of wild bird deaths have been observed in past years. Mortalities occur during the northern hemisphere spring season, as birds arrive at breeding grounds.

H5N1 phylogenetic data and evolution of clade 2.3.2 viruses

H5 HPAI outbreaks worldwide are caused by clade 1 and 2 viruses, particularly clades 2.1, 2.2 and 2.3 for the latter. The following outlines the different clades identified in 2010 (see also Table 2).

All human and animal H5N1 isolates from Cambodia analysed since 2004, including all those from 2010, form part of *clade 1* (genotype Z). Recent viruses are similar to the viruses circulating there in previous years. This is the same clade that circulates predominantly in southern Viet Nam, in the Mekong Delta extending into Cambodia.

Clade 2.1 is known to be circulating in Indonesia, although no 2010 sequence data are available. Data from 2009 show that Indonesian isolates form part of *clade 2.1.3*, and continue to diversify with the greatest variation currently observed for viruses from Sumatra.

Clade 2.2 includes 2010 sequences from Nepal, Bangladesh, Bhutan and India. *Clade 2.2.1* viruses continue to circulate in Egypt. This clade has also been confirmed for an emu isolate from Israel in September 2010, which suggests some movement of H5N1 HPAI in the region, possibly involving "bridge" species. It is interesting to note that in Egypt the 2.2.1 viruses cluster into two distinct phylogenetic groups: A and B. The majority of the samples belong to group B (or group F according to the United States Centers for Disease Control and Prevention [CDC] nomenclature), while the remainder belong to group A (or C according to CDC), to which most human samples belong. Viruses from group A are predominantly from backyard birds, and those from B from vaccinated commercial poultry. Preliminary studies suggest there is little to no human influenza cross-reactivity between the two groups. Epidemiologically, H5N1 HPAI poultry outbreaks in Egypt continue throughout the Nile Delta, mainly in areas of high human and poultry density.

Clade 2.3.4 sequences were obtained from Viet Nam, Lao People's Democratic Republic and Myanmar. *Clade 2.3.4* isolates from Myanmar are similar to 2007 isolates from the Yangon area, suggesting that the 2010 virus originates from a reservoir in domestic duck flocks. Samples from Lao People's Democratic Republic identified as *clade 2.3.4* cluster with viruses seen in that country during previous years. In late 2010, *clade 2.3.2*, which was originally detected from a dead Chinese pond heron in China, Hong Kong SAR in 2004, has become the most common clade in the spread of H5N1 HPAI and its invasion into new territories. Bulgaria, China (including Hong Kong SAR), Japan, Mongolia, Myanmar, Nepal, Romania, the Republic of Korea, the Russian Federation and Viet Nam have all been affected by *clade 2.3.2* since January 2010.


Table 2: Geographic distribution of H5N1 HPAI virus clades, 2010

Clade reported	Country/Territory	Poultry	Wild waterfowl	Other wild bird	Unspecified	Total
1	Cambodia	3			2	5
2.1.3	Indonesia	1 154	1		61	1 216
2.2	Bangladesh	62		1		63
2.2	Bhutan	4			1	5
2.2	India				15	15
2.2.1	Egypt	563			30	593
2.2.1	Israel	1		1		2
1, 2.3.2, 2.3.4	Viet Nam	42			16	58
2.2, 2.3.2	Nepal	5			3	8
2.3.2	Bulgaria			1		1
2.3.2	China		1		1	2
2.3.2	China, Hong Kong SAR	3		3	1	7
2.3.2	Republic of Korea	43	5	1		49
2.3.2	Japan	15	14	7		36
2.3.2	Mongolia		1			1
2.3.2	Romania	2				2
2.3.2	Russian Federation		1			1
2.3.2, 2.3.4	Myanmar	10				10
2.3.4	Lao PDR	1				1
	Total	1 908	23	14	130	2 075

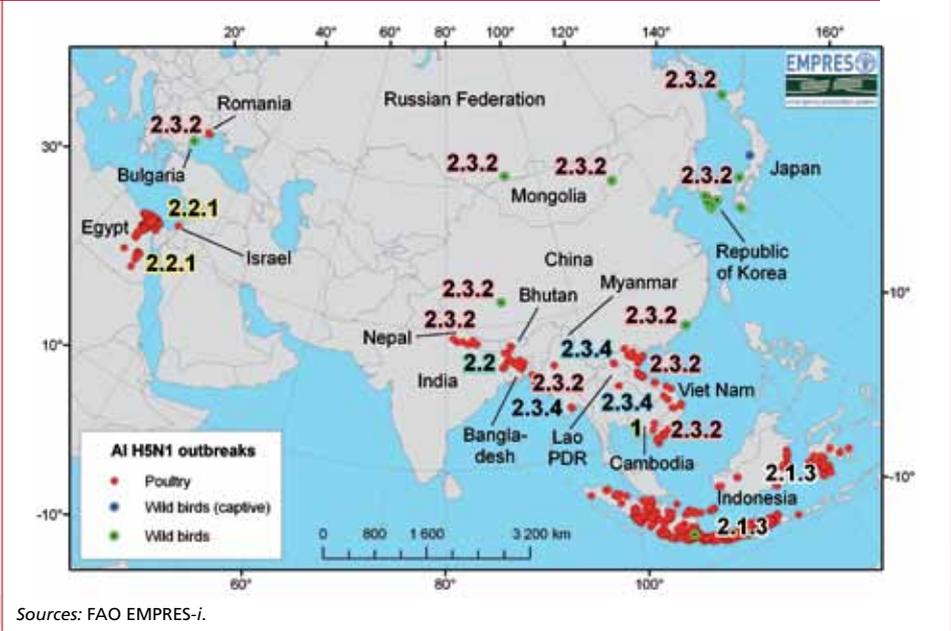
Source: FAO EMPRES-i.

In 2010, Nepal was the first country to detect clade 2.3.2 in the South Asia region. Clade 2.3.2 viruses in Nepal were most closely related to viruses isolated in wild birds in 2009 from the Russian Federation, Mongolia and Bulgaria, and also from poultry outbreaks in Romania. The clade 2.3.2 viruses isolated in wild birds in China, Hong Kong SAR and in poultry in Viet Nam were slightly less closely related to these viruses, probably indicating evolution from the source. The isolate from wild birds found dead in June 2010 in the Republic of Tyva, Russian Federation, close to the border with Mongolia, belonged to clade 2.3.2 of the Asian lineage, with 99 percent similarity to earlier 2009/2010 H5N1 isolates from wild birds in Mongolia, Tyva (Russian Federation) and Qinghai (China).

Most of the recent invasions of clade 2.3.2 may be linked to wild birds. The main clades currently found in wild birds are 2.3.2 and 2.2. The latter has circulated in wild birds since 2005. The predominant clade in 2010 was 2.3.2. For the cases in Bulgaria, China, Hong Kong SAR, Mongolia and the Russian Federation, only wild bird events have been reported, with no poultry affected. The initial clade 2.3.2 incidents in Japan, the Republic of Korea and Romania were also observed in wild birds, and only later did the disease apparently spread to poultry. Other than China, Myanmar and Nepal, all clade 2.3.2-affected countries had been free from the disease for extended periods.

It is likely that the clade 2.3.2 virus first spilled over from poultry to wild birds and

Figure 6: H5 HPAI poultry outbreaks, 1 September 2010 to 8 February 2011, and respective clades isolated



was periodically transported by migratory birds to other locations. Research has demonstrated that some wild waterfowl can shed H5N1 AI virus asymptotically for two to five days, and migration-disease ecology studies conducted by FAO have established the distances wild waterfowl can migrate over this same time frame. Although individual flights can be long (hundreds of kilometres), wild waterfowl's transmission of virus over such distances is more likely to occur through a leap-frog migration pattern, with concurrent transmission of virus from one bird to others at stop-over sites, and the newly infected birds carrying virus to the next site.

Perspectives for 2011

A number of concerns for 2011 must be considered. The endemic foci of disease will continue to pose a threat to countries at risk in Asia and to Egypt, and a long-term approach is required to eliminate H5N1 HPAI from poultry in these areas. The finding of a new clade of H5N1 (clade 2.3.2) in a wide range of wild birds would suggest that another round of outbreaks in a wider geographic area (Palearctic) may occur, certainly in countries in the eastern parts of Asia. The epidemiology of H5N1 in wild birds is far from understood, and the role of the virus's evolution in domestic waterfowl as a source of new viruses for wild birds needs to be defined. If H5N1 viruses are also entrenched in wild bird populations, as was found at Qinghai Lake in China, there will be considerable challenges in keeping poultry populations free from disease. It is likely that the trend of increased numbers of outbreaks in early 2011 will be seen again this autumn, and there is likely to be a parallel increase in human cases.



FAO's Animal Health Service and its Global Programme for the Prevention and Control of H5N1 HPAI continue to contribute to country preparedness, capacity building and outbreak response in affected countries. Between 2005 and 2010, FAO implemented 170 H5N1 HPAI projects, with 28 still ongoing as of February 2011, the majority in Asia. Veterinary epidemiology teams remain at the strategically placed Regional Animal Health Centres. Regional laboratory and epidemiology networks are also being sustained. A special wildlife unit is dedicated to research into the epidemiology of H5N1 in wild birds and wild birds' role in the transmission of the virus.

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Monitoring HPAI in the field to aid in vaccine selection

Highly pathogenic avian influenza subtype H5N1 (H5N1 HPAI) has become enzootic in Indonesia and Egypt. In response, FAO has undertaken two technical projects – one in Indonesia (2007) and one in Egypt (2008) – under the Network of Reference Laboratories, Epidemiology Centres and Groups of Experts on Avian Influenza (OFFLU) banner, and in collaboration with national agencies.

The projects aimed to understand the characteristics and epidemiology of circulating viruses, determine the efficacy of available influenza vaccines for poultry, and develop national systems to support the use of efficacious poultry vaccines as part of a comprehensive strategy to combat HPAI. To improve understanding of the evolution of the H5N1 HPAI virus in Indone-

sia, and the subsequent impact of vaccines applied to poultry, the OFFLU project in that country pioneered the application to avian influenza viruses of antigenic cartography developed to characterize human influenza viruses. The resulting map can be used to help assess vaccine immunity against circulating strains. Capacity building and technology transfer supports these activities in national veterinary laboratories, to develop a sustainable mechanism for monitoring viruses and informing vaccine selection. This is the first coordinated effort of its kind for the monitoring of influenza in poultry at a national level.

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Sampling of infected ducks during participatory avian influenza surveillance programme, Behera Governorate, Egypt, March 2009

National vaccination campaign against avian influenza, Sixth October Governorate, Egypt, March 2009



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Porcine reproductive and respiratory syndrome

Porcine reproductive and respiratory syndrome: virulence jumps and persistent circulation in China and Southeast Asia

Introduction

Porcine reproductive and respiratory syndrome (PRRS) was first recognized almost simultaneously in western Europe and North America in the late 1980s. In retrospect, evidence can be found that PRRS virus (PRRSV) was circulating in China in 1996 and in the Mekong Delta of Viet Nam since 2000, but at this early stage no severe clinical symptoms were associated with it. Since 2006, the pig sectors of China, Viet Nam, the Philippines and Thailand have continuously been hit by outbreaks of severe disease caused by atypical highly virulent strains of PRRSV. In 2010, the severe form of the disease (for convenience, referred to in this article as highly virulent PRRS [HV-PRRS]) affected additional countries in Southeast Asia, including Lao People's Democratic Republic and Cambodia, while outbreaks in Thailand increased in severity. This considerable geographic range underlines the regional burden PRRS represents today.

About the virus and the disease

The causative virus is differentiated into two genetically distinct genotypes: Type 1, or European genotype, with a predominant spread on the European continent; and Type 2, or North American genotype, which is isolated mostly on the American continent (North and South) and in Asia. Infection can occur via the respiratory, oral and venereal routes, as well as through intramuscular, intraperitoneal or intravenous inoculation. With the typical disease, clinical symptoms of PRRS include reproductive failure in breeding stock and respiratory tract illness in young pigs. Viraemia develops in pigs 12 to 24 hours post-infection, with the highest titres at seven to 14 days. Most pigs are viraemic for no longer than 28 days. Mortalities are generally confined to pre-weaning pigs. Cyanosis of the skin, especially the ears, is sometimes observed. Congenitally and post-natally infected piglets remain persistently infected, harbouring the virus in their tonsils and/or lymph nodes. PRRSV can be isolated from muscle and lymphoid tissues up to 24 hours after slaughter (and from muscle that had been frozen at -20°C for one month). Nevertheless, the virus titres decrease with cooling, hardening and freezing, although PRRSV can survive for several weeks at 4°C in bone marrow. Cooking, curing and rendering are sufficient to inactivate PRRSV in meat, minimizing the risk of spread in this way. The real threat occurs when unprocessed infected meat is fed to susceptible pigs (swill feeding).

PRRS and the pig sector: global context and regional peculiarities

■ Developments in pig production

Terrestrial animal meat consumption worldwide is topped by pork. Owing to changes in consumption patterns arising from increasing incomes in developing and transition countries with fast-growing economies, the global demand for pork has been constantly rising over recent decades. Together with poultry, the pig sector is a very fast-

The causative virus is differentiated into two genetically distinct genotypes: Type 1 and Type 2



growing livestock subsector, with numbers that will reach 1 billion head before 2015, representing a twofold increase compared with the 1970s. Pig production is now distributed globally, excluding regions with cultural and religious reservations regarding pork consumption. Pig production worldwide is dominated by an increasing dichotomy of production systems, with mainly subsistence-driven, traditional small-scale production on the one side, and highly specialized, vertically integrated industrialized farms on the other. The latter follows a distribution pattern similar to the intensive poultry sector, concentrating close to centres of urbanization and/or input sources. In an intermediate stage, diverse types of commercial and semi-commercial production systems can be found, usually combining some aspects of industrialized pig production with local husbandry traditions and a reduced dependence on external inputs.

China and Southeast Asia, with their strong cultural background in pig husbandry, have significantly increased their pig densities in recent decades. China alone raises almost 50 percent of the world's pig population, and the process of intensification has picked up enormous speed to supply growing urban centres that have an increased demand for pork and other livestock commodities. On a global scale, however – and definitely in Southeast Asia and China – a large proportion of animals are still kept in small-scale and backyard or free-range settings. In high-pig-density areas in Asia, this leads to the close proximity of production systems of different sizes and biosecurity levels – important factors that determine the scope and effect diseases might have on pig populations.

The linkages and interactions among production systems in a given setting can be quite unique and must be understood when devising disease control and prevention strategies. Such strategies should avoid one-size-fits-all recommendations, leaving enough flexibility to identify epidemiologically significant risk factors at sub-national levels.

Dynamics of highly virulent PRRS in China and Southeast Asia

In the summer of 2006, a new variant of PRRSV appeared in China and was first reported as high fever disease (HFD). It was later identified as an atypical form of PRRS, which according to the China Animal Disease Control Center (CADC) affected almost 2 120 000 pigs and caused 400 000 deaths. Clinically, HV-PRRS differs greatly from the typical PRRS and is characterized by high fever (40 to 42 °C), petechiae, erythematous blanching rash and high mortality rates of up to 100 percent in single production units, for swine of all ages, including grown and fattening pigs.

The disease persisted in its epidemic form in 2007, with serious impacts on the pig population. From 1 January to 22 August 2007, statistics released by the Chinese Government reported 826 outbreaks of PRRS in 26 provinces, autonomous regions and municipalities, including 257 000 diseased pigs, 68 000 dead pigs and 175 000 pigs destroyed (culled). Among these 26 provinces, those along the Yangtze River in the south of China were the most affected (Hebei, Shanghai, Jiangsu, Zhejiang, Anhui, Fujian, Jiangxi, Shandong, Henna, Hubei, Hunan, Guangdong, Guangxi, Hainan, Chongqing, Ningxia, Xinjiang, Tianjin, Liaoning, Gansu).

**China and Southeast
Asia have significantly
increased their pig
densities in recent decades**

During 2007, highly virulent strains of PRRSV appeared in Viet Nam and the Philippines (typical PRRS strains were first reported there in 1998). The spread pattern in Viet Nam (2007 to 2010) suggests the appearance of these new strains in the northern part of the country in March 2007. This coincided with the Tet Holiday, one of the major “harvest times” in pig production, with increased movement of people and product within the country. A second wave of infection, apparently with the same virus strain, occurred in June 2007 in the south of the country. The 2010 surveillance data from northern Viet Nam revealed a “new” 2010 PRRSV variant, while a mix of new and older variants was detected in the southern part of the country.

In the Philippines, the disease has been spreading mainly in areas with higher pig densities and increased commercial pig production. The number of detected cases has been rising each year (2010 results are not yet available). During surveillance, it became clear that most positive cases also tested positive for other pig pathogens such as classical swine fever (CSF) virus, porcine circovirus type 2 (PCV2) and swine influenza virus (SIV). Secondary bacterial infection may also contribute to the clinical appearance of HV-PRRS.

Thailand reported HV-PRRS for the first time in 2008 but, even including 2009 data, case numbers were low (25 in 2008 and 33 in 2009). In 2010, the disease caused an epidemic wave of major concern on small-scale commercial farms, with 145 outbreaks as of October 2010 (latest available information). Co-infections with other swine diseases were also reported, but seemed to be less prevalent than those reported from the Philippines.

The latest countries to report this new highly virulent variant of PRRS were Cambodia and Lao People’s Democratic Republic, both reporting their first cases in 2010 in small commercial units. Myanmar had not found positive cases, but with the epidemic wave in neighbouring Thailand in 2010, surveillance was increased. The spread of PRRS in the region over time and space is summarized in Figure 2.

■ Summarizing the spread pattern and country reactions

One possible explanation of the 2006/2007 PRRS epidemic in China and, later, Viet Nam is that the ancestor PRRSV of North American origin (Type 2) evolved into a highly virulent strain under selection pressure in China, which was driven by changes in pig husbandry practices, the epidemiological linkage of a large number of animals under very diverse production settings, and environmental factors (temperature and relative humidity in summer).

With its emergence in 2006 in areas of high pig density in China, the virus has made its way around Southeast Asia and, at least for the greater Mekong region, it seems evident that the disease was following the path of the intensification of pig production as it spread and became established first in countries with a larger share of commercial production units and high animal densities (Viet Nam, Thailand and the Philippines). It later entered countries with a less developed commercial sector (Cambodia and Lao People’s Democratic Republic), owing to lack of biosecurity in value chains and the absence of regulations and incentives for controlling pig diseases. In these more diffuse production environments, the absence of disease surveillance at the community level



The global context: drivers and risks

The almost simultaneous emergence, in the 1980s on separate continents, of two genetically highly distinct genotypes of PRRSV has been a source of ongoing speculation. The current knowledge on PRRSV epidemiology in wild boar and low-pig-density farming landscapes leaves the industrialization of swine production as the driver of virus evolution and shift in virulence. The intensification of production involves massive changes in pig husbandry practices: the moving of pigs indoors, increases in the sizes of herds sharing airspace, the breakdown of the traditional farrow-to-finish system into highly specialized multi-site production systems, and increased use of artificial insemination. These factors have led to a pig production chain that provides a host contact network structure conducive to sustained circulation of infectious viruses such as PRRSV, including highly virulent strains.

Geographic and trade corridors linking different livestock sub-populations pose increasing epidemiological challenges. They explain how HV-PRRS, as well as other diseases including foot-and-mouth disease and CSF, spread in eastern Asia. These disease dynamics are reinforced and sustained by farming landscapes where smallholder farming and intensive production coincide, resulting in the increased vulnerability of eastern Asia to livestock disease epidemics.

■ Impact on the pig sector

With the growing importance of pig production in many regions of the world, the emergence of a highly virulent strain of PRRS virus that has already reached pig populations in some regions in Asia can be considered a serious animal health threat for other regions around the globe. It has the potential to lead to a major socio-economic impact on the livelihoods of millions of pig farmers.

HV-PRRS has emerged in the area of intensification of pig production in eastern Asia, where the virus apparently encountered the right conditions for a virulence jump. This has not happened in other regions of high pig densities. The virus then spread through this production environment; whether or not the highly virulent PRRSV will find its way to other regions of the world depends on the movement and trade patterns of the commercial pig sector. Genetic material of improved pig breeds usually travels from Western Europe and North America to other parts of the world, because the leading breeder companies have their nucleus herds in these regions, and trade regulations make retrograde imports of animals and semen from Asia very difficult – reducing the risk of disease introduction. The growing markets in South America, Mexico and Eastern Europe that may have an interest in linking with Asian marketing chains will face considerable risks should the trade flow include the transport of genetic material into their countries.

Socio-economic impact

PRRS is considered to be the most economically important viral disease of intensive swine farms in Asia, Europe and North America. Financial losses are mainly due to increased mortalities, poor reproductive performance, and the costs of ancillary control measures, vaccines and medications. Secondary diseases following a PRRS outbreak on

HV-PRRS has emerged in the area of intensification of pig production in eastern Asia



a farm can lead to additional costs. In addition, costly diagnostic testing and herd monitoring are necessary after a PRRSV introduction, to develop comprehensive control or eradication strategies. PRRS has been estimated to cost approximately USD 560.32 million in losses for United States swine producers each year. The HV-PRRS outbreak in China and Viet Nam caused extensive losses and a significant rise in pork prices.

In general, socio-economic assessments of PRRS and pig diseases in developing countries are not abundant. Socio-economic assessments of PRRS in the swine industry and smallholders in China or Viet Nam have not been carried out.

FAO response and main recommendations

FAO has been supporting Southeast Asian countries' PRRS control since 2007, by providing technical assistance to help understand the epidemiology of PRRS, capacity building to improve diagnostic capacities in the different contexts and countries, and support to the implementation of national disease strategies under a regional framework. In November 2010, FAO brought together a number of Southeast Asian countries at a workshop to review their activities on swine disease surveillance and swine health management.

Main recommendations for PRRS control

- Improving the timely exchange of epidemiologically relevant information among affected countries, within a regional framework that feeds into national control strategies.
- Conducting risk and impact assessments along the production chains, to complete the understanding of PRRS epidemiology.
- Designing and pursuing a national strategy, harmonized with existing strategies for diseases affecting the pig sector, to detect and control PRRS outbreaks.
- Increasing risk-based surveillance for swine diseases and capacities at all levels, including national laboratory networks.
- Increasing awareness among all stakeholders along the production chain regarding the disease and the overall impact on people's livelihoods.
- Encouraging support to pig producers of all sized units, to improve biosecurity according to the capabilities of their production systems.
- Promoting the appropriate use of safe and efficient vaccine matching with circulating strains, as a tool to reduce clinical symptoms.
- Avoiding the culling of animals when compensation of producers is not legislated.

Extracted from: K. Dietze, J. Pinto, S. Wainwright and C. Hamilton. 2011. Porcine reproductive and respiratory syndrome (PRRS): virulence jumps and persistent circulation in Southeast Asia.

FAO Focus. www.fao.org/docrep/013/al849e/al849e00.pdf.

Rinderpest

A world free from rinderpest Global Rinderpest Eradication Programme Symposium, 13 to 14 October 2010.

Since its foundation in 1945, the Food and Agriculture Organization of the United Nations (FAO) has fought rinderpest. This has involved implementing vaccine campaigns on behalf of member countries, supplying vaccine and other materials and equipment, providing training and technical advice/assistance and, over the past 17 years, coordinating the Global Rinderpest Eradication Programme (GREP). With an increased role, GREP coordinated and assisted national and regional campaigns against the few remaining foci of infection in Africa and Asia, with the last confirmed case of rinderpest in the world reported in 2001. Since then, all continuing surveillance for the disease and virus has failed to find any evidence that rinderpest is occurring naturally anywhere in livestock or wildlife populations. FAO and the World Organisation for Animal Health (OIE) have established a Joint Committee to review the evidence of freedom from disease that has been provided by all countries; it is anticipated that when the committee submits its final report in 2011, FAO and OIE will jointly declare that rinderpest has been eradicated from the planet. This will be only the second virus, and the first pathogen causing a disease in livestock, to be eliminated globally. In view of this, FAO has halted field operational activities against rinderpest, some 60 years after it started them.

However, there are at least two areas where FAO will continue its involvement in rinderpest eradication. The first is in developing a science-based post-eradication strategy to safeguard the now highly susceptible world cattle population against inadvertent escape of the virus from laboratory environments. Development of this strategy has been entrusted to the FAO/OIE Joint Committee, which will submit a proposal and recommendations by mid-2011. The second area of continued involvement is in assessing the overall history and roadmap that led to rinderpest eradication, to highlight and record lessons learned in the process. It will then be useful to see how these lessons might be applied to other diseases, particularly peste des petits ruminants (PPR), a disease of sheep and goats caused by a virus closely related to rinderpest virus and with similar epidemiological characteristics. To address this second point, FAO convened a symposium in Rome from 13 to 14 October 2010, bringing together animal health scientists and other specialists from several countries. More than 100 experts from international and regional organizations, national field staff from countries that played key roles in rinderpest eradication campaigns, and individual scientists and veterinarians who had made significant contributions participated in the symposium.

The symposium ended with the following two recommendations to FAO:

1. The success of the global eradication of rinderpest should be widely and intensively publicized and promoted. This should emphasize:
 - a. the roles played by all stakeholders, including livestock owners;



- b. the benefits that eradication has brought and will continue to bring, to individuals as well as the wider community;
 - c. the lessons learned during the eradication process, and their potential application to other diseases;
 - d. the post-eradication strategy, including the sequestration of all stocks of virus and the archiving of all documentation (papers, books and reports on rinderpest), to ensure global livestock safety; and the need for adequate international and national resources to ensure this.
2. International and regional organizations and all stakeholders should apply the lessons learned from the eradication of rinderpest to other diseases, particularly the progressive control and eventual eradication of PPR. This could be implemented within a larger programme of improved small ruminant health, and also within specific regional and national projects and activities. FAO should play the lead role in organizing the preliminary steps necessary for initiating this global initiative and in identifying appropriate partnerships to drive and implement the activities required.

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Workshops

Strengthening Systems of Prevention and Control of Transboundary Animal Diseases in the Maghreb and Egypt

In support of the animal health programme in North Africa, the Government of Spain, through the Spanish Agency for International Cooperation for Development (AECID), provided an additional contribution of USD 2.5 million under project GCP/RAB/010/SPA “Strengthening Systems of Prevention and Control of Transboundary Animal Diseases in the Maghreb and Egypt: Towards a Mediterranean Animal Health Network” (REMESA). Through this network, the project aims to strengthen regional cooperation and information sharing for epidemiological surveillance, laboratories, communication and socio-economics. The priority diseases are foot-and-mouth disease, Rift Valley fever, peste des petits ruminants, highly pathogenic avian influenza, rabies, bluetongue and West Nile fever. The three-year project officially started in June 2010.

REMESA is a regional network associating the five Maghreb countries (Algeria, the Libyan Arab Jamahiriya, Mauritania, Morocco and Tunisia), Egypt and southern countries of Western Europe (France, Italy, Portugal and Spain). It was established in Avila (Spain) in April 2008 by the countries, the Food and Agriculture Organization of the United Nations (FAO), the World Organisation for Animal Health (OIE), the Arab Maghreb Union (AMU) and the European Union (EU). The network promotes cross-border cooperation in animal health by facilitating the coordination of animal disease control strategies, the sharing of experiences, and the regular exchange of information on the zoo-sanitary situation in the region.

REMESA is managed by a joint permanent committee (JPC), chaired alternately by its member countries. FAO and OIE are both members of the JPC and coordinate the network within the framework of the FAO/OIE Regional Animal Health Centre (RAHC) for North Africa, a regional platform associating the FAO Emergency Centre for Transboundary Animal Disease Operations for North Africa (ECTAD-NA) and the OIE Sub-Regional Representation for North Africa. FAO ECTAD-NA will provide secretariat support to the network until December 2011.

REMESA member countries and other countries around the Mediterranean Basin are all within the same geo-sanitary zone, which means they face similar epidemiological risks for many transboundary animal diseases and zoonoses that threaten animal resources, population health and national economies. REMESA countries engage in a process of political and economic rapprochement, through AMU and

Inception workshop on Strengthening Systems of Prevention and Control of TADs in the Maghreb and Egypt



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broader cooperation initiatives, such as the Euro-Mediterranean Partnership (EUROMED) and its Barcelona Process, and the proposed Union for the Mediterranean (UPM). All these geo-political factors reinforce the relevance of REMESA and its supporting programmes and projects.

To improve exchange, coordination and technical capacity at the national and regional levels, REMESA also relies on a platform/information site,¹ which was recently opened for documentation and information exchange among its member countries.

FAO ECTAD-NA organized the inception workshop from 29 November to 1 December 2010 in Tunis, with some 40 participants from project beneficiary countries – Algeria, Egypt, the Libyan Arab Jamahiriya, Mauritania, Morocco and Tunisia – as well as ECTAD-NA and FAO Headquarters. From each of these countries, there was at least one expert on each REMESA thematic area: epidemiology, socio-economics, laboratories and communication.

The technical objective of the inception workshop was to enable representatives of the six countries to develop the concepts of the project, foster ownership and identify activities under each thematic area. Participants were divided into working groups supporting the four REMESA sub-networks:

- RELABSA: animal health laboratories sub-network;
- REPIVET: epidemiological surveillance sub-network;
- RECOMSA: animal health communication sub-network;
- RESEPSA: socio-economic sub-network for production and animal health.

Each working group developed specific activities to support the countries and REMESA sub-networks in different intervention areas, in line with regional strategies for the coordinated prevention and control of priority animal diseases.

A further objective of the workshop was to present proposed work plans to the senior animal health officials of network countries, the donor organization, and potential collaborators and donors. On the workshop's last day, the Chief Veterinary Officers of participating countries, the OIE Sub-Regional Representative for North Africa, representatives of AECID and Tunisia-based donor agencies, and other stakeholders joined the workshop to review and discuss the work plans of the thematic working groups. FAO presented a general overview of the project and the workshop outcomes, which was followed by detailed presentations of the issues discussed and the resulting work plan matrices of each working group. The workshop concluded with a plenary session to present and discuss the recommendations concerning project implementation formulated by participants. A comprehensive report of the workshop is available on the ECTAD-NA website.²



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The Communication Focal Points of Algeria, the Libyan Arab Jamahiriya, Mauritania, Morocco and Tunisia work together

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¹ www.remesanetwork.org.

² www.fao-ectad-tunis.org/.



Emergency Prevention System for Transboundary Animal and Plant Pests and Diseases Wildlife Health and Ecology Unit conducts One Health Workshop in Southern Africa

Among its other efforts, the Emergency Prevention System for Transboundary Animal and Plant Pests and Diseases (EMPRES) Wildlife Health and Ecology Unit undertakes activities that aim to build the capacity of animal health services to undertake surveillance for wildlife diseases and investigation of disease outbreaks. This work has increasingly focused on the application of a One Health approach to understanding and investigating infectious diseases that occur at the interface of livestock, wildlife and people. In November 2010, FAO and its partners – the University of Pretoria Department of Veterinary Tropical Diseases, the Agreement on the Conservation of Populations of European Bats (EUROBATS) group of the Convention on Migratory Species (CMS), the Zoological Society of London (ZSL) and the Wildlife Conservation Society (WCS) – held a human-animal-environment interface workshop on “Wildlife Investigation and Livestock Disease (WILD): Implications for Public Health”.

The workshop was conducted over five days in Johannesburg, South Africa with the participation of 27 professional officers from ministries of agriculture, the environment and health of 12 countries: Angola, Botswana, Ghana, Lesotho, Malawi, Mauritius, Mozambique, Seychelles, South Africa, Swaziland, Zambia and Zimbabwe. Topics covered included wildlife diseases, wildlife ecology, disease surveillance strategies, outbreak response, epidemiology and drivers of disease emergence. To facilitate the application of theoretical concepts, problem-based learning activities were used to encourage the diverse participants to work together and develop a One Health approach/solution to likely disease scenarios. Teams were formed and asked to develop multi-sectoral responses and management plans

for the disease monitoring, outbreak investigation and control programmes required to address issues arising from an outbreak at a particular interface.

Colleagues from FAO’s Emergency Centre for Transboundary Animal Disease Operations (ECTAD) Gaborone office presented the ongoing buffalo-cattle disease interface study in Botswana as an example of a successfully implemented field project involving collaboration between the livestock and wildlife sectors. Among other diseases, this project had considered the control of two zoonotic diseases – brucellosis and tuberculosis (TB). One day of the workshop was dedicated to bat ecology, the pathogens for which bats are reservoirs, conservation challenges, and field techniques for bat surveillance. This was led by colleagues affiliated to CMS- EUROBATS, who used bat trapping equipment and live bats to demonstrate proper handling and sampling techniques for conducting surveillance for bat-borne diseases.

Pre- and post-workshop testing on the topics covered showed that participants’ knowledge had improved significantly, particularly regarding important emerging diseases; the agricultural, biological, ecological and epidemiological factors involved



Trainers and participants at the South African WILD training



in the risk of disease transmission between wildlife and livestock and relevant human populations; and the importance of an inter-ministerial and multidisciplinary approach to disease investigation and control. Participants stressed that the problem-based interactive activities and interdisciplinary work were the most valuable elements of the course.

This was the first WILD training activity to be conducted in the Africa region. It built on four previous wildlife capture, handling and sampling training sessions, conducted by the African Union Interafrican Bureau for Animal Resources (AU-IBAR)³ and FAO as part of the Support Programme to Integrated National Action Plans (SPINAP)⁴ project. With partners including AU-IBAR, CMS-EUROBATS and the Royal Veterinary College (United Kingdom), FAO plans to implement three additional WILD training courses over the next six months, in East, Central and West Africa, with support from the United States Agency for International Development (USAID)/RESPOND component of the Emerging Pandemic Threats (EPT) project.



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Dr Paul Racey of CMS-EUROBATS demonstrating bat handling

Contributor: Tracy McCracken (FAO)

³ www.au-ibar.org/index.php/en/who-we-are/overview.

⁴ www.au-ibar.org/index.php/en/projects/current-projects/spinap.



Meetings

Increasing concern moves African swine fever up the international animal health agenda

In response to the incursion and establishment of African swine fever (ASF) in the Caucasus since 2007, the Emergency Prevention System for Transboundary Animal and Plant Pests and Diseases (EMPRES) has been providing regular updates and epidemiological assessments about the situation, and has been emphasizing the need for a more concerted and committed approach to this disease. There is mounting concern in the international animal health community about the spread of this disease, and in 2011 dialogue among Eastern European countries, European Union (EU) member countries and relevant international organizations has developed increased impetus.

A concrete outcome of this concern was the Veterinary Expert Meeting on African Swine Fever held in January 2011 to share updates on the disease spread and applied control measures, and to draft action points for a joint way forward. This meeting was organized and chaired by Dr Karin Schwabenbauer, Chief Veterinary Officer (CVO) of Germany, and attended by representatives from FAO, the EU, OIE, Austria, Denmark, Germany, Italy, Latvia, Lithuania, Norway, the Russian Federation, Spain and the United States of America. The agenda included presentations by leading ASF research groups and participating international organizations. FAO emphasized that while there was an understandable emphasis on eastern Europe and the Caucasus, the global context of ASF must not be overlooked. This context includes the endemicity of all known ASF genotypes in the natural virus reservoirs in sub-Saharan Africa, and preparedness for potential future epidemic waves in currently unaffected regions such as eastern Asia, where more than 55 percent of the world's domestic pig population is raised.

The First Veterinary Forum for Southeast Europe was organized in February 2011 in Budapest, Hungary by FAO and the European Commission for the Control of Foot-and-Mouth Disease (EUFMD), under the umbrella of the Global Framework for the Progressive Control of Transboundary Animal Diseases (GF-TADs) for Europe. The forum provided a platform for discussing ASF dynamics, with special emphasis on preparedness and early detection in southeastern European countries, which are currently under increased threat of disease introduction into their territory. Participating countries welcomed the opportunity to discuss and compare the different stages of ASF contingency planning and the current situation of ASF control projects in the region. The need for continued dialogue on these topics was emphasized.

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FAO International Workshop on Challenges of National, Regional and Global Information Systems and Surveillance for Major Animal Diseases and Zoonoses

FAO Headquarters, Rome, Italy, 23 to 26 November 2010

Organized by the Food and Agriculture Organization of the United Nations (FAO), this three-day meeting – referred to as an international workshop – consisted of a series of scientific presentations by 44 experts from all geographic areas, representing different aspects of global animal health promotion and disease prevention systems, including a broad array of international and regional organizations; national veterinary, medical and other health-related services; and academic institutions and non-profit organizations.

This report summarizes participants' discussions on surveillance and information systems, which explored issues raised in the presentations and focused on the operation, characteristics, objectives, conceptual design, needs and future directions for national, regional and global animal health surveillance/information systems.

The meeting was based on the following principles:

- Disease surveillance designed to reduce disease burden and poverty is a global public good.
- Because pathogens do not respect geographic or species differences, health information systems should be designed to cross geographic boundaries and encompass human and animal health, where appropriate.
- Early detection and early warning are of paramount importance in allowing health systems to respond to events, reduce risk and mitigate the consequences of disease emergence.

The four objectives articulated for meeting participants were to:

1. identify successes and challenges faced by current national, regional and global surveillance systems, and propose means of overcoming the challenges, including strategies to facilitate data sharing and technology transfer among national, regional and global health information systems;
2. discuss the standardization of mechanisms for exchanging data among information systems, based on the use of open-source software and technologies;
3. identify appropriate methods for improving the collection, management, analysis and use of geo-referenced data on transboundary animal diseases (TADs), zoonoses and other emerging diseases;



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*Participants of the meeting,
FAO, Rome, Italy*

4. seek consensus on protocols for the sharing of official and unofficial data among national, regional and global animal health information systems.

The recommendations and final report from this meeting are available at: www-data.fao.org/ag/againfo/programmes/en/empres/surveillance_2010.html.

Contributor: Julio Pinto (FAO)

Network of Reference Laboratories, Epidemiology Centres and Groups of Experts on Avian Influenza, Third Annual Technical Meeting

FAO Headquarters, Rome, Italy 16 to 17 November 2010

Leading scientists from the Network of Reference Laboratories, Epidemiology Centres and Groups of Experts on Avian Influenza (OFFLU)⁵ and the public health sector, including the World Health Organization (WHO) and United States Centers for Disease Control and Prevention (CDC), met in Rome, Italy, from 16 to 17 November 2010, to discuss a range of technical and other challenges related to animal influenza viruses. OFFLU is an open network of expertise on animal influenza established jointly in

2005 by the World Organisation for Animal Health (OIE) and the Food and Agriculture Organization of the United Nations (FAO). It supports international efforts and facilitates collaborative relationships to improve control of influenza infections in animal species; improve data sharing between animal health and public health partners involved in the surveillance and laboratory diagnosis of influenzas; and build laboratory capacity

for detecting, diagnosing and monitoring influenzas, on a global scale.

The meeting focused on identifying priorities for research and further actions to improve and coordinate global surveillance and control. Scientists from more than 30 countries and from fields of expertise that included equine, swine, avian and human influenza shared their latest experiences, ideas and research findings.

Following emergence of the human pandemic H1N1 (2009) virus, which contains genetic components from swine and avian viruses, network resources have been mobilized to support international efforts to combat this new global threat; OFFLU's contribution to the WHO human influenza vaccine strain selection process was formalized in January 2011. OFFLU will continue to strengthen links within animal health networks and to collaborate with the WHO influenza network on matters relevant to public health.

The meeting also provided an opportunity to highlight OFFLU's successes, which include providing global guidance on surveillance, control and biosafety related to



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*Participants of the meeting,
FAO, Rome, Italy*

⁵ www.offlu.net/index.html.



highly pathogenic avian influenza (HPAI); helping individual countries to develop effective avian influenza vaccination strategies; and rapidly responding to pandemic H1N1 by providing urgent technical advice on the animal health aspects of this newly emerged disease.

A number of joint WHO-OFFLU projects were described, and the meeting was important for both the animal and the human health sectors. Experts from these sectors agreed to collaborate on a landmark initiative to look at ways of predicting the possible emergence of new threats by examining the genetic sequences of viruses collected through global animal influenza surveillance. Other notable outputs included an OFFLU influenza research agenda for equine, swine, poultry and wild birds; a mechanism for global coordination of swine influenza surveillance; a worldwide proficiency testing network; an expert group to monitor virus mutations; a roadmap for improved capacity building; and recommendations for improving the effectiveness of vaccine use.

Through its multidisciplinary knowledge base and existing links with international collaborators, OFFLU plays a pivotal role in strengthening technical links between human and animal laboratories at the national, regional and global levels. Significant progress has been made in animal influenza (H5N1) vaccine selection and efficacy, vaccination strategies, genetic mapping, the nurturing of relationships, and capacity building of national veterinary services. It is now clear that OFFLU offers a strategic global-level technical platform for promoting the activities needed to respond to animal influenzas on a global scale.

The main OFFLU action points emerging from the meeting

1. OFFLU (OIE/FAO) will deliver a guiding statement on the use of material transfer agreements for sharing virus strains and other biological material among institutes.
2. The OFFLU Applied Epidemiology Group will review influenza surveillance data requirements for existing infection and/or disease reporting mechanisms.
3. OFFLU has produced a standard H5 antiserum, and will submit a dossier to OIE for establishment as an OIE standard.
4. The OFFLU technical activity for proficiency testing will coordinate an international proficiency test for detection of influenza A viruses via real-time polymerase chain reaction (PCR).
5. OFFLU will develop a technical activity for the global coordination of swine influenza virus surveillance and research.
6. OFFLU will publish its research agenda on the OFFLU Web site.
7. WHO, OIE and FAO will formalize OFFLU collaboration in the human influenza vaccine virus selection process.

Contributors: Gwenaelle Dauphin (FAO, OFFLU), Filip Claes (FAO, OFFLU) and Mia Kim (FAO, OFFLU)



News

Meetings and publications

Meetings and events

- One Health Workshop, FAO, Rome, Italy, 4 to 6 May 2011
- World Conference on Veterinary Education, VetAgro Sup, Campus Vétérinaire, Lyons, France, 12 to 16 May 2011
- 79th General Session of the World Assembly of OIE Delegates, Paris, France, 22 to 27 May 2011; including Rinderpest Eradication, Recognition of Remaining Countries and Resolution, 25 May 2011 (www.oie.int/eng/session2011/infos.htm)
- 6th International Symposium on Emerging and Re-emerging Pig Diseases, Barcelona, Spain, 12 to 15 June 2011
- Towards a Safer World – Practical Approaches to Advance Disaster Preparedness, Rome, Italy, 15 to 17 June 2011 (organized by the World Food Programme [WFP])
- Symposium on Rinderpest Eradication: Achievements and Obligations, FAO, Rome, Italy, 27 June 2011 (for Chief Veterinary Officers and special guests)
- Conference's Plenary Session (Declaration of Global Freedom from Rinderpest), FAO, Rome, Italy, 28 June 2011.
- 3rd International Conference on Sustainable Animal Agriculture for Developing Countries, Nakhonratchasima, Thailand, 26 to 29 July 2011 (www.saadc2011.com/home.php)
- Global Conference on Rabies Control, Seoul, Republic of Korea, 7 to 9 September 2011
- 31st Conference of the International Scientific Council for Trypanosomiasis Research and Control (ISCTRC), Bamako, Mali, 12 to 16 September 2011 (www.au-ibar.org/index.php/en/media/calendar-of-events/details/49-31st-conference-of-the-isctrc-bamako-mali)
- World Rabies Day, 28 September 2011 (www.worldrabiesday.org/)
- 7th European Congress on Tropical Medicine and International Health (ECTMIH), Barcelona, Spain, 3 to 6 October 2011 (www.ectmihbarcelona2011.org/homeweb.aspx)
- Joint Ministerial Meeting (JMM) on Avian Influenza, Cancun, Mexico, 10 to 14 October 2011
- 30th World Veterinary Congress 2011: Caring for Animals: Healthy Communities, Cape Town, South Africa, 10 to 14 October 2011
- International Closing Ceremony of the World Veterinary Year, Cape Town, South Africa, 10 to 14 October 2011
- 2nd World Conference on Biological Invasions and Ecosystem Functioning, Mar de la Plata, Argentina, 21 to 24 November 2011

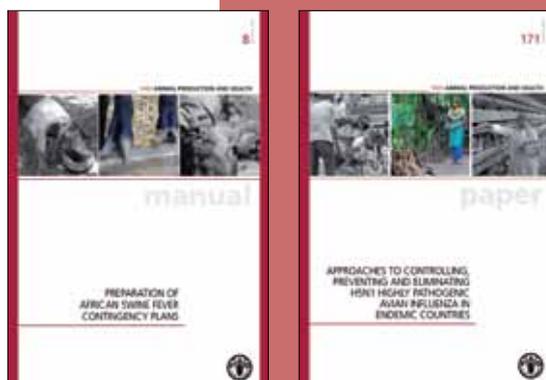


Regional Global Regional Eradication Programme (GREP) meetings:

- Nairobi, Kenya, 5 to 8 May 2011
- Bangkok, Thailand, 7 to 10 June 2011
- Rabat, Morocco, 14 to 17 June 2011
- Addis Ababa, Ethiopia, training on biosafety, sequestration and molecular diagnosis of rinderpest, 4 to 8 July 2011

FAO Animal Production and Health Publications

- **FAO Animal Production and Health Manual No. 8:** *Preparation of African swine fever contingency plans* (in English, French, Russian, Spanish, Armenian and Georgian) (available at www.fao.org/docrep/012/i1196e/i1196e00.htm).
- **FAO Animal Production and Health Paper No. 171:** *Approaches to controlling, preventing and eliminating H5N1 highly pathogenic avian influenza in endemic countries* (available at www.fao.org/docrep/014/i2150e/i2150e.pdf).



New staff

Caryl Lockhart

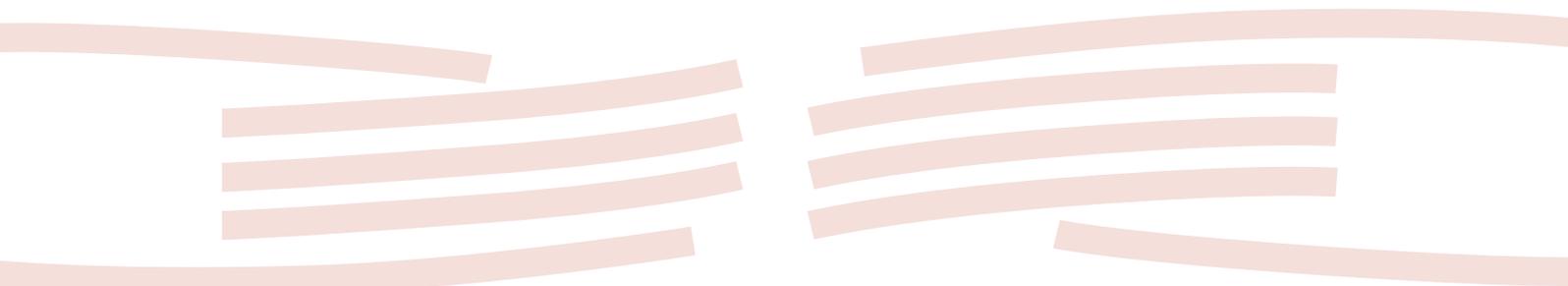
Caryl Lockhart (DMV, M.Sc., Ph.D.) joined the Global Early Warning and Response System for Major Animal Diseases, including Zoonoses (GLEWS) Animal Health Service Group in October 2010 as Disease Intelligence Officer. She previously worked with FAO as a Veterinary Epidemiologist on the Avian Influenza Control Programme in Indonesia and on the Caribbean Amblyomma Programme in Antigua, and with the Ministry of Agriculture in Dominica, West Indies as Veterinary and Livestock Officer. She received a doctorate in veterinary medicine from the *Instituto Superior de Ciencias Medicas de Habana* in Cuba, a master of science in tropical livestock production from the *Universidad Pedro Henriquez Urena* in the Dominican Republic, and a doctor of philosophy (Ph.D.) in veterinary epidemiology from Massey University, New Zealand.

Fulvio Biancifiori

Fulvio Biancifiori (DVM, Epidemiologist), has joined FAO to support the FAO/OIE Global Framework for the Progressive Control of Transboundary Animal Diseases (GF-TADs) Secretariat. He first worked at the *Istituto Zooprofilattici Sperimentali* (IZS) in Perugia, Italy (1974) doing research into the diagnosis of infectious diseases of livestock. In 1984, he joined FAO as Chief Technical Adviser for a series of United Nations Development Programme (UNDP)-FAO projects in Africa, the Near East, South-east Asia and Latin America. In 1991, he joined the former FAO-AGOW in Rome for



West Africa countries, and took part in a regional project in Central America and the Caribbean with the primary objective of standardizing and harmonizing laboratory diagnostic methods and veterinary regulations in the region. In 1994, he moved to IZS Teramo (Italy), as coordinator of the biotechnology laboratories. In 1997, he rejoined IZS Perugia for the process of gaining accreditation under International Organization for Standardization (ISO) 9001 and Italian national standard UNI EN 45001, and was coordinator of biotechnology and molecular biology labs. He set up the education and training service and planned and validated new radio frequency identification of products (RFID) technologies for the traceability of animals and their products "from farm to fork". He edited the book *Benessere animale* ("Animal welfare"), which was published (in Italian) in 2010.





Contributions from FAO Reference Centres

FAO/OIE World Reference Laboratory for FMD, Pirbright, United Kingdom

Report from World Reference Laboratory for FMD, July to December 2010

Country/Territory	No. of samples	Virus isolation in cell culture/ELISA ¹								RT-PCR ² for FMD ³ (or SVD) ³ virus (where appropriate)			
		FMD virus serotypes							NVD ⁵	NT ⁶	Positive	Negative	NT
		O	A	C	SAT 1	SAT 2	SAT 3	Asia 1					
Afghanistan*	81	-	-	-	-	-	-	-	4	77	73	8	-
Botswana	5	-	-	-	-	5	-	-	-	-	5	-	-
Cambodia	5	5	-	-	-	-	-	-	-	-	5	-	-
Ethiopia	12	-	-	-	-	-	-	-	12	-	8	4	-
China (Hong Kong SAR)	3	3	-	-	-	-	-	-	-	-	3	-	-
Iran (Islamic Republic of)	52	34	11	-	-	-	-	-	7	-	48	4	-
Mongolia	18	8	-	-	-	-	-	-	10	-	9	3	6
Mozambique	7	-	-	-	-	7	-	-	-	-	7	-	-
Myanmar	2	-	-	-	-	-	-	-	1	1	1	-	1
Nepal	51	10	-	-	-	-	-	-	41	-	27	24	-
Pakistan**	52	36	-	-	-	-	-	-	16	-	48	4	-
Senegal	4	-	-	-	-	-	-	-	4	-	-	4	-
Turkey	33	20	3	-	-	-	-	-	10	-	30	3	-
Thailand	8	8	-	-	-	-	-	-	-	-	8	-	-
Viet Nam	13	12	1	-	-	-	-	-	-	-	11	-	2
Zambia	4	3	-	-	-	-	-	-	1	-	4	-	-
Zimbabwe	4	-	-	-	-	2	-	-	2	-	4	-	-
Total	273	139	9	-	-	14	-	-	104	1	218	37	9

¹ FMD (or SVD) virus serotype identified following virus isolation in cell culture and antigen detection enzyme linked immunosorbent assay (ELISA).

² Reverse transcriptase-polymerase chain reaction for FMD (or SVD) viral genome.

³ Foot-and-mouth disease.

⁴ Swine vesicular disease.

⁵ No FMD, SVD or vesicular stomatitis virus detected.

⁶ Not tested.

* All but four samples from Afghanistan were supplied in ribonucleic acid (RNA) later for PCR analysis.

** One sample from Pakistan contained a mixture of type O and A FMD viruses.



**FAO/OIE Reference Laboratory for Rinderpest and Peste des Petits Ruminants,
Montpellier, France**

Report from FAO Regional Reference Laboratory for PPR, International Cooperation Centre of Agricultural Research for Development (CIRAD), Montpellier, France, July to December 2010

Country/ Territory	Species	Sample	Number of tests	Number of PPRV positives/doubtful	Test	Nature of the test: confirmatory or tentative
PPRV¹ with differential diagnosis with RPV²						
Djibouti	Dromedary	Sera	2	0	C-ELISA ³	Confirmatory
	Oryx gazella beisa	Sera	2	0	C-ELISA	Confirmatory
	Caprine	Sera	10	8	C-ELISA	Confirmatory
France (Mayotte)	Caprine	Sera	114	0	C-ELISA	Confirmatory
	Bovine	Sera	1	0	C-ELISA	Confirmatory
	Caprine	Blood	10	0	RT-PCR/QPCR ⁵	Confirmatory
	Bovine	Blood	1	0	RT-PCR/QPCR	Confirmatory
	Caprine	Lung	2	0	RT-PCR/QPCR	Confirmatory
Senegal	Caprine/Ovine	PCR product	24	16	RT-PCR ⁴ /Sequencing	Confirmatory
	Caprine/Ovine	Tissue	224	41	RT-PCR/Sequencing	Confirmatory
	Caprine/Ovine	Sera	224	150/6	C-ELISA	Confirmatory
Vaccine						
Jordan	-	PPR vaccine	2		Quality Control ⁶	Pass

¹ Peste des petits ruminants virus.

² Rinderpest virus (all samples remained negative).

³ Competitive enzyme linked immunosorbent assay.

⁴ Reverse transcriptase-polymerase chain reaction.

⁵ Quantitative RT-PCR.

⁶ Sterility test + PCR (RPV, PPRV, bovine viral diarrhoea virus, mycoplasma) + titration (cytopathic effect) visualized by immunofluorescence test using an anti-PPR monoclonal antibody (anti-PPRV Mab) + sequencing.



Stop the press

From January to May 2011, since the last EMPRES Transboundary Animal Diseases Bulletin (No. 36), there have been reports of more transboundary animal diseases (TADs) across the world.

Porcine reproductive and respiratory syndrome (PRRS) cases were confirmed for the first time in Mongolia and Myanmar in February 2011. In Mongolia, the PRRS was confirmed in a far in Darkhan-Uul Aimag (north of Ulaanbaatar) in February, then in another farm in Tuv Aimag (South of Ulaanbaatar) in May. In Myanmar, up to 12 May 2011, pig farmers in three townships were facing high mortalities in their predominantly subsistence-driven production. With FAO support, the country continues to conduct surveillance and will work on national vaccine production. It has not yet been confirmed whether the virus circulating in Myanmar is a highly pathogenic strain related to those that are currently circulating in other Southeast Asian countries.

Foot-and-mouth disease (FMD) serotype O was reported in Bulgaria, China (Guizhou, Taiwan and Xinjiang Provinces), the Democratic People's Republic of Korea, Israel, the Libyan Arab Jamahiriya (December 2010 outbreaks reported in February 2011), the Republic of Korea, the Russian Federation and Viet Nam. FMD serotype SAT2 was reported in Botswana and Zimbabwe. FMD was also reported in South Africa, in cattle (serotype SAT 1) and buffaloes (serotype SAT 3).

Update on the article on page 14 on the FMD epidemiological situation in southeast Bulgaria: Emergence of an additional cluster of seven FMD serotype O outbreaks in livestock (in Sredets and Malko Tarnovo Municipalities, Burgas Province, as of 5 May 2011), coupled with results of sero-surveillance in wild boar in Turkey and phylogenetic analysis of all Bulgarian isolates strongly suggest the involvement of wild boar, and possibly other wildlife, in the recent incursion of FMDV into Bulgaria. FAO and EUFMD continue to monitor the situation, and plan further follow-up activities in the region.

African swine fever (ASF) continued to be reported in pigs and wild boar in the Russian Federation, particularly in the endemic areas (Southern Federal Okrug) and also in a number of new locations in Murmansk, Nizhniy Novgorod and Arkhangelsk Oblasts, which are thousands of kilometres to the north. The disease was also reported in Chad, Kenya and the United Republic of Tanzania.

Peste des petits ruminants (PPR) outbreaks were officially reported for the first time in Algeria in March 2011 and in Tunisia in May 2011.

Rift Valley fever (RVF) outbreaks have been reported again in South Africa (Eastern, Northern and Western Cape Provinces) since January 2011. Stamping out policy has been applied to control the disease.

Contagious bovine pleuropneumonia (CBPP) was reported for the first time in Gabon in January 2011. The disease was reported also for the first time in neighbouring the Republic of Congo in 2010.

Highly pathogenic avian influenza (HPAI): During the first quarter of 2011, H5N1 HPAI outbreaks were regularly reported in poultry in areas where the disease is endemic, such as Bangladesh, China (Hong Kong SAR), Egypt, Indonesia and Viet Nam; since April 2011, the number of officially reported outbreaks has been progressively declining. H5N1 HPAI outbreaks were also reported in Cambodia, India, Israel, Japan, Myanmar, the Republic of Korea, and the West Bank and Gaza Strip. A number of wild bird cases were reported during the same period in Bangladesh, China (Hong Kong SAR), Japan, the Republic of Korea and Mongolia. Japan and the Republic of Korea have reported an unexpectedly high number of outbreaks in this reporting period.



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