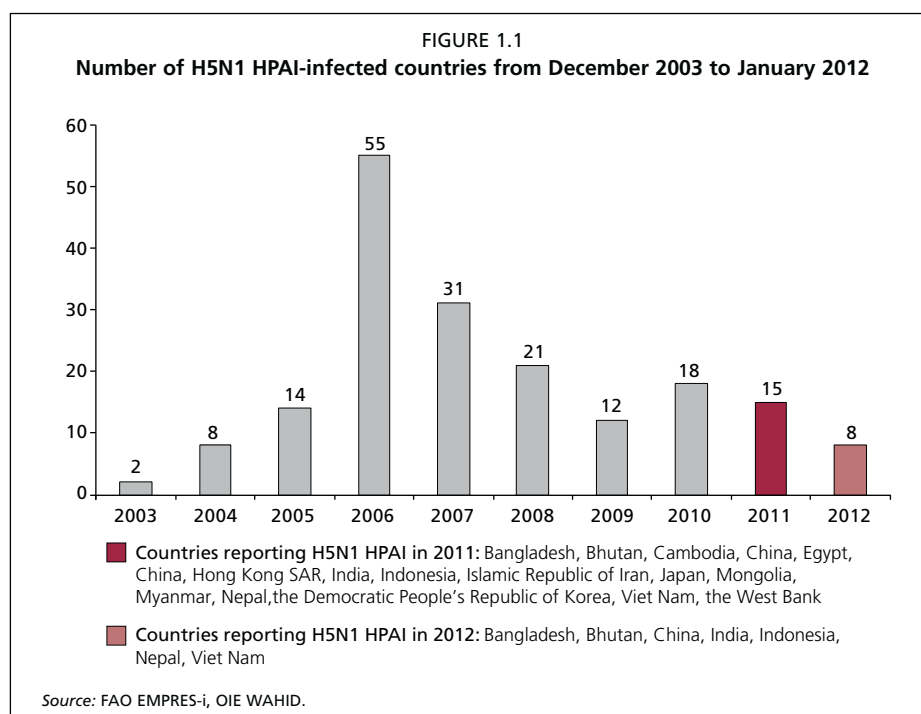


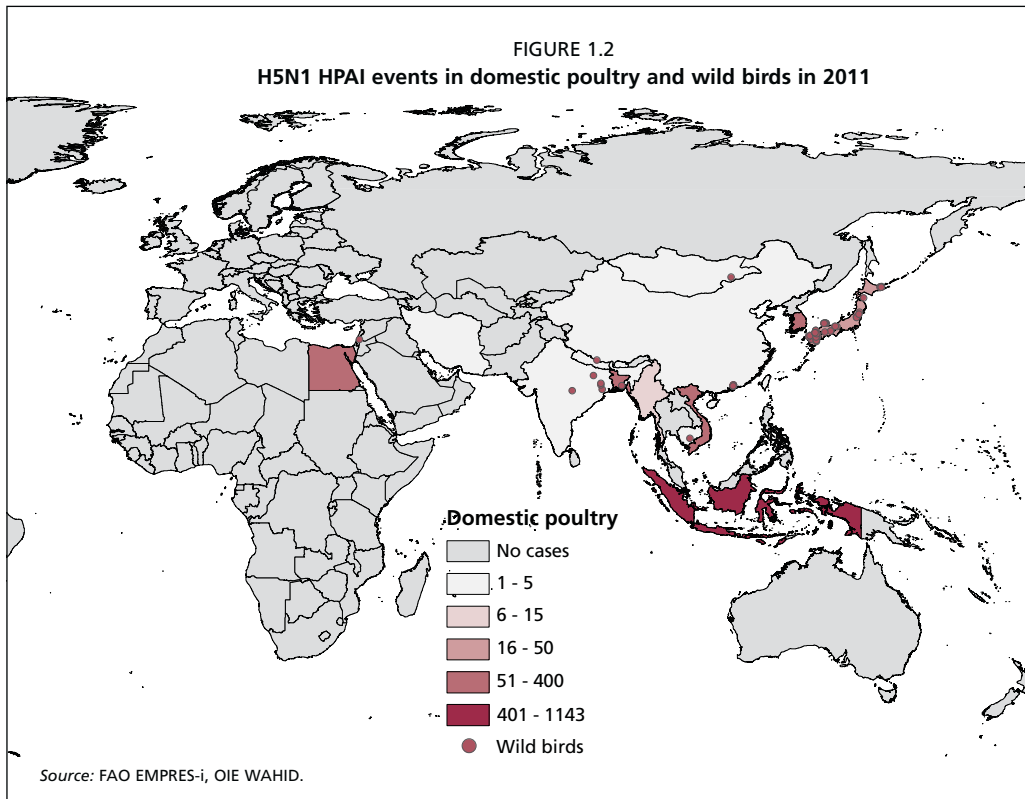
Chapter 1

H5N1 highly pathogenic avian influenza and other diseases situation update (January 2011 to January 2012)

OVERALL H5N1 HIGHLY PATHOGENIC AVIAN INFLUENZA INCIDENCE INCREASED IN ANIMALS IN 2011

H5N1 HPAI has affected sixty-three countries/territories in Asia, Europe and Africa since the beginning of the epizootic in poultry, wild birds or captive wild birds in 2003. Of these, 15 countries (14 in Asia; and 1 in Africa) experienced outbreaks during 2011 and 2012 (see Figures 1.1 and 1.2; Table 1.1), against 18 in 2010 and 12 in 2009 (see Figure 1.1). H5N1 HPAI continues to be a major concern, with a slight decrease in the overall number of infected countries/territories in 2011 and 2012. However, the disease is entrenched in poultry populations only in Bangladesh, China, Egypt, Indonesia, Viet Nam and parts of India. In these settings, progressive control and elimination remains the long-term goal.





The overall number of reported outbreaks/cases of H5N1 HPAI worldwide increased in 2011 compared to the same period in 2010, partly due to unusual reporting from previously infected countries particularly associated with wild bird events. There was a general decrease in outbreak numbers at the country level during 2011, with the exception of Japan, the Republic of Korea and Bangladesh where increases were observed (see Table 1.1). In Bangladesh, the situation appears to have worsened considerably during 2011, where a five-fold increase in outbreak numbers was observed. The peak of disease activity in 2011 was, once again, observed in the cooler months of January to March (see Figure 1.3).

Since 2004, an improvement in disease awareness worldwide can be noted, but as has been reported previously there are still some concerns about the efficiency of surveillance systems. Outbreaks/cases of H5N1 HPAI are still likely to be underestimated and under-reported in some countries owing to limitations in the capacity of veterinary services to implement sensitive and effective disease surveillance, or to perform epidemiological investigations. Most animal disease surveillance systems depend on livestock owners to report suspicious incidents, but the general weakness of compensation schemes means there are poor incentives for disease reporting by owners.

FOUR HIGH-BURDEN COUNTRIES REMAIN ENZOOTIC

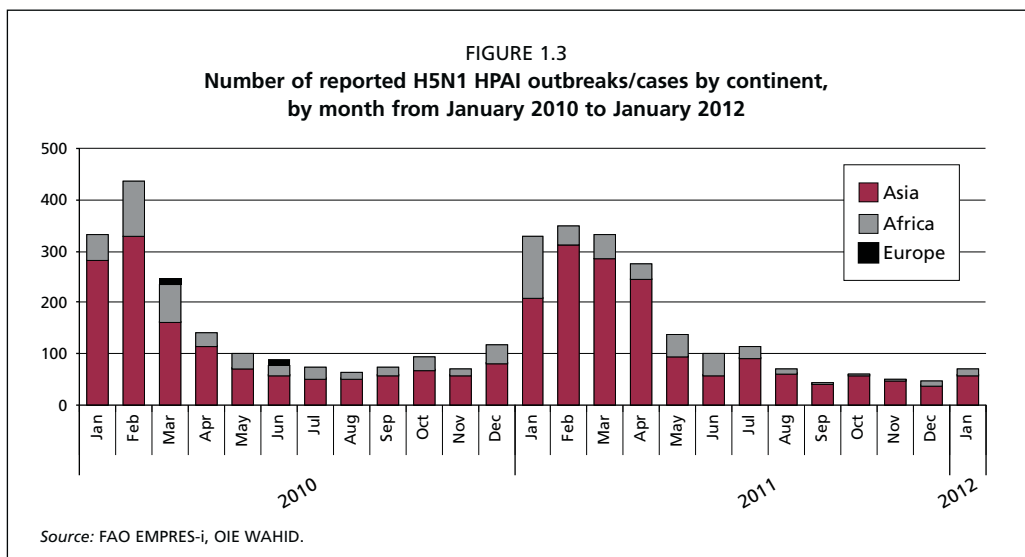
The majority of outbreaks in 2011 and early 2012 occurred in four high burden countries (see Table 1.1): Indonesia (60 percent), Egypt (20 percent), Bangladesh (8 percent), and

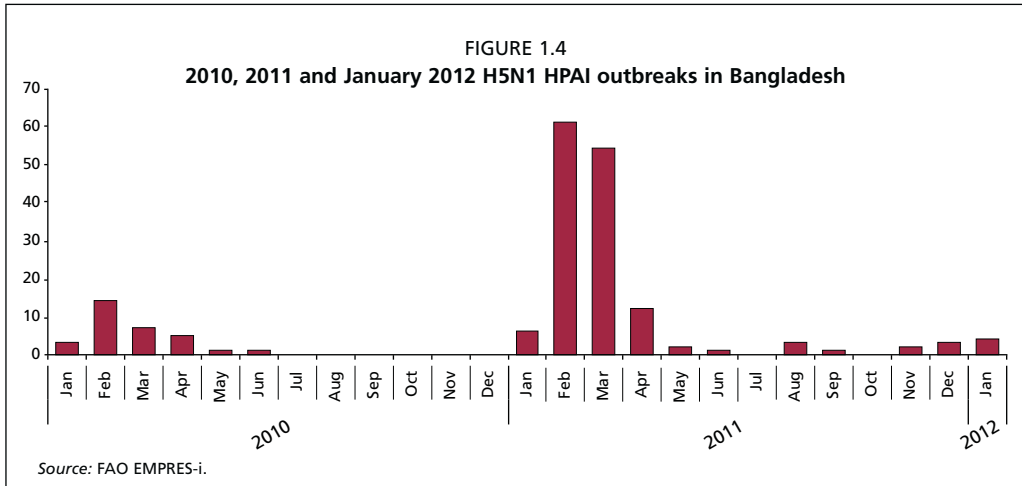
TABLE 1.1
Number of outbreaks during 2009-2010

	Bangladesh	Bhutan	Bulgaria	Cambodia	China	Egypt	Germany	India	Indonesia	Israel	Iran	Japan	Lao People's Democratic Republic	Mongolia	Myanmar	Nepal	Republic of Korea (the)	Romania	Russian Federation (the)	Viet Nam	west Bank
2009	32	0	0	1	19	176	1	10	1502	0	0	0	5	2	0	2	0	0	2	56	0
2010	31	5	1	2	3	443	0	15	1204	2	0	5	1	1	3	8	8	2	1	51	0
2011	145	2	0	5	9	378	0	6	1155	0	3	74	0	1	9	1	53	0	0	47	3
2012	4	3	0	0	6	15	0	7	22	0	0	0	0	0	0	4	0	0	0	8	0

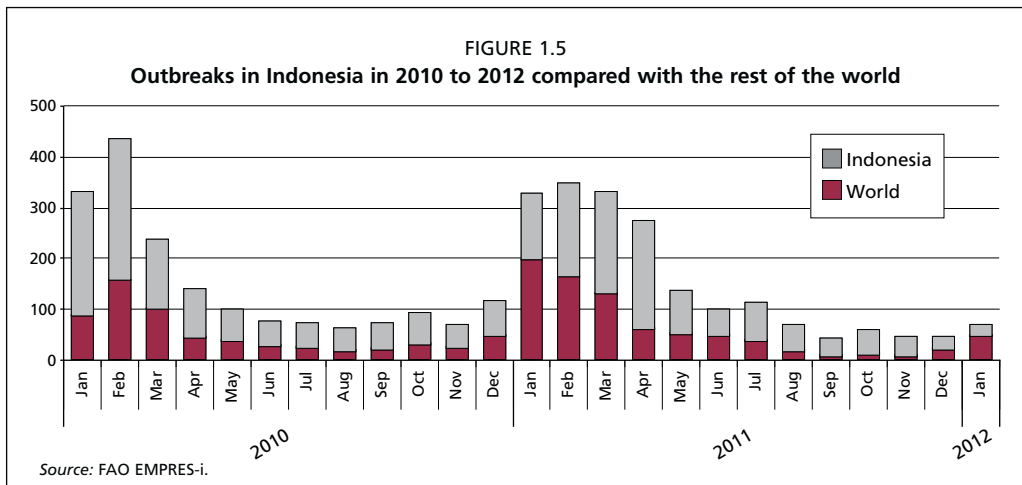
Viet Nam (3 percent) as well as countries like Japan (4 percent) and the Republic of Korea (3 percent) where the disease is considered sporadic. This result is slightly different from the situation in 2010 and may be attributed to expansion of clade 2.3.2.1 in Asia.

During 2011, **Bangladesh** (see Figure 1.4) experienced an increase in outbreak numbers in poultry (from 31 in 2010 to 145 in 2011), mostly in commercial poultry from five areas, three of which were infected during 2010. Areas affected in Bangladesh were Barisal, Chittagong, Dhaka, Khulna, Rajshahi and Sylhet. Although, like previous years, most outbreaks occurred between January and April, outbreaks were observed during 10 out of 12 months. A new incursion of clade 2.3.2.1 was observed for the first time in Bangladesh (in crows and chickens) in January and February, and this is now the dominant strain with some evidence of spillover into India. Virus clades from outbreaks between April and June 2011 belonged to clade 2.3.2.1 and 2.2.2. Clade 2.3.4.2 was identified in poultry in February 2011 in the Chittagong District. The virus isolates from the 2010 outbreaks belonged to clade 2.2, sublineage III and clustered with sequences of viruses from Bangladesh isolated from 2007 to 2009.





Indonesia continued to report a high number of H5N1 HPAI outbreaks in poultry during 2011. Pursuant to past years, there appears to be a non-significant reduction from the previous year (1204 in 2010 versus 1155 in 2011). More outbreaks were reported in the country itself than the rest of the world combined (see Figure 1.5). H5N1 HPAI is considered endemic on the islands of Java, Sulawesi and Sumatra, with sporadic outbreaks reported elsewhere. High incidence areas are recognized at both provincial and district levels on Java (especially Yogyakarta) and in the south of Sumatra (Lampung). Only one of Indonesia’s 33 provinces (Maluku) has never reported the occurrence of H5N1 HPAI. The high number of reports each month is partially explained by the implementation of FAO’s Participatory Disease Surveillance and Response (PDSR) programme which targets village poultry production systems (mainly backyard) and reports outbreaks at the village level. Clade 2.1 was isolated in 2009, but no sequence data is available for isolates from 2010 or 2011 outbreaks. Indonesian virus sequences from 2009 to 2010 show that these isolates remain in clade 2.1.3. Presently, no 2011 sequence data from animal viruses are available. The data shows that within Indonesia clade 2.1.3 continues to diversify with the largest variations observed in viruses from Sumatra.



In **Viet Nam**, between January 2011 and January 2012, the Department of Animal Health (DAH) officially reported 55 H5N1 HPAI outbreaks in 22 of 64 provinces (34 province-level prevalence) involving ducks and chickens in northern, central and southern parts of the country. This result is comparable to that observed in 2010 with 21 out of 64 provinces affected. Surveillance and molecular genetics have indicated the presence of four circulating virus clades in Viet Nam since 2003. These are: (1) clade 1.1 (predominant in southern Viet Nam from 2004 until now); (2) clade 2.3.4 (predominant in northern Viet Nam from 2007 to the first half of 2010); (3) clade 7 (detected in poultry seized at the Chinese border and at markets near Hanoi in 2008); and (4) clade 2.3.2 (detected in 2005 for the first time and reappearing in late 2009). Virus clade 2.3.2.1 has become predominant in northern Viet Nam since late 2010 until now. It was also detected in the south-central area of Viet Nam. In a vaccine efficacy trial, it was observed that the current vaccines in use in Viet Nam provided poor protection against one particular virus strain within virus clade 2.3.2.1. This virus strain forms a distinct cluster from most of the other virus strains of clade 2.3.2.1 in the HA gene phylogeny. This strain was detected in seven northern provinces of Viet Nam during the period 2011 to 2012. In 2011, Viet Nam temporarily halted government-sponsored vaccination in the northern and central areas of the country in response to the emergence of this new clade of H5N1 virus, when the vaccine in use was found to be ineffective against it. However, vaccination continues in the south and an emergency stock of vaccine for ring vaccination is maintained for use in the country.

Egypt continued to report large numbers of outbreaks predominantly in backyard systems during 2011 to January 2012 in most of its 29 governorates. Compared to 2010, there has been a slight reduction in outbreaks from 443 in 2010 to 378 in 2011, possibly due to reduction in surveillance activities as the result of civil unrest. In Egypt, detection of HPAI is the result of surveillance conducted in high-risk governorates by community animal health outreach (CAHO); (similar to PDSR in Indonesia), as well as active surveillance conducted in the commercial and village poultry sectors. Egyptian viruses isolated in 2011 belonged to the 2.2.1 group (the so-called classical or A group). Viruses belonging to the variant or B group, now the fourth order clade 2.2.1.1, were not isolated in 2011.

SPORADIC H5N1 HPAI EVENTS STILL PREDOMINANTLY IN ASIA

Southeast Asia

Cambodia experienced four H5N1 HPAI poultry outbreaks and one wild bird event during 2011 in five areas representing an increase from 2010 (two poultry outbreaks). Affected areas in 2011 were Banteay Meanchey, Takeo, Battambang and Kandal. Of these, only Takeo was infected in 2010. Like previous outbreaks in Cambodia, poultry outbreaks in 2011 were identified after reports of human cases, particularly in Banteay Meanchey. All available human and animal isolates since 2004, including all those from 2011, are clade 1.1 (genotype Z) and most closely related to clade 1.1 viruses previously circulating in Cambodia. This clade is also the same that circulates predominantly in southern Viet Nam.

The Lao People's Democratic Republic did not report H5N1 HPAI outbreaks during 2011, but results from active surveillance in high-risk areas have positive swab samples for HPAI H5N1, clade 2.3.2.1 in the Vientiane Capital. These results imply that the virus is still circulating in the country despite the lack of outbreak reports. The 2011 active surveillance

was carried out in the nine highest-risk provinces based on the location of historical HPAI outbreaks. The surveillance focused on ducks in live bird markets (LBMs), and villages with high duck populations and farms. A total of 33 markets, 40 villages and 19 farms were visited during two rounds.

Myanmar experienced an increase in H5N1 HPAI outbreaks in poultry during the first four months of 2011 (11 outbreaks reported compared to 3 in the same period in 2010). Outbreaks were concentrated in Rakhine and Saigang, in the south and northwest of the country, respectively. Similar to 2010, viruses circulating in 2011 belonged to separate clades: clade 2.3.4.2 and clade 2.3.2.1.

East Asia

China reported one outbreak of HPAI H5N1 in poultry in Tibet in December 2011 and a number of H5N1 HPAI related events in poultry and wild birds in **China, Hong Kong SAR** during the first and last quarter of 2011 and January 2012. Specifically, in China, Hong Kong SAR, there were four wild bird events and four outbreaks in reported poultry during 2011. In addition to the wild bird events in December, one positive chicken carcass was identified in a LBM as part of ongoing active surveillance. This latter finding led to the immediate culling of 19 451 poultry, including 15 569 chickens, 810 pigeons, 1 950 pheasants and 1 122 silky fowls in China, Hong Kong SAR. In January 2012, there were one poultry outbreak and six wild bird events.

Though no outbreaks were reported during the first three-quarters of 2011 on mainland China, ongoing active surveillance in LBMs at national and provincial levels during March, June and July resulted in virus-positive samples, implying that H5N1 viruses are still circulating in many provinces in domestic poultry and that disease outbreaks go unnoticed by the authorities. Virus-positive provinces identified during 2011 include Anhui, Chongqing, Guangdong, Guangxi, Hubei, Hunan, Fujian, Zhejiang, Guizhou, Henan, Sichuan, Yunnan, Zhejiang, Jiangxi and Jiangsu. All the clades of Asian-lineage H5N1 HPAI virus found globally have been detected in China. Of particular interest is the recent expansion of clade 2.3.2.1 which was originally isolated in 2004 from a dead Chinese pond heron in China, Hong Kong SAR and has now expanded its geographic range to include Mongolia, the Russian Federation, Nepal, Romania and Bulgaria. In China, Hong Kong SAR, viruses from clade 2.3.4 were also detected in wild birds and poultry in 2009. The recent positive events in wild birds and poultry carcass are associated with clade 2.3.2.1.

Japan experienced a new incursion of H5N1 HPAI outbreaks in poultry ($n = 26$) and wild birds ($n = 48$) during the first two months of 2011 throughout the country. These events followed on H5N1 HPAI events in wild birds identified during late 2010 in a number of Prefectures (Kagosima, Tottori and Toyama). In 2011, as in 2010, virus isolates belonged to clade 2.3.2.1.

The **Republic of Korea** reported 53 H5N1 HPAI outbreaks in poultry (ducks and chickens) during the first five months of 2011, unlike 2010 during which only wild bird event was identified during November and December. Outbreaks in poultry during 2011 were distributed across six provinces (Chollabuk-do, Chollanam-do, Chungchongnam-do, Kyonggi-do, Kyongsangbuk-do and Pusan). Most outbreaks were in Chollanam-do (23 out of 53) and Kyonggi-do (19 out of 53). Viruses circulating in 2011 were clade 2.3.2.1.

In 2011, similar to 2010, one H5N1 event was confirmed in **Mongolia** in wild birds in April (whooper swans at Zegst Lake, Suhbaatar Province). Phylogenetic analyses confirmed the virus responsible was clade 2.3.2.1.

South Asia

Bhutan reported five H5N1 HPAI outbreaks in poultry during December 2011 and January 2012 in backyard birds. Though the clade responsible for these outbreaks is not yet known, outbreaks during 2010 were associated with clade 2.2 viruses detected in India and Bangladesh.

India experienced an unusual number of wild bird events in crows ($n = 5$) as well as outbreaks in poultry ($n = 4$) during 2011 and January 2012. Wild bird events were observed in crows during October, November and January in Orissa, Bihar and Maharashtra, with high levels of mortality. The clade involved is 2.3.2.1.

Nepal reported one clade 2.3.2.1 H5N1 HPAI outbreak in poultry in the central area during November 2011. In January 2012, one crow and three poultry outbreaks related to 2.3.2.1 viruses were reported.

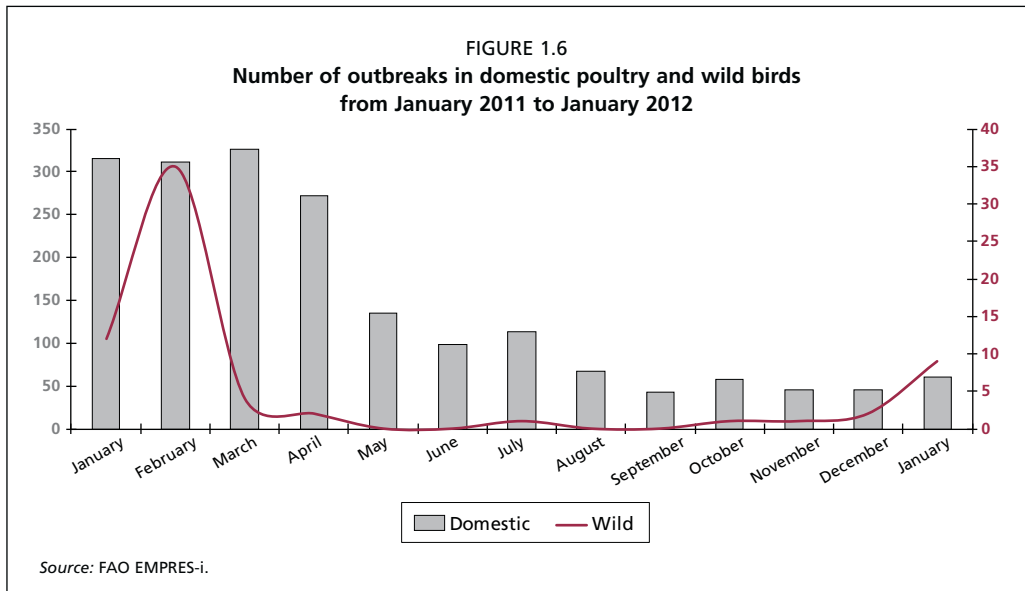
Middle East

In the **West Bank** three H5N1 HPAI events were observed in 2011; one in wild birds and two in domestic turkeys. This report was the first record of H5N1 HPAI in wild birds in this country and the first report in poultry since 2006. The source of the outbreaks is unknown. The outbreaks in poultry were associated with virus clade 2.2.1; isolates that were previously found in poultry outbreaks in Israel and Egypt in 2010.

KNOWLEDGE GAPS REMAIN ON THE ROLE OF WILD BIRDS

During January 2011 to January 2012, there were reports of wild bird events/mortalities due to H5N1 HPAI in seven countries in Asia involving over 27 species. Affected countries/territories were Bangladesh (2011), Cambodia (2011), China, Hong Kong SAR (2011 and January 2012), India (2011 and January 2012), Japan (2011), Mongolia (2011), the West Bank (2011) and Nepal (January 2012). What is most relevant during this period is the large crow die-offs (greater than 1 143) observed from October 2011 in India associated with virus clade 2.3.2.1 with no apparent link to poultry outbreaks. Additionally, there were simultaneous reports of wild bird mortalities in Nepal in crows also associated with virus clade 2.3.2.1. The number of outbreaks in the January 2011 to January 2012 period represents an increase from 2010 (14 to 58), due primarily to increased reports from Japan ($n = 48$) and India ($n = 7$). (See Figure 1.6).

Compared to the number of outbreaks reported globally in domestic poultry in 2011 (see Figure 1.6), wild bird event reporting continues to be considered as rare. The wild bird species infected in January 2011 to January 2012 included several species of waterfowl, typically implicated in sustaining avian influenza virus transmission. These included dabbling and diving ducks (Northern Pintail, *Anas acuta*; Mandarin Duck, *Aix galericulata*; Common Pochard, *Aythya farina*; Greater Scaup, *Aythya marila*; Tufted Duck, *Aythya fuligula*; and unidentified species of ducks), swans (Black Swan, *Cygnus atratus*; Tundra Swan, *Cygnus columbianus*; Whooper Swan, *Cygnus Cygnus*; and an unidentified species of swans) along



with an unidentified species of geese. Other water birds, normally closely associated with congregations of waterfowl, were infected with H5N1 HPAI. These were grebes (Little Grebe, *Tachybaptus ruficollis*; Great Crested Grebe, *Podiceps cristatus*; and an unidentified species of grebe), cranes and herons (Hooded Crane, *Grus monacha*; Little Egret, *Egretta garzetta*; Grey Heron, *Ardea cinerea*), gulls (Black-headed Gull, *Chroicocephalus ridibundus*; and an unidentified species of gull). In the past, a number of predatory species of birds, including one owl, were found to be positive (Marsh Harrier, *Circus aeruginosus*; Peregrine Falcon, *Falco peregrinus*; Crested Goshawk, *Accipiter trivirgatus*; Goshawk, *Accipiter* sp.; Ural Owl, *Strix uralensis*) most likely as a result of feeding on infected prey. Typical scavengers, such as crows (House Crow, *Corvus splendens* *Corvus* sp.) were also reported as well as one species of small passerines (Oriental Magpie Robin, *Copsychus saularis*). Since the beginning of the H5N1 epizootic, over 100 species from 13 orders of bird have been infected with H5N1 AI virus.

The epidemiological role of water birds, particularly waterfowl, in the introduction and spread of H5N1 HPAI, has been significantly clarified but remains controversial because the presence of wild birds at a location when a new HPAI outbreak occurs only increases suspicion about their role. The actual transmission mechanism among wild birds and poultry remains unconfirmed. However, the H5N1 HPAI virus incursion into Japan and the Republic of Korea during 2011 occurred during a period of significant negative surface air temperature anomalies; conditions that were similar to those observed during the clade 2.2 invasion into Europe and other regions in 2006.^{14, 15, 16} While it is clear that virus transmission takes place among wild bird populations for low pathogenic avian influenza (LPAI) viruses, and that there is likely some leap-frog transmission cycle that contributes to longer movement of HPAI H5N1 virus among waterfowl along specific flyways, they do not appear to be the HPAI H5N1 reservoir and they do not have the capacity to efficiently sustain a year-round transmission.^{17, 18, 19, 20}

BOX 1.1

H5N1 HPAI infections in wild birds

The predominant virus clade involved in wild bird events during 2011 was 2.3.2.1 in Bangladesh, Nepal, China, Hong Kong SAR, India and Mongolia. One wild bird event in Cambodia was associated with clade 1.1. The main clades identified in wild birds since 2005 include 2.2 and 2.3.2. Clade 2.2 virus was the predominant clade circulating in wild birds from 2005 to 2010, and was succeeded by clade 2.3.2 from 2010 onwards when the virus was isolated from outbreaks in Japan, the Republic of Korea, Mongolia and the Russia Federation. This clade has also been found during poultry outbreaks in the Republic of Korea, Bangladesh, Japan, China, and the Lao People's Democratic Republic from poultry samples collected via active surveillance.

Though there is limited information to support the role of wild birds/poultry in the introduction and spread of virus clade 2.3.2, it is likely that this virus clade may circulate in poultry and spill over from poultry into wild birds, and is periodically transported by wild birds to other locations. Research has demonstrated that certain wild waterfowl can shed H5N1 HPAI virus asymptotically for between two to five days, and migration disease ecology research conducted by FAO has characterized distances wild waterfowl can migrate over this time frame. While individual migration flights can be long (hundreds of kilometers), for wild waterfowl to be transmitting virus over such distances it is more likely that this occurs through a 'leap-frog' migration pattern, with concurrent transmission of virus from one bird to many others at stopover sites, and newly-infected birds carrying viruses to the next site. To date, based on sampling of more than 750 000 healthy wild birds, no H5N1 HPAI wild bird reservoir has been found.

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- ¹⁵ Reperant, L. A., Fuckar, N. S., Osterhaus, A. D. M. E., Dobson, A. P. & Kuiken, T. (2010) Spatial and temporal association of outbreaks of H5N1 influenza virus infection in wild birds with the 0°C isotherm. *PLoS Pathog*, 6(4): e1000854 doi10.1371/journal.ppat.1000854 (available at <http://www.plospathogens.org/article/info%3Adoi%2F10.1371%2Fjournal.ppat.1000854>).
- ¹⁶ Ottaviani, D, de la Rocque, S., Khomenko, S., Gilbert, M., Newman, S. H., Roche, B., Schwabenbauer, K., Pinto, J., Robinson, T. P. & Slingenbergh, J. (2010) The cold European winter of 2005-2006 assisted the spread and persistence of H5N1 influenza virus in wild birds. *Ecohealth* 7(2): 226-36 (available at <http://www.ncbi.nlm.nih.gov/pubmed/20686815>).
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- ¹⁸ Cappelle, J. N., Gaidet, S. A., Iverson, J. Y., Takekawa, S. H., Newman, B., Fofana, B. & Gilbert, M. (2011). Characterizing the interface between wild ducks and poultry to evaluate the potential of transmission of avian pathogens. *International Journal of Health Geographics*, 10:60 (available at <http://www.ij-healthgeographics.com/content/10/1/60>).
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- ²⁰ Prosser, D. J., Takekawa, J. Y., Newman, S. H., Yan, B., Douglas, D. C., Hou, Y., Xing, Z., Zhang, D., Tianxian, L., Yongdong, L., Zhao, D., Perry, W. M. & Palm, E. C. (2009). Satellite-marked waterfowl reveal migratory connection between H5N1 outbreak areas in China and Mongolia. *Ibis*, 51(3): 568-576 (available at <http://onlinelibrary.wiley.com/doi/10.1111/j.1474-919X.2009.00932.x/abstract>).

INCREASE IN HUMAN CASES DURING 2011 TO JANUARY 2012

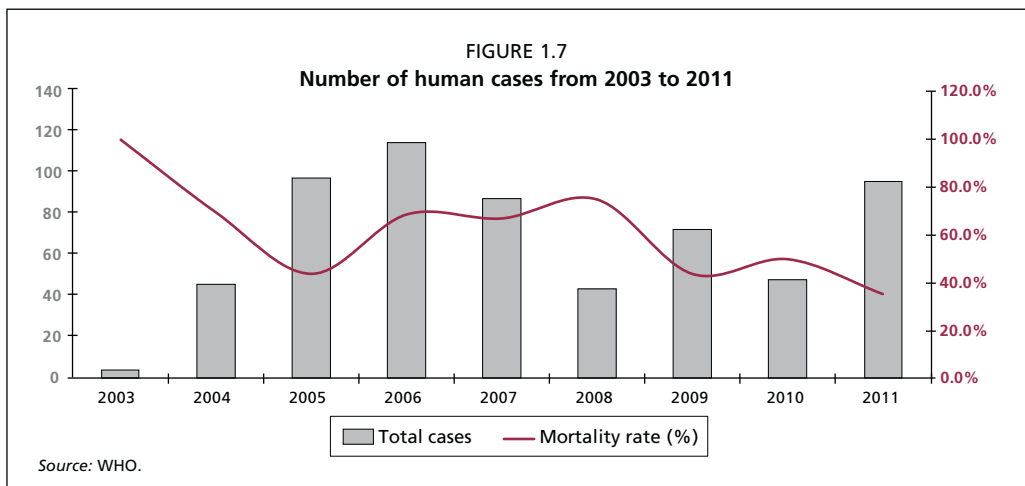
In 2011 to 2012, WHO reported 67 human cases – of which 35 were fatal – in six countries: Cambodia (9 cases; 9 fatalities), Bangladesh (2 cases; 0 fatalities), China (2 cases; 2 fatalities), Egypt (40 cases; 15 fatalities), Indonesia (13 cases; 11 fatalities) and Viet Nam (1 cases; 1 fatality) (see Figure 1.7). Overall, the number of human cases and the number of countries reporting H5N1 infections in humans has increased from 2010 to 2011. In 2011, 62 cases (and 34 fatalities) were reported in comparison to the 48 human cases (and 24 fatalities) in 2010. Viet Nam experienced a decrease in human cases from 2010 to 2011 (from 7 to 1, respectively). As of the end of January 2012, the total number of human cases reported globally was 583 (of which 344 were fatal).

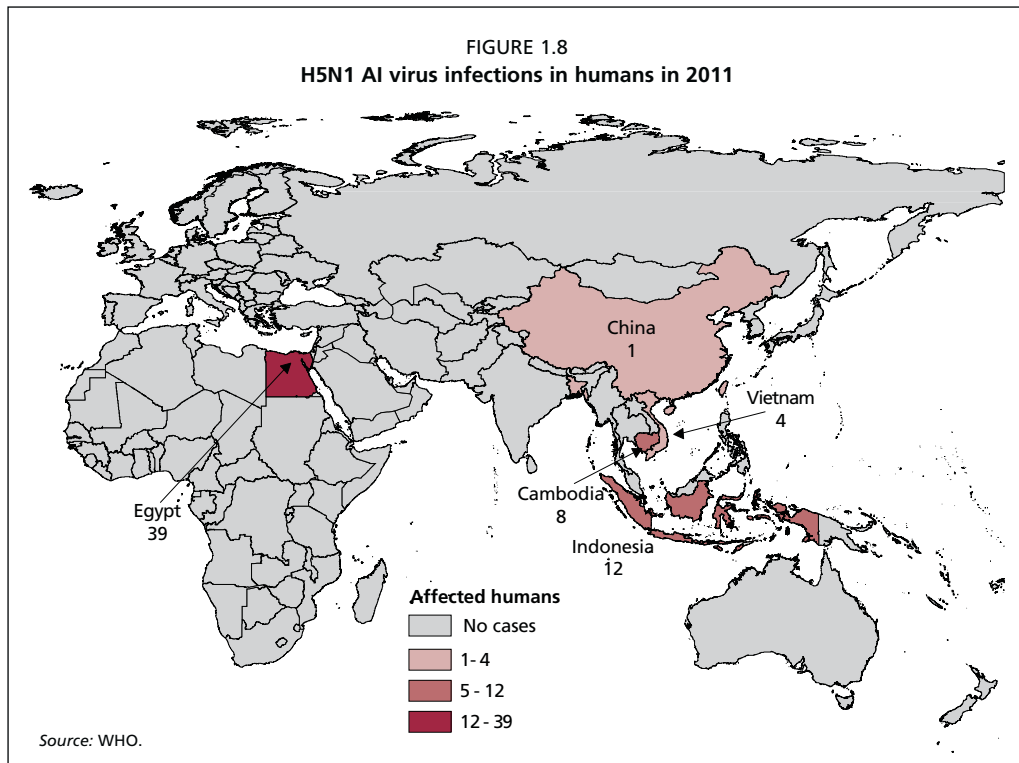
GLOBAL SURVEILLANCE OF H5N1 HPAI AND OTHER ANIMAL DISEASES AT THE ANIMAL/HUMAN/ECOSYSTEM INTERFACE: GLEWS

Surveillance for H5N1 HPAI remains a high priority for FAO at global, regional and national levels. However, it is also a difficult area for national animal health services to maintain investment in because of the costs involved and the declining interest in H5N1 HPAI among animal health field services and poultry producers, in particular, in endemic countries.

The public health and human pandemic threat dimensions of the global H5N1 HPAI enzootic also made such analysis difficult. This situation will remain, as it continues to be difficult to demonstrate the link between poultry health surveillance and human cases. While rare, in some places it has been the occurrence of human cases that has been the sentinel for H5N1 disease in poultry, which has not been identified by farmer reporting systems. In general, as H5N1 HPAI is a relatively uncommon event, active surveillance for disease is relatively inefficient and it is difficult to assess the impact of such surveillance on the overall control of the disease. One of the benefits of active surveillance is that it creates a stronger link between producers and official animal health services, resulting in enhanced farmer awareness and implementation of control measures.

Beyond H5N1 HPAI, emerging and re-emerging animal diseases have increased over the past decades with over 75 percent of emerging diseases affecting humans having their origin in animals (livestock and wildlife). Therefore, managing and coping with the unpre-





dictability of infectious disease events is imperative. The increased threats to human, animal and environmental health through existing and emerging pathogens is triggered by multiple, often inter-related factors driven by global development trends (population growth, urbanization, increasing demand for animal products, intensifying farming systems, land use change, increased human mobility, trade liberalization). Traditional approaches to animal disease prevention and control are based on disruption of pathogen transmission. While these have proven to be effective in some cases (e.g. in the global eradication of rinderpest), they have been less successful in others (e.g. the persistence of H5N1 HPAI despite significant elimination efforts). There is increasing recognition that, in isolation, conventional approaches may be insufficient and that the root causes of disease emergence and maintenance need to be addressed for more efficient and sustainable prevention and control of infectious diseases. Therefore, there is a need to broaden the current reactive approaches to health protection to include proactive measures of disease risk mitigation.

During 2011, the GLEWS initiative implemented in partnership by FAO, OIE and WHO, continued to strengthen its capacity in terms of disease hazards analysis, early warning and forecasting. In particular, integrated risk assessment of pathogen transmission at the animal–human interface is a focus of GLEWS analysis activities.

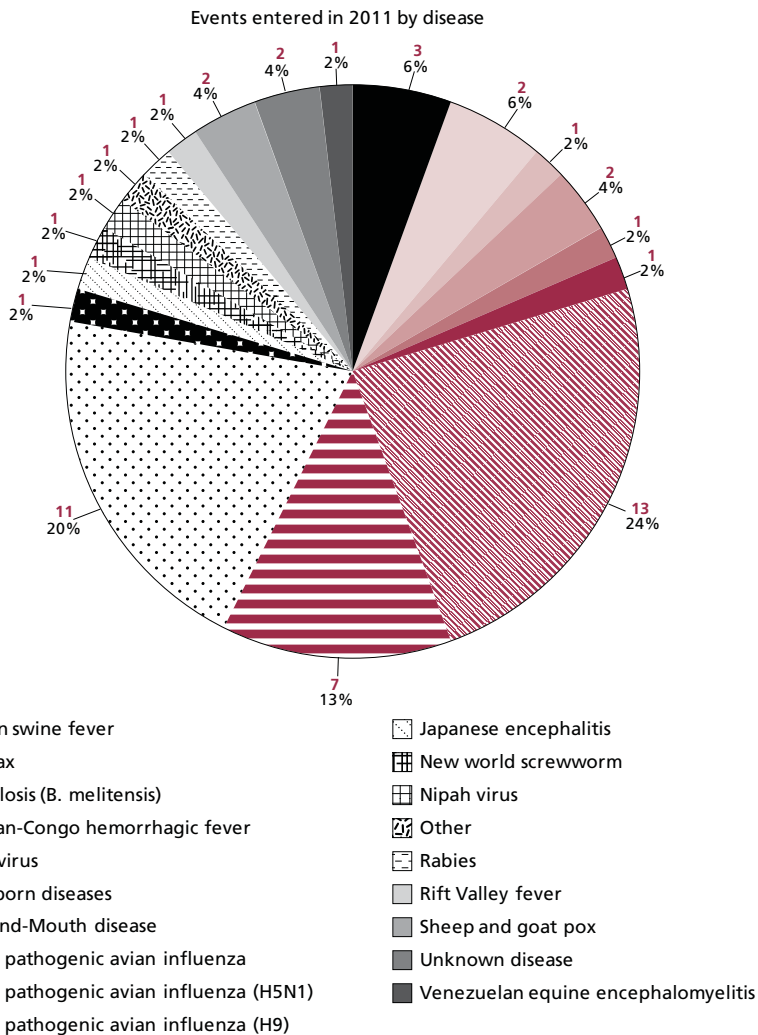
GLEWS activity in 2011 included requests for verification of suspected disease events, disease surveillance reports, epidemiological analysis and specific risk assessments for priority diseases. The joint GLEWS electronic platform²¹ is currently hosted by FAO, has

²¹ Available at <http://www.glews.net/Glews-Platform/>

been operational since February 2009 and was designed for data sharing. During 2011, an average of five relevant disease outbreak events per month were investigated jointly by the three partner organizations and information was shared through the GLEWS electronic platform. Some of these events triggered a response from the FAO/OIE CMC-AH or World Health Organization Global Alert and Response (WHO GAR).

The GLEWS platform is password protected to safeguard sensitive or confidential data and provides a disease event management tool that facilitates and links information exchange between the focal points of the three partner organizations. In 2011, a wider and

FIGURE 1.9
GLEWS events entered and verified by FAO/OIE/WHO in the GLEWS platform
(January 2011 to January 2012)



Source: FAO GLEWS, 2012.

increased range of diseases was covered in comparison to 2009 and 2010, where H5N1 HPAI reporting was predominant (Figure 1.9). A real-time disease map has been available online since November 2009 and is accessible through the GLEWS website (www.glews.net), showing events that were tracked through the GLEWS platform and officially confirmed or denied by OIE and WHO. Since its launch in March 2009, the number of visitors to the GLEWS website has been steadily increasing to almost 9 000 in December 2010, reaching around 11 000 visitors in January 2011, followed by an average of between 6 000 and over 8 000 visitors a month through January 2012.

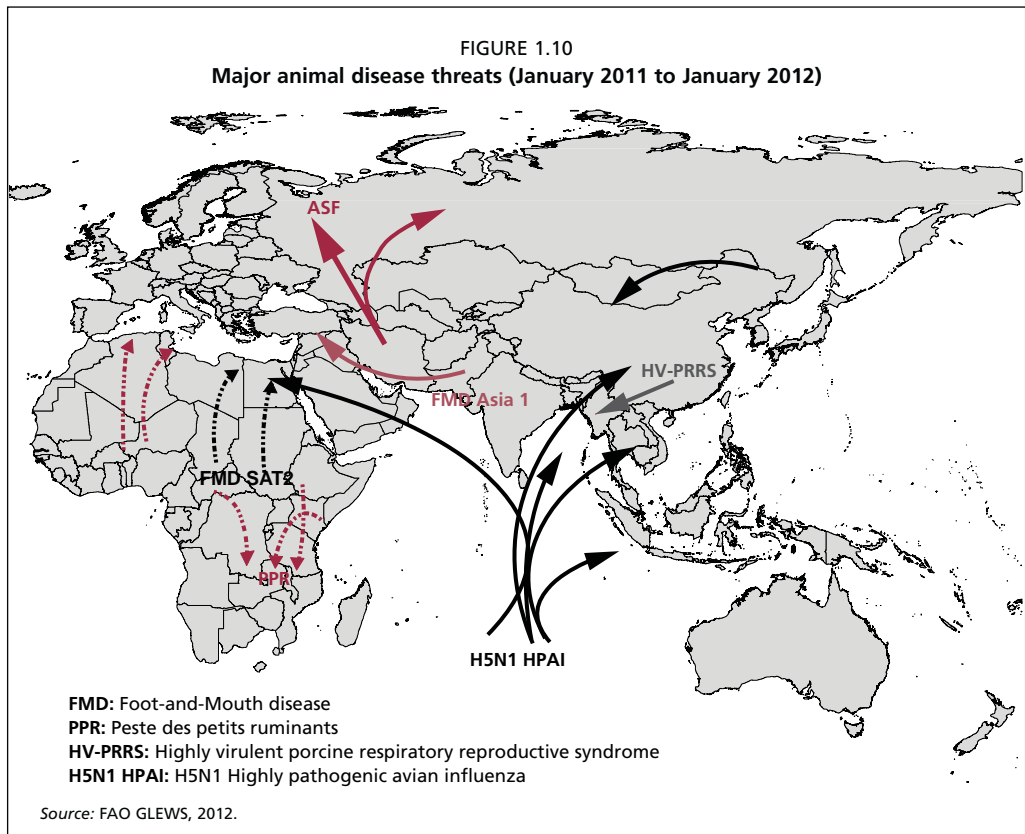
Since the beginning of the H5N1 HPAI epidemic in late 2003, the FAO-GLEWS team has been editing, on a weekly basis, a summary of the global H5N1 HPAI situation in poultry and wild birds from official and unofficial sources as well as human H5N1 disease occurrence. A weekly *HPAI Update* describing the main HPAI events and a monthly overview of H5N1 HPAI are published by FAO. They describe global trends, epidemiological analysis and events occurring during the reporting period. For instance, full access to animal data provided by OIE and FAO has been available to WHO to assess the risk of people contracting H5N1 infection.

H5N1 HPAI continued to be a major concern in 2011, in particular, in endemic countries, but other emergent diseases are monitored regularly by GLEWS. During 2011, other animal diseases also continued to spread in different regions of the world, disrupting livestock production, rural economies and people's livelihoods and food security. This spread has been due largely to the limited capacity of veterinary services to contain animal diseases in endemic settings, and to disease drivers such as high intensification of animal production, increased trade of animal and animal products and intensified contact between animal, human and wildlife populations. This significant flare-up of disease events in 2011 include: the continued and uncontrolled spread of African swine fever (ASF) in Eastern Europe and the Russian Federation, FMD spread in North Africa (type SAT 2) and Central Asia (type Asia 1), PPR moving through Eastern and North Africa (Algeria and Tunisia), and highly virulent porcine reproductive and respiratory syndrome (hVPRRS) in Southeast Asia (Figure 1.10). During 2011, a significant emergence of a new disease, Schmallenberg virus disease (SVD), is occurring in Europe causing congenital malformations in domestic ruminants. SVD belongs to the *Bunyaviridae* family, within the *Orthobunyavirus* genus and the spatial and temporal distribution suggests that the disease is transmitted by insect vectors and then vertically, in utero.

PROSPECTIVE FOR 2012

Globally, H5N1 HPAI in poultry and H5N1 human cases continue to be a global threat for poultry, wild birds and human populations. H5N1 HPAI still present a seasonal pattern as seen in previous years in endemic countries, which is reflected in increased of cases in poultry and humans from October each year until April. Emergent virus H5N1 clade (sub-strain) 2.3.2.1 remains circulating in eastern Asia and the Ganges Delta threatening wild birds and poultry populations.

Other TADs such as ASF will continue to spread to the western part of the Russian Federation in areas close to European Union countries and, potentially, to eastern borders with China, threatening China's and Southeast Asia's swine population. This is a disease for which there is no available vaccine. Other emergent diseases in swine will continue to



expand geographically into new areas such as has been observed during the last five years with hvPRRS spreading from China to countries in Southeast Asia.

Some countries in North Africa and the Middle East have been facing civil instabilities since 2011 and it is expected that the spread of TADs including H5N1 HPAI, FMD and PPR will expand to geographical areas where these diseases have been absent or not reported regularly. The FMD situation will continue to be fluid in Egypt, Libya and the Middle East with three different strains detected at the end of 2011 and the beginning of 2012 (Type A O5 Islamic Republic of Iran, Type A African origin and SAT 2 related to FMD SAT 2 strains detected in Sudan). There is a significant risk that other viruses circulating in eastern Africa readily find the way to Egypt/North Africa causing regional epidemics of FMD. In Libya, for instance, outbreaks of FMD types O and the new SAT 2 are spreading within the country, and FMD Asia 1 has been spreading since 2009 from Afghanistan, Pakistan, and Islamic Republic of Iran and recently, in 2012, into Turkey. FMD types will continue to spread. FMD types Asia 1 and FMD Sat 2 are spreading through Central Asia (Afghanistan, Pakistan, Turkey) and North Africa (Libya, Egypt) and the Middle East (Bahrain), respectively from endemic areas. Understanding of livestock trade routes and factors triggering incursions of new types in endemic areas is of paramount importance since vaccination against FMD covers only some circulating types with serious implications for routine vaccination campaigns against known types. Surveillance efforts need to be enhanced in endemic areas to detect

incursions of new types causing large epidemics affecting livestock, food security and livelihoods. The absence of a vaccine protecting against all FMD types is an important gap in the control of FMD since vaccines need to be regularly updated to guarantee the efficacy of vaccination programmes against all endemic types circulating or to face incursions of new types into this endemic areas.

In Africa, PPR distribution includes the sub-Saharan countries that lie between the Atlantic Ocean and the Red Sea where the disease has been recorded in almost every country. However, 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, in recent years, has already become endemic; first in Kenya and then in the United Republic of Tanzania, sometimes without the presence of overt disease. An incursion of PPR in 2008/09 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 findings of PPR sero-positive animals in Algeria in early 2011, and in Tunisia in early 2012.

The emergence of rabies from endemic areas into new areas and livestock species from wildlife reservoirs in some regions have to be carefully considered since this disease continues to be the most relevant zoonoses in terms of humans affected and deaths. Wildlife (e.g. bats, foxes) play an important role in rabies transmission to livestock. Increased encroachment of domestic and wildlife populations is facilitating contact rates between species compartments and the emergence of rabies in some regions. However, traditional canine rabies remains the most important mechanism for transmission of rabies from animals to humans.

Vector-borne diseases (VBD) are expanding and will continue to expand their geographical distribution associated with climate change and global warming effects. The geographical expansion of Bluetongue serotypes into northern regions of Europe during recent years and the emergence and spread of the new SVD detected and spread within Western Europe are clear examples of this new VBD dynamic. Geographical expansion of VBDs and adaptation of pathogens to new hosts or vectors need to be closely monitored in all regions for the serious implications of VBD such as West Nile virus (WNV) and Congo-Crimea haemorrhagic fever (CCHF) on public health.