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GLOBAL ANIMAL DISEASE INTELLIGENCE REPORT



JANUARY – DECEMBER 2016

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Summary

Animal Disease Overview

Several remarkable animal health events occurred during 2016. As in previous years, a continuous circulation of highly pathogenic avian influenza (HPAI) H5 subtypes was observed in China and other Asian countries. At the same time, however, a notable global spread of subtype H5N8 took place. Starting from migratory birds' summer breeding sites in Asia, and driven by subsequent bird movements, this subtype was able to spread across the whole of Europe and reach sub-Saharan countries in Africa.

As concerns vector-borne infections, lumpy skin disease (LSD) continued to spread across the Balkan countries and in the southwestern zones of the Russian Federation, supported by the presence of vectors and, possibly, informal movements of infected animals. Climatic conditions, and average precipitation in particular, were probably associated with the occurrence in August 2016 of Rift Valley fever (RVF) in Niger, where around 400 human cases with more than 30 deaths were observed.

Weather conditions were also associated with an unusual outbreak of anthrax in Siberia (Russian Federation) in July 2016, when reindeer and humans were affected. Abnormally high temperatures in the spring and early summer facilitated permafrost melt, disturbing the soil and bringing anthrax spores to upper soil layers.

During 2016, African swine fever (ASF) continued to spread in Eastern Europe, due to uncontrolled contacts between backyard pig farms and to the infection's persistence in wild boar populations.

Wildlife was also involved in a large outbreak of Peste des petits ruminants (PPR) in Mongolia, where more than 4 000 Mongolian saiga antelopes (*Saiga tatarica ssp. mongolica*) were found dead due to the disease.

Risk assessment of emerging infections

MIDDLE EAST

H5N1 Highly pathogenic avian influenza

A risk assessment published by FAO (<http://www.fao.org/3/a-i6155e.pdf>) in September 2016 estimated the likelihood of spread of H5N1 HPAI from Lebanon and Iraq to other countries in the Middle East as a result of the movement of live poultry and related products, and the migration of wild birds. Although the overall risk of H5N1 spread in the Middle East region was considered as medium, Turkey, the Syrian Arab Republic and Iran were found to face a higher likelihood of introduction. Countries and territories at medium risk of incursion were identified as the West Bank and Gaza Strip, Israel, Kuwait and Saudi Arabia. In addition, Armenia, Azerbaijan and Georgia were considered potentially threatened because they are on the spring migration flyways of northward-bound wild birds, although the risk through this pathway was considered low.

CENTRAL AFRICA

H5N1 Highly pathogenic avian influenza

Following H5N1 HPAI outbreaks in Cameroon in May and September 2016, FAO published a risk assessment (<http://www.fao.org/3/a-i6348e.pdf>) evaluating the chances of the virus spreading into neighbouring countries (also considering that H5N1 HPAI is regarded as endemic in Nigeria). The likelihood of H5N1 spreading through live poultry trade with Central African Republic, Chad and Congo was considered low through legal trade, but moderate through informal trade.

EAST AFRICA

H5N8 Highly pathogenic avian influenza

In January 2017, massive mortality due to H5N8 HPAI infection among white-winged terns (*Chlidonias leucopterus*) was reported along the shores of Lake Victoria, in Uganda. From there, the disease spread from wild to domestic birds in nearby villages and areas. A rapid risk assessment, conducted by FAO with the support of international experts, estimated that the probability of infection spreading to Kenya was between 66 percent and 90 percent, while chances of incursion into Tanzania and Rwanda were more even, at between 33 percent and 66 percent. Uncertainty for these estimates was high.

Rift Valley fever in East Africa

In March 2016, Uganda declared the country's first outbreak of Rift Valley fever, with two human cases in the Kabale district, to the southwest. Both patients had been in close contact with livestock. Subsequently, one goat was found positive after serological samples were taken from flocks and herds. Despite the strong 2015–2016 El Niño phenomenon and associated abnormal rainfall in East Africa, no substantial climatic anomalies were observed in the Kabale area during the 2016 epidemic. Moreover, the area's physical and environmental characteristics placed it outside of the RVF vector suitability map produced by NASA (Anyamba *et al.*, 2009). Consequently, this area was not identified by climate-based models as being at risk of RVF vector amplification (FAO, OIE, WHO, 2015). No further outbreaks of RVF were detected in Uganda, nor were any registered in neighbouring countries.

WEST AFRICA

Rift Valley fever

Since August 2016, there have been 384 human cases of RVF, 33 of them fatal, notified in Niger's Tahoua region (Tahoua department and Keita district). Analysis of climate data recorded between 2000 and 2016 for the affected area showed above-average precipitations from January to mid-September 2016. A rapid risk assessment carried out by FAO in October 2016 (http://www.fao.org/ag/againfo/programmes/en/empres/news_031116.html) highlighted that RVF infection in Niger posed a medium risk (a mean score of 5.75 on a scale of ten) to the country's public health, and a medium-high risk (6.5) to animal health. Considering only the likelihood of occurrence, the experts consulted during the assessment considered RVF was likely/very likely (66%–99% probability) to occur in neighbouring Mali during the same vector season. Occurrence of the disease in the other neighbouring countries – Burkina Faso, Benin and Nigeria – was considered less likely (10%–30% probability) or substantially even (33%–66%). The predictions, made in October, were confirmed in January 2017 with notification of the first RVF outbreak in small ruminants in Mali.

EUROPE

Lumpy skin disease

During 2016, Lumpy Skin Disease spread rapidly through southeast Europe, involving Bulgaria, Greece, Kosovo, the Former Yugoslav Republic of Macedonia, Serbia and Albania, with further outbreaks reported in the Russian Federation and Georgia. With the exception of the last two countries, control efforts centred on vaccinating susceptible animals in regions where the presence of the disease had been established. The main pathways for LSD introduction into free areas were considered to be the movement of infected animals and vectors. Spread of LSD in Greece was mitigated by a vaccination campaign and movement restrictions imposed in the affected areas. A risk assessment by the European Food Safety Authority (EFSA) concluded that vaccination had a greater impact in reducing LSD spread than stamping out, despite low vaccination effectiveness (40 percent). However, EFSA found that vaccination was most effective if protection had already been developed at the time of virus entry, more so than large-scale vaccination after virus entry. The assessment concluded it was important to carry out prior vaccination of the entire susceptible cattle population in at-risk regions (EFSA, 2016).

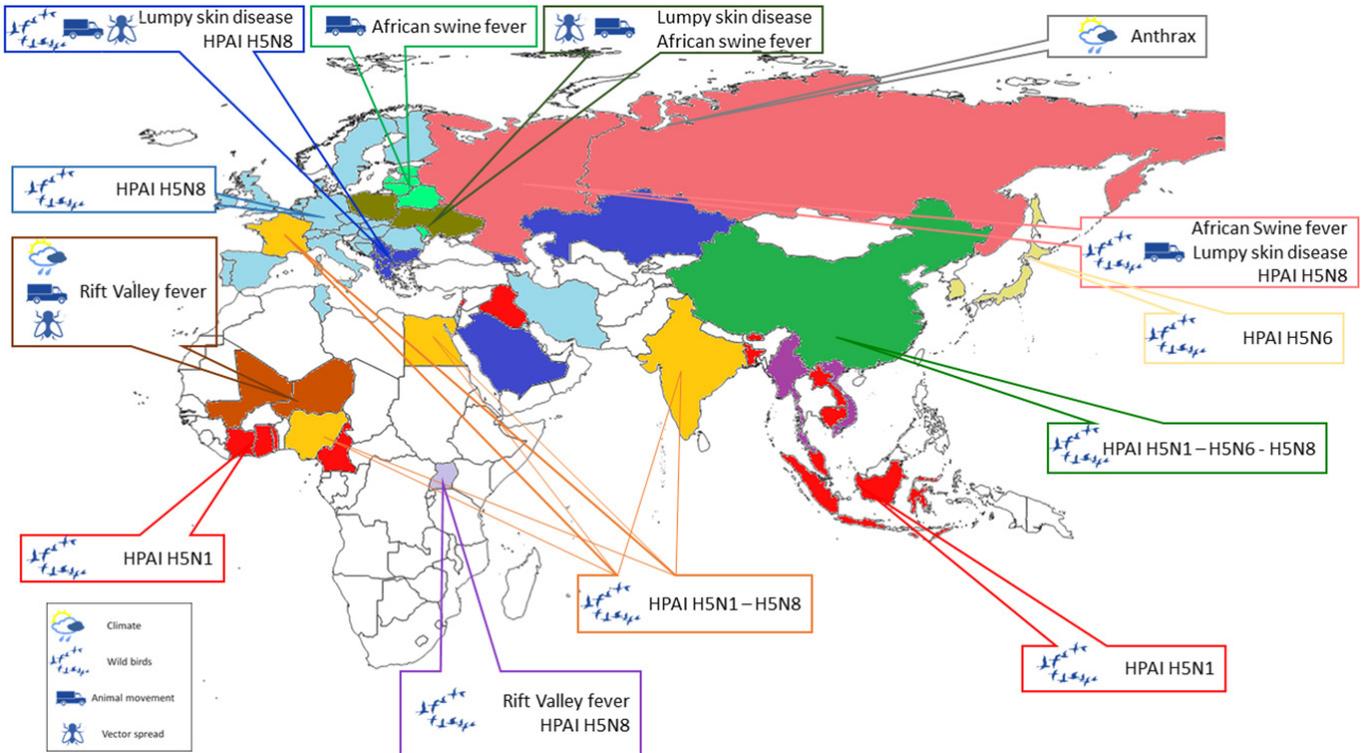
African swine fever (ASF)

After its introduction into Poti, Georgia, in 2007, the first wave of an epidemic of African swine fever spread across Lithuania, Poland, the Russian Federation and Ukraine in January and February 2014. The virus then entered Estonia in September and an incursion was reported in the Republic of Moldova two years afterwards. The virus has continued to circulate in wild boar populations, with seasonal fluctuations linked to wild boar ecology. No incursions into new countries have been observed since September 2016, however, although new zones have been affected in Ukraine. Informal and uncontrolled animal movements, and poor biosecurity in pig farms, are considered the main drivers for the disease's spread. Anecdotal reports speak of infected pork products sold to military facilities and of improper waste management as having possibly contributed to infection in some Eastern European countries. Tourists and visitors taking pork products from infected areas and leaving food waste in the environment can help spread ASF. But wild boar populations also play a crucial role in maintaining and spreading the disease, significantly hampering eradication efforts. Strategies using conventional wild boar management approaches, including bans on feeding them, and targeted hunting of reproductive females, were found to become effective slowly, over several generations (Lange, 2015).

Anthrax

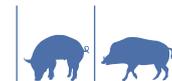
Anthrax spores can persist in the soil for long periods, even under extreme environmental and climatic conditions, and transmit the disease when the situation becomes more favourable. A large outbreak of anthrax affecting reindeer and humans was reported in Siberia (Russian Federation) in July 2016. It was the first appearance of the disease in the affected region in 75 years, the previous outbreak having occurred in 1941. The recent upsurge could be associated with climate change and the abnormally warm temperatures registered in 2016, which may have substantially reduced the snow cover and the permafrost in the area. Over the past two decades, substantial climate-driven changes have been observed in northern Siberia, including the outbreak area. Snow cover there decreased significantly between 1999 and 2016, together with ice in the Arctic Ocean. In addition 2015 and 2016 were characterized by strong El Niño conditions and snowmelt began 20 days earlier than normal, with the ground generally becoming snow-free in just two weeks instead of a month. This may have contributed to permafrost melting in the outbreak area, disturbing the soil and bringing anthrax spores up to the soil surface and into plants, which were then eaten by browsing reindeer. Human cases occurred among people who had been in contact with infected animals or had consumed reindeer meat or blood.

Main animal disease events and related drivers – 2016



Animal disease situation

African swine fever

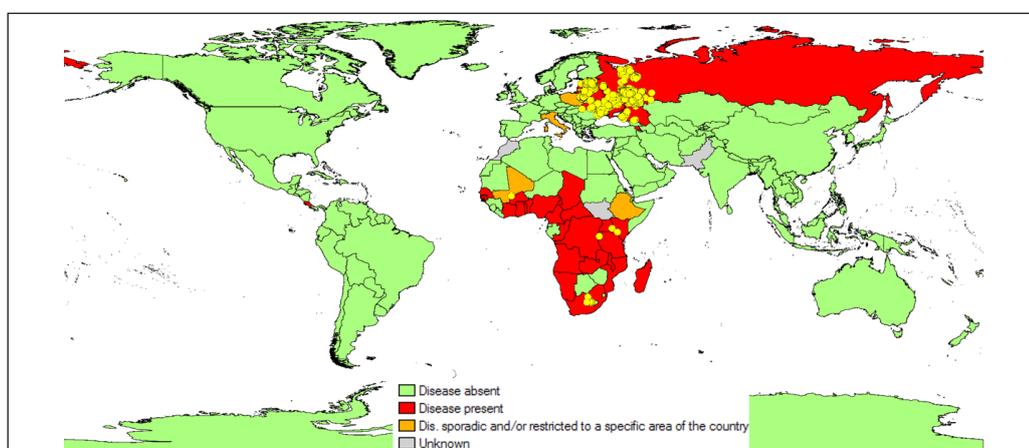


During 2016, ASF continued to spread in Eastern Europe and outbreaks were notified in Belarus, Estonia, Latvia, Lithuania, Republic of Moldova, Poland, the Russian Federation and Ukraine (Figure 1).

insecurity, and the occurrence of uncontrolled animal movements are considered the main drivers of the spread of ASF in the region. Furthermore, the presence of a significant and dense wild boar population plays an important role in maintaining the infection in the area while hampering control efforts.

The presence of a large number of backyard pig farms with low bi-

Figure 1. African swine fever – global situation, 2016



Anthrax



Anthrax is endemic in many countries and in all continents, and it (re)emerges regularly in specific areas in association with favourable climatic and soil conditions (Figure 2). In July 2016, a number of anthrax outbreaks occurred in the Yamalo-Nenets region of Siberia (Russian Federation), affecting reindeer and humans. Out of a population of 41 000 susceptible reindeer, 2 649 cases were confirmed, with 2 349 deaths (88.7% fatality). In addition,

24 people, including nine children, of whom one died, were confirmed as having anthrax. It is thought that, due to abnormally high temperatures in the area, the permafrost slowly melted, bringing anthrax spores closer to the surface.

Animals were infected when they ingested contaminated vegetation while grazing.

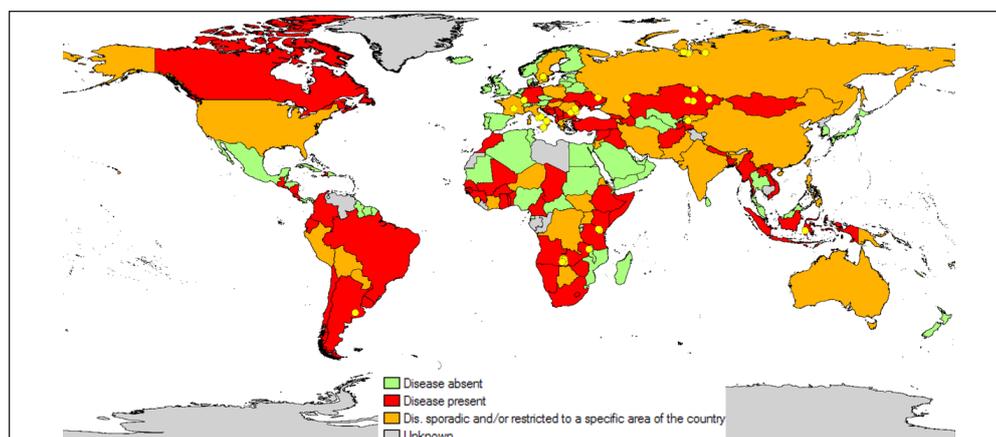


Figure 2. Anthrax – global situation, 2016

1) Sources: FAO EMPRES-i for disease outbreak locations and OIE-WAHIS for 2016 country disease status

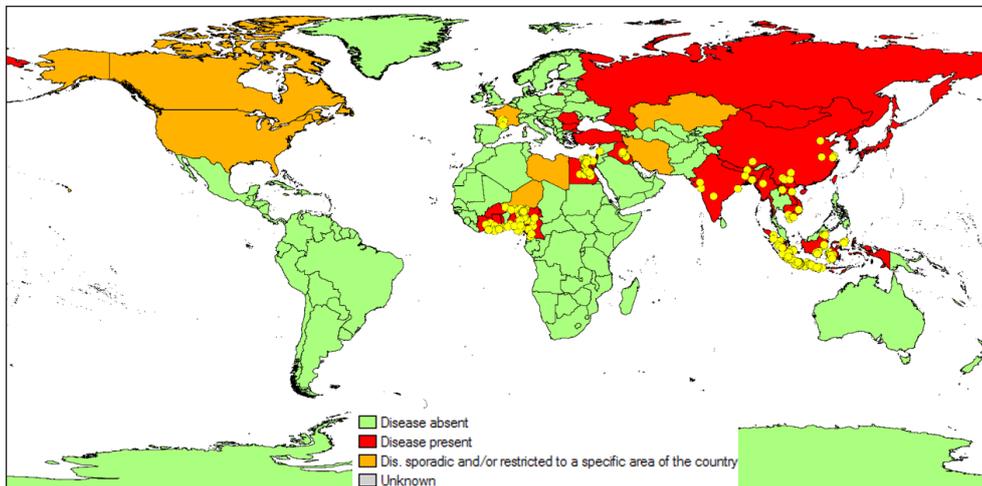


Highly pathogenic avian influenza H5N1

Several outbreaks of H5N1 HPAI infection occurred in 2016 (Figure 3). The disease continued to be reported in China, Indonesia and other southeastern Asian countries. The virus was also detected in Egypt, where a number of human cases were confirmed.

In addition, following its incursion in December 2014, H5N1 HPAI was still circulating in western Africa, including Cameroon, Togo, Côte d'Ivoire, Ghana, Burkina Faso, Niger and Nigeria.

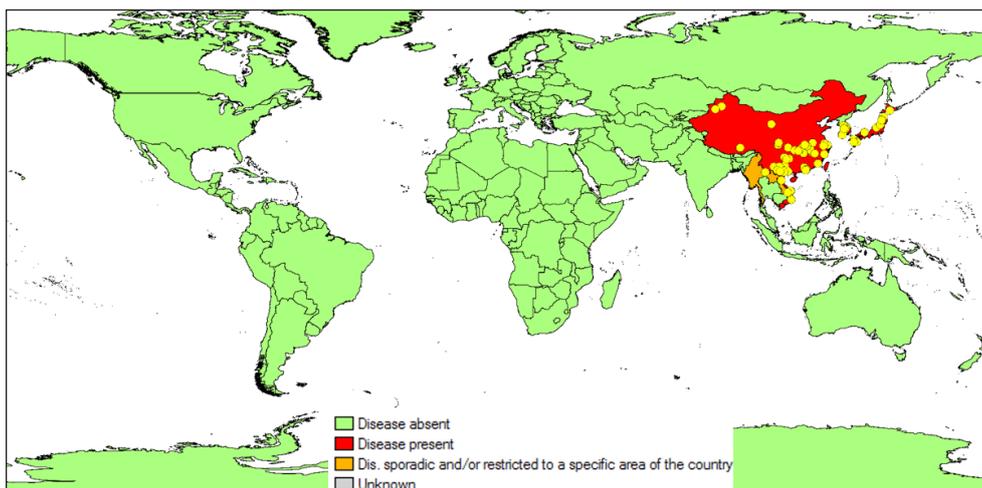
Figure 3. Global situation of H5N1 HPAI, 2016

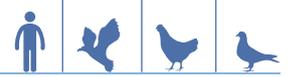


Highly pathogenic avian influenza H5N6

In 2016, H5N6 HPAI circulated extensively in China, where the infection was confirmed in poultry farms and in humans (Figure 4).

Figure 4. Global situation of H5N6 HPAI, 2016



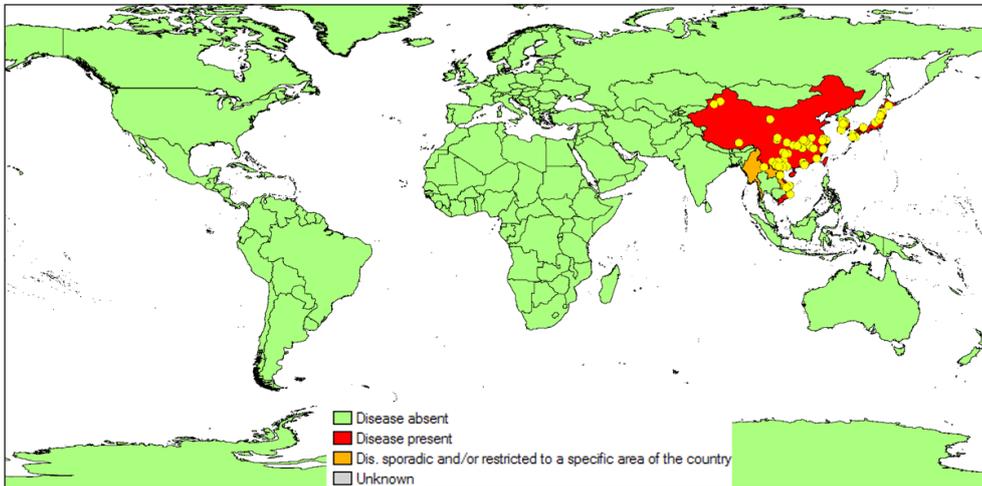


Highly Pathogenic Avian Influenza H5N8

A global epidemic of H5N8 HPAI driven by wild bird movements occurred during 2016 (Figure 5a). Starting from the summer breeding sites of migratory birds in Asia, the infection spread

across the whole of Europe and into African countries along migratory flyways. No human cases of H5N8 infection have been reported to date.

Figure 5a. Global situation of H5N6 HPAI, 2016



Middle East respiratory syndrome – coronavirus (MERS-CoV)



During 2016, 13 outbreaks of MERS-CoV in camels were reported to the OIE – 11 from Saudi Arabia and two from Jordan.

while rest were in Qatar (three), Thailand (two), Austria (one), Bahrain (one), Oman (one) and United Arab Emirates (one) (Figure 5b).

In 2016, a total of 255 human cases with 96 deaths were reported globally. Most of the cases (246, or 96.5%), occurred in Saudi Arabia,

Most cases (64.4%) of MERS-CoV infection in humans were classified as primary (32.0% of them involving a known history

Figure 5b. MERS-CoV cases distribution in humans and animals in 2016

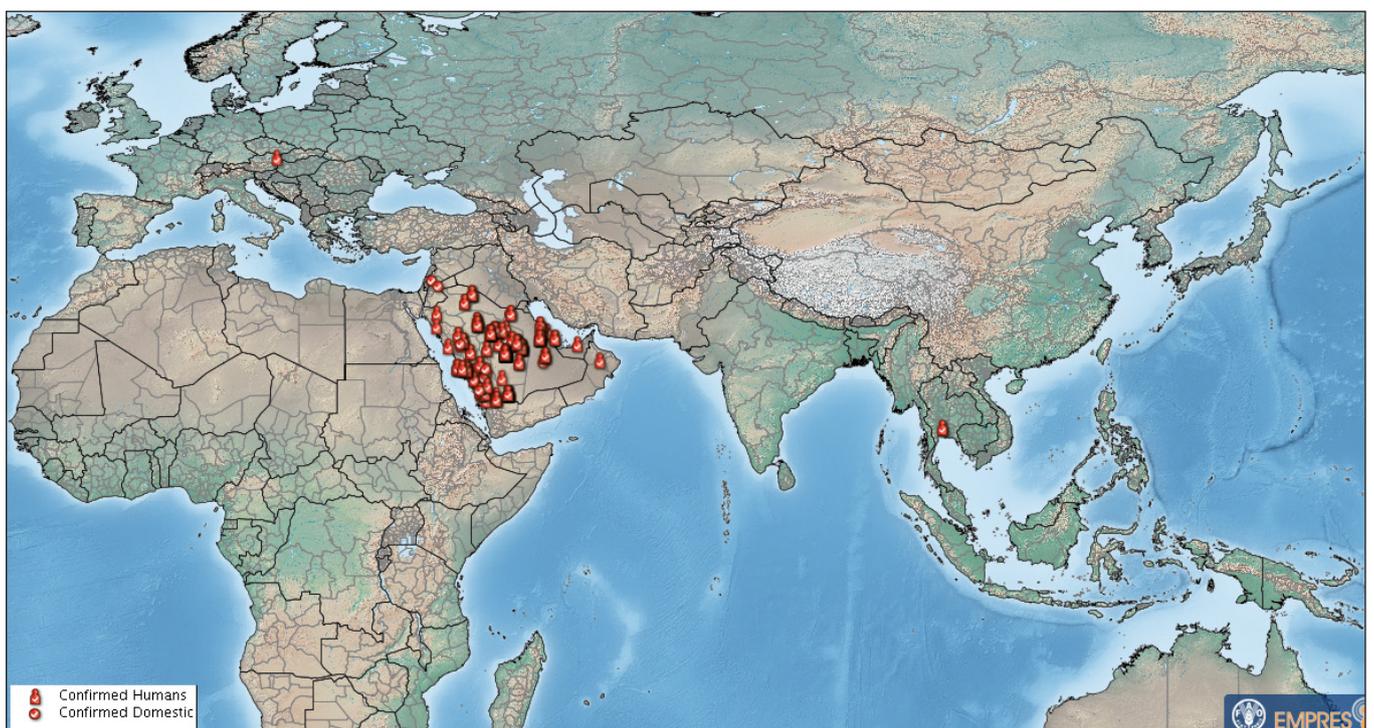
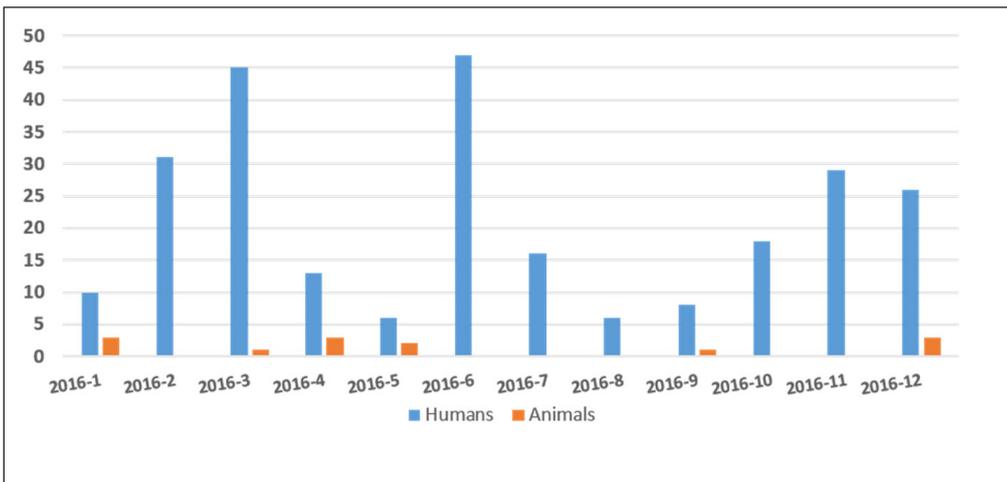


Figure 5c. Number of cases of MERS-CoV in humans and animals in 2016 (by month of onset)

of contacts with camels), while 31.3% were reported as secondary infections contracted by household members, roommates or health workers (Figure 5c).

With about 30 million heads, the global camel population has more than doubled during the past 50 years. This growth is linked to the intensification of camel production systems and a decrease in nomadic camel populations in favour of permanent or semi-permanent settlements, often close to cities (Faye, 2016). Approximately 95 percent of the global camel population consists of dromedaries, 60 percent of which are in East African countries with significant camel exports to the Arabian Peninsula and Egypt (Funk *et al.*, 2016). The ecology and epidemiology of MERS-CoV, its pathways and the risk factors for transmission between camels and between animals and humans are still poorly understood. A recent study based on interviews with experts (Funk *et al.*, 2016) found that dromedaries are considered the leading source of MERS-CoV infection of other dromedaries, and that the risk of transmission was particularly high during calving or weaning.

According to the study, dromedaries infected with MERS-CoV and asymptomatic humans were likely to play the main role in human infection, with bats and other species presenting a possible, but still undefined risk. Direct and indirect contacts between humans and dromedaries were identified as a major risk factor – far greater than consumption of camel products such as meat or milk. In MERS-CoV infection among dromedaries, the major risk factors were: bringing dromedaries to markets; introducing new dromedaries into the herd; high dromedary population density; and watering dromedaries at communal water-points.

In 2016, the epidemiologic patterns of MERS-CoV were the same across the Middle East: multiple transmission from dromedaries to humans and secondary transmission in health-care settings. Transmission among close family members within households remained limited for unclear reasons. Until zoonotic transfer of the virus from infected dromedaries to human populations is halted, there will be a continuing risk of further health-sector-related outbreaks in the Middle East and beyond (WHO, 2016).

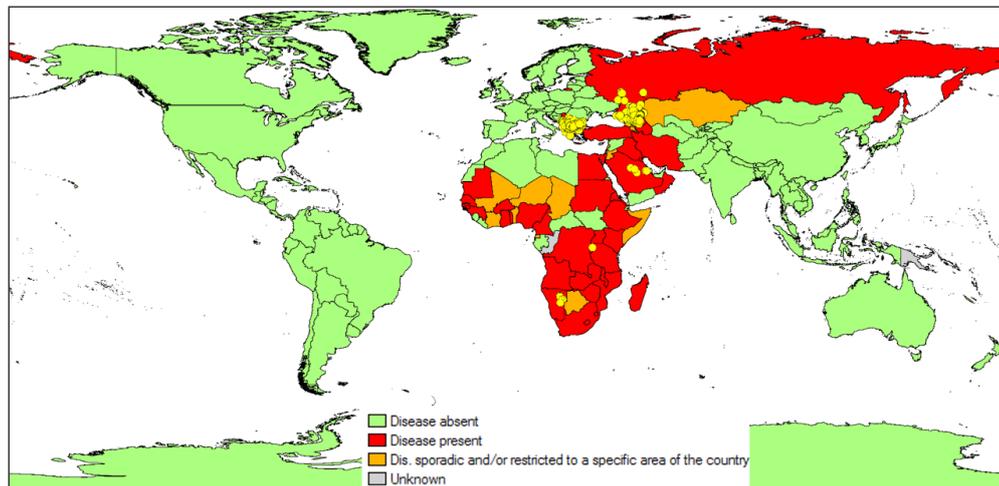
Lumpy skin disease



During 2016, LSD continued to spread from Greece to several Balkan countries (Albania, Bulgaria, Montenegro, Serbia and the Former Yugoslav Republic of Macedonia). Georgia and southwestern parts of the Russian Federation were also involved (Figure 6).

Although it is not known exactly what vectors are dominant in spreading the disease, their contribution is considered the epidemic's main driver in Eastern Europe, together with informal movements of infected animals.

Figure 6. Lumpy skin disease – global situation, 2016



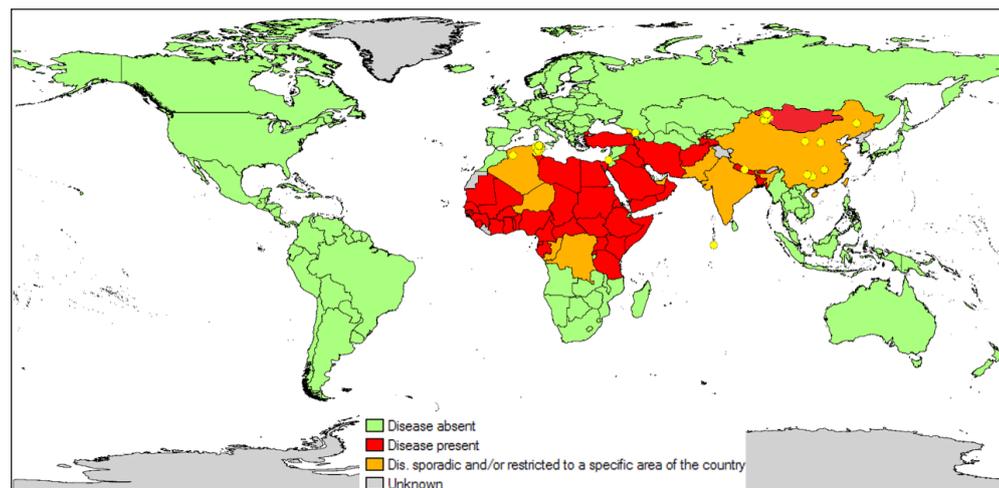
Peste des petits ruminants



The disease is affecting several African and Middle Eastern countries where PPR is endemic (Figure 7). During 2016, outbreaks occurred in Tunisia and in the Caucasus (Georgia). The disease

also involved wild ruminants in Mongolia, where more than 4 000 Mongolian saiga (*Saiga tatarica* spp. *mongolica*) were found to have died of PPR.

Figure 7. Peste des petits ruminants – global situation 2016



Drivers of animal diseases

Factors/drivers influencing the dynamics of animal and zoonotic diseases globally include changes in land use, animal and food product movements and trade, changes or intensification of contacts at the wildlife and livestock or human interfaces, migrations due to wars and civil unrest, and the effects of climate and climate-related phenomena.

This section describes briefly the changes observed in major drivers that could have influenced the patterns of diseases observed during 2016. Given the complex nature of the interaction between drivers and disease occurrence, this section does not attempt to provide proof of association or causation, but highlights some key risk factors that may allow some insight into the incursion and spread of animal diseases in different ecosystems.

El Niño Southern Oscillation (ENSO)

Extreme precipitation and drought events occurred across the world in 2016. The global climate during the year was influenced by the continuation of strong El Niño conditions in the winter (January–March 2016), its transition into a neutral phase during the summer season (June–September), and the development of La Niña conditions in October–December 2016.

Precipitation, flooding and droughts

El Niño's impact on global precipitation was significant in the early months of 2016, and then declined during the year. Between July 2015 and June 2016, precipitation was well below average in Indonesia and the islands of the tropical Western Pacific, most of southern Africa, and the northern half of South America along with parts of Central America and the Caribbean. From January to September 2016, well-above-average precipitation occurred across a region extending from northern Scandinavia, southeast across western and southern European Russia, to Kazakhstan. Other major regions with well-above-average rainfall included eastern Australia south of the tropics, Alaska and Arctic Canada, the eastern side of the Andes in Argentina and the Yangtze River Basin in China. The basin experienced its most significant flood season since 1999, with rainfall about 140 percent of average from April to July.

Regions with well-below-average precipitation during January–September included central Siberia, Chile, and scattered regions in the Amazon basin and southern Africa.

Monsoon-season rainfall in the Sahel was generally above average, determining significant flooding in the Niger River Basin. In upper Niger, the river reached its highest level since 1964 at Mopti, Mali, in early September. Flooding also occurred downstream, particularly in Niger and northern Nigeria, and was also reported in other parts of West Africa, including Gambia, Senegal, and Ghana. In addition, significant flooding occurred in South Sudan, Sri Lanka, and various parts of India during the monsoon season, particularly in the Ganges Basin.

In contrast, rainfall in Kenya and Tanzania was generally below average during the “long rains” season (March–May), and significantly below average during the “short rains” (October–December).

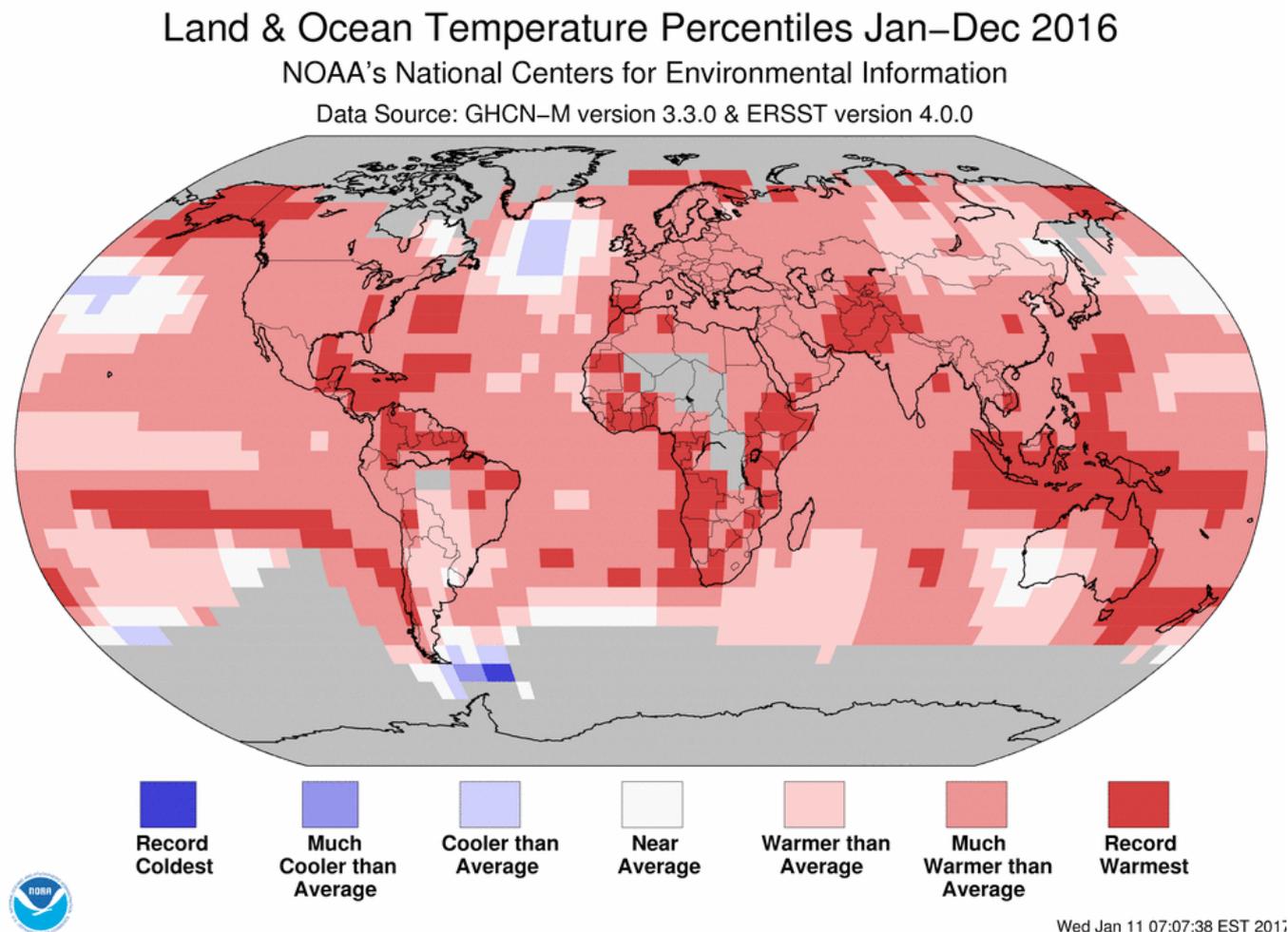
Major droughts affected much of southern Africa in 2016. The region has experienced two consecutive poor rainy seasons, with rainfall well below average since 2014. Among the most-affected countries were Malawi, Angola, Zambia, Zimbabwe, Mozambique, Madagascar and Lesotho. Other regions with significant droughts in the early months of 2016 included much of northern South America and nearby areas of Central America and the Caribbean; the Mekong basin in Southeast Asia, particularly in Vietnam; parts of India; Indonesia, the Philippines and various islands in the tropical Western Pacific; northern and central Ethiopia; and parts of eastern Australia.

During the autumn season, very dry conditions were observed in northern Europe, particularly in Finland, United Kingdom, France and Austria.

Above-average precipitations were probably associated with the occurrence of RVF in Tahoua region (Niger) in August 2016. From January to mid-September 2016, total rainfall in the region was 355 mm, about 80 mm more than the average (mean = 274 mm) for the area – the highest in 16 years. Peaks in rainfall occurred in April (usually a dry month in the area), late May, July and late August 2016.

Temperature

The year 2016 was the warmest in the 137-year period of record, and the third consecutive hottest year at global level. Average global temperature across land and ocean surfaces in 2016 was 0.94 °C above the 20th-century average of 13.9 °C, surpassing the previous record year of 2015 by 0.04 °C. It was the 40th consecutive year (since 1977) that the annual temperature has been above the 20th-century average. In 2016, the first 16 years

Figure 8. Land and ocean temperature percentiles in 2016

of the 21st century ranked among the 17 warmest on record, and the five warmest years have all occurred since 2010. Overall, the global annual temperature has increased at an average rate of 0.07 °C per decade since 1880 and at an average rate of 0.17 °C per decade since 1970.

The global temperatures in 2016 were influenced by strong El Niño conditions at the beginning of the year. Much of the record heat can be attributed to the temperature of the world's oceans, which, between January and July, reached some of their highest monthly levels in the 137-year record. The monthly temperature in January–March was at least 0.8°C above average. Although El Niño dissipated in the spring and was replaced by weak La Niña conditions near the end of the year, global ocean temperatures remained high, with the temperature in December 0.61 °C above the 20th-century average.

Land surface temperatures also reached record highs. The global annual land surface temperature for 2016 was 1.43 °C above the 20th-century average, surpassing the previous, 2015 record by 0.11 °C. In 2016, the highest monthly temperature anomalies

occurred in March, February and April (with +2.35 °C, +2.24 °C and +1.85 °C above last century's average respectively).

Most of the world's land surface experienced above-average annual temperatures, e.g.: the far-eastern Russian Federation, Alaska, far-western Canada, eastern United States, much of Central America and northern South America, southern Chile, much of eastern and western Africa, north central Siberia, parts of south Asia, many Southeast Asian island nations and Papua New Guinea, and parts of Australia, especially along the northern and eastern coasts (Figure 8). Unusually hot weather during the year also affected southern Africa, Thailand, India, Kuwait, Iraq, and Iran. Europe experienced its third warmest year and Africa its second warmest.

No land areas were cooler than average during the year. Nevertheless, extreme temperature lows occurred in Asia in late January 2016, from eastern China to Thailand.

Ocean warming and the resulting decrease of ice cover in the Arctic Ocean was a main determinant of permafrost melting

earlier in the year. The phenomenon could have contributed to the emergence of anthrax in Siberia (Russian Federation) in July 2016 by bringing anthrax spores closer to the soil surface, with consequent contamination of water and forage for animals.

Animal trade

The globalization of trade in live animals and products, together with increased international travel, is facilitating disease incursion into free areas. The protection formerly offered by natural barriers is now becoming ineffective. Significant amounts of natural or agriculture-based resources harvested or produced in developing countries are further processed or consumed in economically more advanced countries, providing regular routes for hitchhiking organisms. Similarly, developing countries are often not self-sufficient in various food commodities and, when importing them, run the risk of bringing in new pests or pathogens (Richardson *et al.*, 2016). According to the last available live animal **production** figures (FAOSTAT 2014), no major changes have taken place in the volumes of cattle, poultry (*Gallus gallus*, ducks, geese, turkeys and guinea fowls), small ruminants (sheep and goats), pigs and camels produced, nor in the rankings of top producing countries.

The last available data on international trade in live animals recorded by the United Nations is for 2015. A slight decrease compared to the previous year in overall export and import values

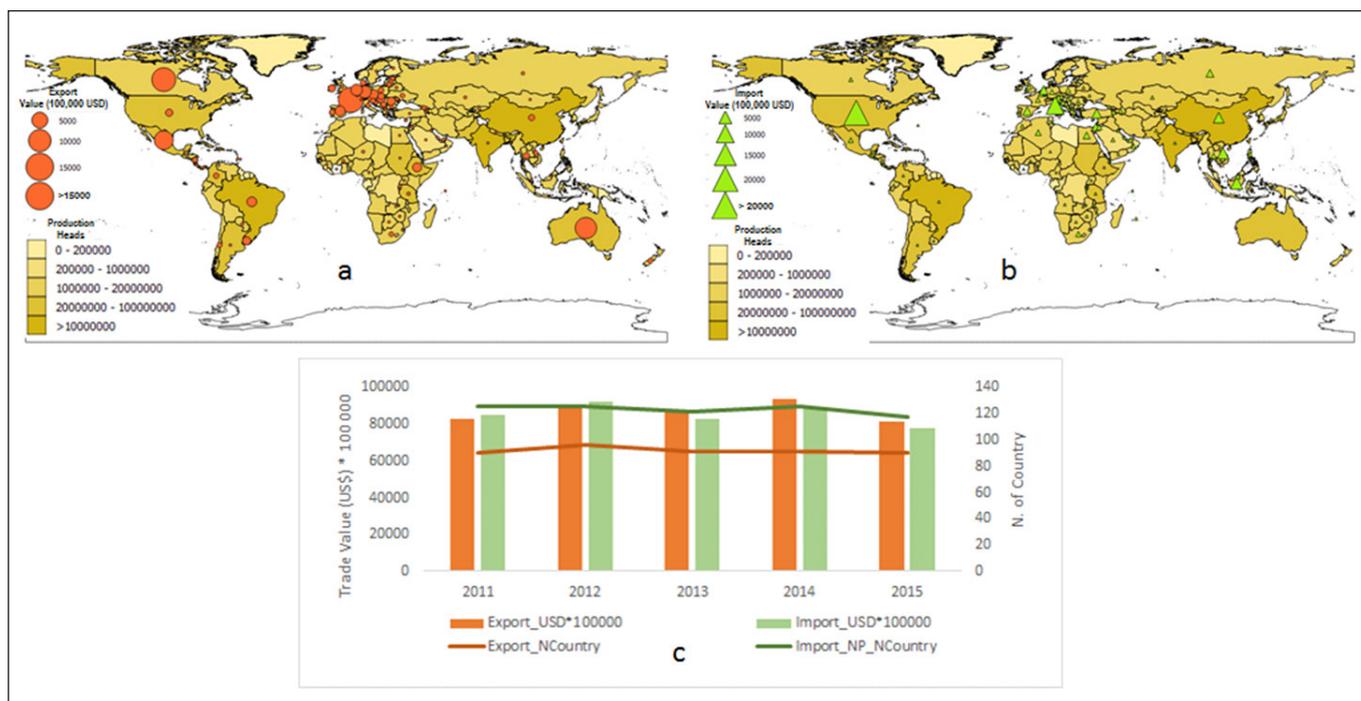
was seen for pigs, poultry and camels, while an increase was registered for small ruminants. No major changes took place in the rankings of top exporting and importing countries. The general trend in global meat prices for 2015 was down: the 2016 meat price index declined to 156.2 from 168.1 in 2015, and from 198.3 in 2014. During 2016, the index fluctuated due to changes in poultry, mutton and pork prices. Although not reflected in global trade data, price differentials across regions and borders are well known to encourage unregulated movements of animals and animal products, thus increasing the risk of the risk of pathogens and disease spreading.

Cattle (Figure 9). Brazil, India, China and the United States continued to be the principal cattle producers. Much as in previous years, major exporter of live bovines in 2015 were France, Canada and Australia, while the major importers were Italy and the United States.

Live pigs (Figure 10). China produces 49 percent of the world's live pigs. The Netherlands, Denmark and China were the major exporters, while Germany alone accounted for 33 percent of global pig imports in terms of value.

Small ruminants (Figure 11). In 2014, China, India, Nigeria and Pakistan produced 35 percent of the world's small ruminants. In 2015, Sudan, Jordan, Australia and Romania dominated export trade while countries in the Arabian Peninsula accounted for 75 percent of the value of imports (Saudi Arabia alone for 50 percent).

Figure 9. Live cattle exports (a) and imports (b) in 2015, and temporal trend from 2011 to 2015 (US dollars x 100 000).



Poultry (Figure 12). In terms of live poultry, in 2014 China produced almost 25 percent of the global poultry stock, while Germany and the Netherlands dominated both exports and imports. Increased production of poultry and low-biosecurity production environments in Southeast Asia are relevant drivers for the emergence and spread of LPAI and HPAI in poultry value chains and live bird markets (LBMs).

Camels. Somalia, Sudan and Kenya were the major camel producers in 2014, while Oman, Ethiopia and Saudi Arabia the major camel exporters. Qatar, Saudi Arabia and United Arab Emirates were the top importers.

Figure 10. Live pig exports (a) and imports (b) in 2015 and temporal trend from 2011 to 2015 (US dollars x 100 000).

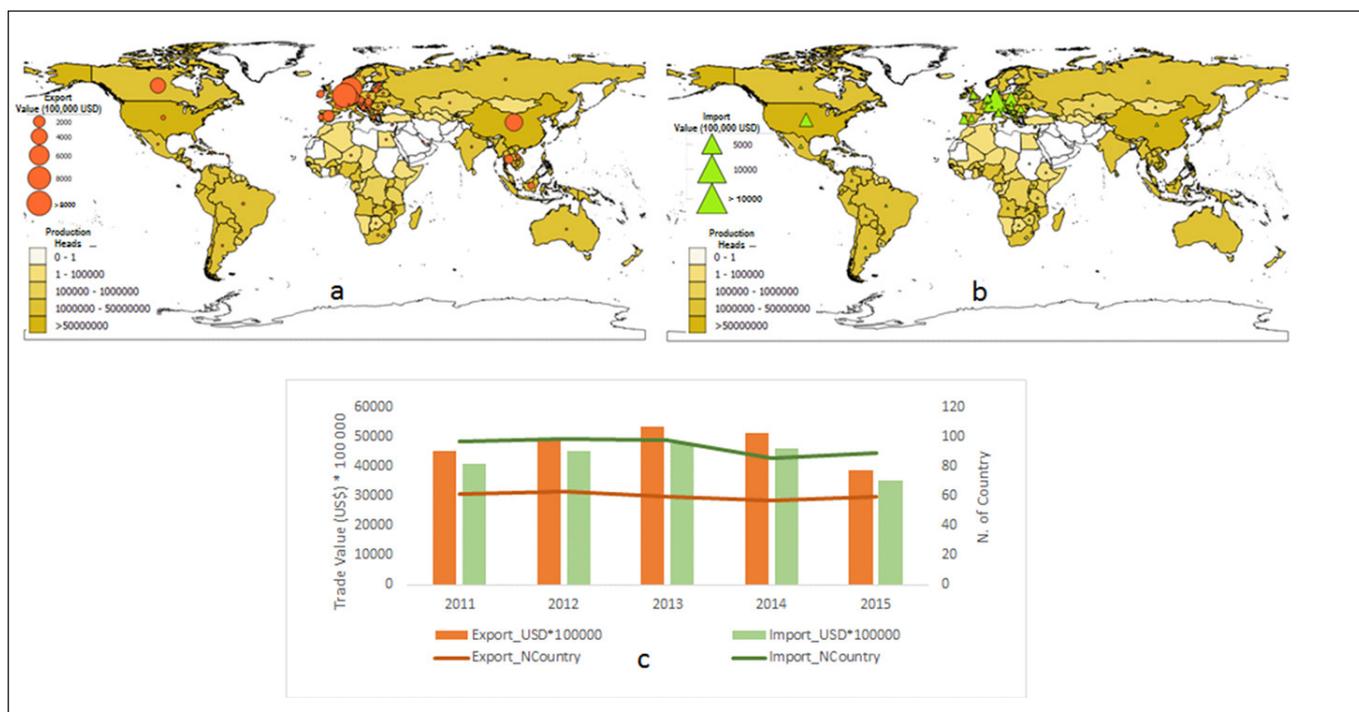


Figure 11. Live small ruminant exports (a) and imports (b) in 2015, and temporal trend from 2011 to 2015 (US dollars x 100 000).

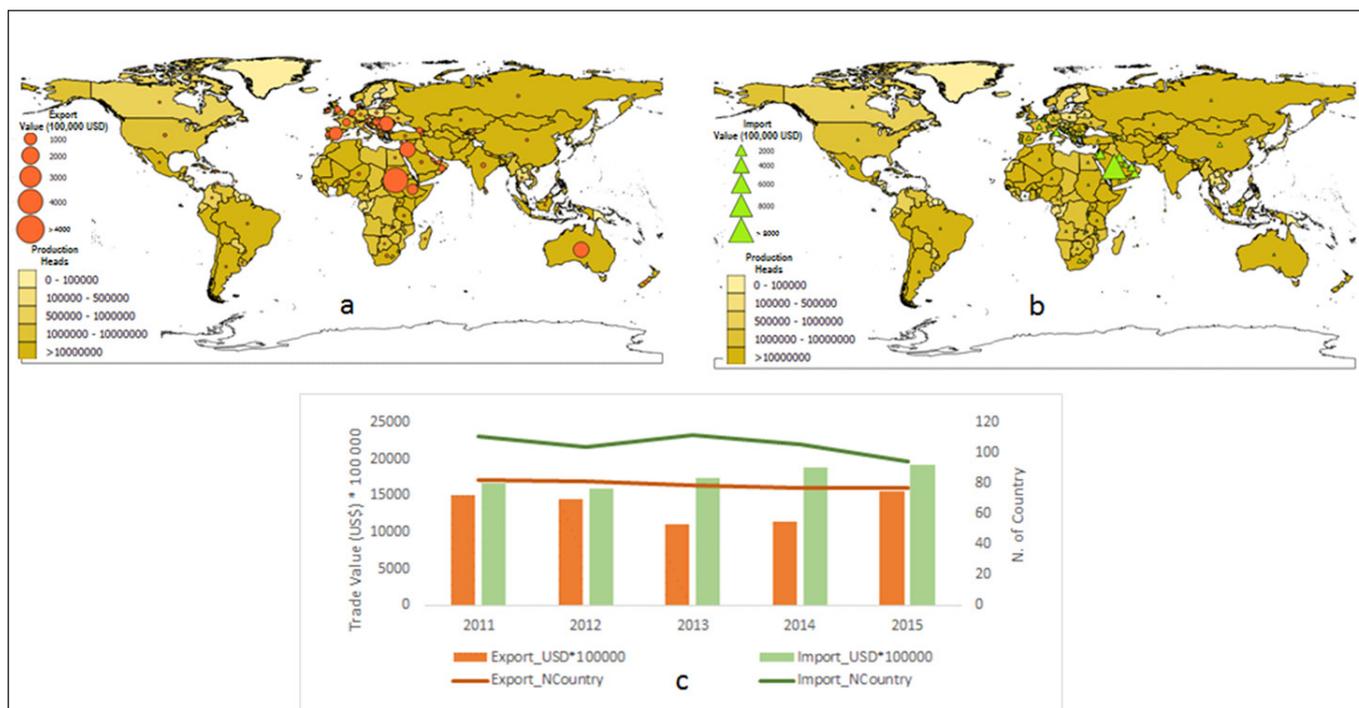
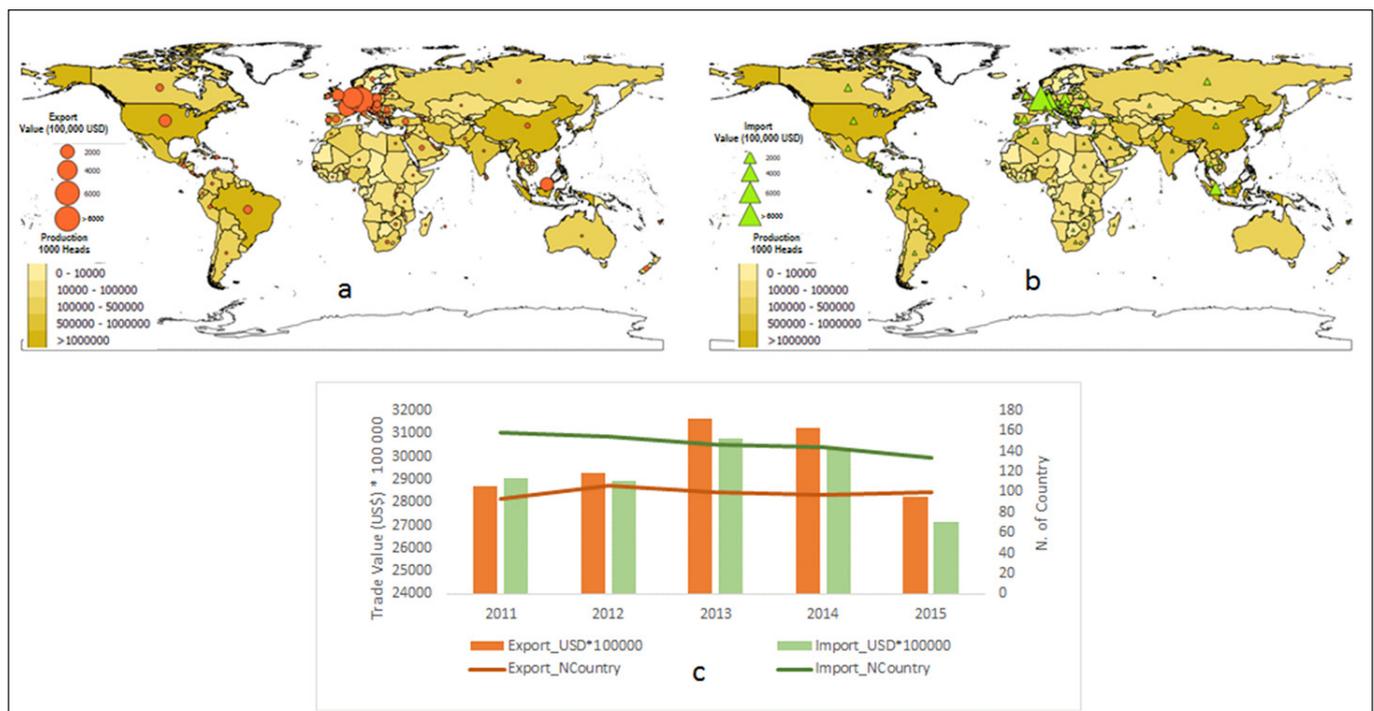


Figure 12. Live poultry exports (a) and imports (b) in 2015, and temporal trend from 2011 to 2015 (US dollars x 100 000).

Festivals and traditions

In various countries around the world, many traditional feasts and festivals are celebrated every year, often boosting demand for animal products, with consequent increased animal trade and movements, as well as human travel.

A number of countries in South and Southeast Asia (including China, Myanmar, the Republic of Korea and Viet Nam) celebrated Chinese New Year in February 2016 – with a resulting surge in trade and in animal and human movements. Mass travel by people within China, or returning to their hometowns, from abroad is often seen as one of the main drivers for increased person-to-person infections such as seasonal influenza and respiratory diseases in general.

During Muslim celebrations too, large numbers of sheep and goats are traded for ceremonial slaughter, and this increased movement of animals is considered one of the main factors driving the spread of livestock diseases (such as RVF or PPR) in West and northeastern Africa.

Major Muslim festivals include the Lesser Bairam (Eid al-Fitr) at the end of Ramadan, and the Greater Bairam (Eid al-Adha), 70 days later, at the end of the Islamic year.

Wildlife

Many scientific papers dealing with disease control and prevention consider wild animals reservoirs of pathogens and the key actors in the (re)emergence of epidemic threats.

Leaving aside the issue of whether today's wild animals, confined to natural reserves or subject to indirect human intervention, are "truly" wild, non-farmed animals share the same environment as, and interact with, humans, farmed animals and pathogens.

From an ecological perspective, wild animals may play a maintenance function, allowing the conservation of pathogens within ecosystems. A maintenance host (or reservoir), is therefore a host population (a single population) or a community/host complex (several populations) in which pathogens may persist even in the absence of transmission from other hosts (Caron *et al.*, 2015). But wild animal populations, given their capacity to transmit infections to farmed animals and human beings, are monitored by veterinary and public health authorities. From the epidemiological point of view, wild species may act as reservoirs that maintain pathogens in the environment, as bridge species involved only in the transmission of pathogens, or they may play both roles (Caron *et al.*, 2015).

A recent review identified the ten zoonotic diseases most often discussed in scientific papers dealing with the wildlife–livestock interface (Wiethoelter *et al.*, 2015). First among them was avian

influenza (both low- and highly pathogenic). That is not surprising, considering the crucial role played globally by wild bird populations in the emergence of new virus subtypes and in their maintenance and spread. In many instances waterfowl (e.g. ducks, geese, waders, gulls, and terns) act as the maintenance hosts for avian influenza viruses, and since several migratory wild bird species travel over long distances, they also act as bridge hosts facilitating virus transmission to farmed poultry (Caron *et al.*, 2015). For example, a recent analysis of H5N8 HPAI covering viral sequences, epidemiological data, waterfowl migration, and poultry trade was able to demonstrate that the virus spread along two main long-distance migration routes: one from the Korean peninsula, northward to the Arctic coast of the Eurasian continent and then west to Europe (the virus was introduced into the Korean peninsula in 2013-2014 by wild birds migrating over long distances, which acquired it from the pool of H5 HPAI viruses circulating in domestic anseriformes in China); and the other north from the Korean peninsula, then east across the Bering Strait, and south along the northwest coast of North America. The reconstruction did not indicate any spread between Europe and North America (Global Consortium for H5N8 and Related Influenza Viruses, 2016). All these virus-spread mechanisms are clearly governed by the wild bird flyways connecting breeding and wintering areas. In fact, several wild bird species with known HPAI H5N8 sequences are long-distance migrants at different stages of their migratory cycle: five of the nine species found positive to H5N8 in the Republic of Korea studied in the winter of 2013–2014 were long-distance migrants at their wintering sites, or were engaged in spring migration. Both in North America and Europe, two of the four species found in the winter of 2014–2015 were long-distance migrants at their wintering sites or engaged in autumn migration (Global Consortium for H5N8 and Related Influenza Viruses, 2016). But resident and local waterfowl also play a key role as bridge hosts in virus introduction into poultry farms. The results of outbreak investigations on affected poultry farms in North America and Europe show that the likelihood of virus introduction via contaminated water, feed, and poultry was negligible and no links between the outbreaks in one country and those in other countries could be attributed to personnel contacts or trade in live animals, feed, or products of animal origin. In contrast, many affected poultry farms were in areas where wild waterfowl were abundant, and direct contact with infected wild birds or indirect contact with materials (e.g. bedding, boots, and vehicle wheels) contaminated by wild bird faeces were considered the most likely route of introduction (Global Consortium for H5N8 and Related Influenza Viruses, 2016). Recognition of the likely role of wild birds in the spread of HPAI reinforces the need to improve biosecurity on poultry farms and strengthen surveillance over waterfowl at the crossroads of migratory flyways, both in wintering and breeding sites.

Another disease at the wildlife-domestic animal interface of major concern is African swine fever. In 2007, the disease was reported in Georgia, most probably originating from southeast Africa (Rowlands *et al.*, 2008). From Georgia, the virus spread into Armenia, Azerbaijan and into several states of the Russian Federation. In 2013 it reached Belarus and Ukraine and later, in 2014, it entered Lithuania, Poland, Latvia and Estonia, affecting both domestic pigs and wild boar. Based on the characteristics of the virus and on the epidemiological findings, the introduction into the Baltic countries and into Poland was most probably from Belarus (EFSA, 2015). More than a year after its arrival in Poland and the Baltic countries, ASF is still spreading in wild boar in the eastern member states of the European Union, with a few spillovers into the domestic pig population, while in Ukraine and in the Russian Federation the virus continues to spread in both wild boar and domestic pigs (Bellini *et al.*, 2016). Different risk factors have been considered for the disease's massive spread across Eastern Europe: illegal movements of infected animals and pork meat, swill feeding habits, and scarce application of biosecurity principles, especially in the backyard sector, which is clearly playing an important role in the maintenance of the infection in some countries. However, in the Baltic countries and in Poland, it was observed that wild boar habitat suitability and the distance from infected wild boar and domestic pigs, were the main risk factor for the spread of the virus through infected wild boar. Different studies highlighted the extensive geographical distribution of wild boar, wild boar management (hunting systems, winter feeding), local density and size of the infected population, together with direct contact with dead infected wild boar, as the most relevant risks for the spread and the persistence of the virus in wild boar populations (Bellini *et al.*, 2016). Wild boar are susceptible to ASFV and they show clinical signs and mortality similar to those of domestic pigs, with comparable virus elimination times and concentrations. When wild boar die, infected carcasses, if not promptly removed, remain in the environment and they can, directly or indirectly, infect other susceptible pigs, continuing the epidemiological cycle of the disease. ASF virus is very resistant to a range of environmental conditions from hot/humid to very cold. Wild boar can also contribute to spreading the virus during the infectious period of the disease, since they eliminate the virus into the environment through their excretions and secretions. Hunting is allowed in most of the forested areas of northeast Europe, and wild boar are one of the more intensively hunted ungulate species in the region. Yet, wild boar have expanded throughout Europe during the last 40 years thanks to their high reproductive rate, which can double populations after each reproductive season. Since hunting wild boar implies blood contamination of the soil and transportation of dead animals, which facilitate virus dispersion in the environment, basic biosecurity measures should be adopted during hunting to minimize the risk of spreading the disease (Bellini *et al.*, 2016). Furthermore, indiscriminate and unreg-

ulated hunting pressure can also facilitate the spatial dislocation of significant parts of a wild boar population, thus facilitating the territorial spread of the infection.

Wild animals can be victims of infections introduced by domestic animals. The recent case of Peste des petit ruminants infection in saiga antelopes (*Saiga tatarica ssp. mongolica*) in Mongolia is just one such spillover events. Mongolian saiga are an extremely rare species, to be found only in the Altai-Sayan ecoregion of Mongolia. Thanks to conservation efforts, the saiga population rose to 14 600 in 2015. But with the PPR infection, which killed more than 4 000 animals, the survival of this species is being challenged again.

Risk assessment of emerging infections

Middle East

H5N1 Highly pathogenic avian influenza

A risk assessment conducted by FAO (<http://www.fao.org/3/a-i6155e.pdf>) estimated the likelihood of spread of H5N1 HPAI from some infected countries (Lebanon and Iraq) to other countries in the Middle East region and in neighbouring territories as a result of the movement of live poultry (both legal and illegal), poultry-related products and the migration of wild birds (Figure 13). The overall risk of H5N1 HPAI introduction into the unaffected countries of this region ranged from low to high, with moderate to high levels of uncertainty. The overall risk for spread in the Middle East region was medium, with medium uncertainty. Countries at high risk of introduction of H5N1 were Turkey, Syrian Arab Republic and Iran (Islamic Republic of). Countries or territories at medium risk of incursion were identified as the West Bank and Gaza Strip, Israel, Kuwait and Saudi Arabia. In addition, Armenia, Azerbaijan and Georgia were considered exposed to the infection because of their location along the spring migration pathways of wild birds travelling northward, although the risk of H5N1 HPAI spread through this pathway was considered low. Finally, Cyprus was considered at negligible risk of incursion from Lebanon and Iraq. The main risk factors contributing to the introduction and spread of the virus in the region were identified as:

- **Political regional instability.** The civil war in the Syrian Arab Republic has resulted in large-scale, uncontrolled displace-

ment of people and animals across the region, with Iraq, Jordan, Lebanon and Turkey being the main destinations.

- **Wild bird migration and climate.** Iraq and Lebanon are a concentration points for migratory birds on the Western Siberian-Mediterranean- East Africa flyway, on their way from breeding areas in Eastern Europe and western/central Siberia to wintering areas in the Middle East. This passes over the river systems of the Arabian Peninsula, the Nile system in Egypt, Ethiopia, Israel and Sudan, across the southeastern Mediterranean countries and along the Rift Valley/Red Sea flyway and the Caspian Sea (Figure 14).
- **Poultry production, movements and trade.** Overall, production has increased across the region since 2004, with important producers including Israel, Saudi Arabia, Turkey and Yemen. Anecdotal evidence points to the existence of trade along the borders of northern Iraq and Turkey, as well as Iran in the mainly Kurdish areas.
- **Wild bird informal trade.** Wild birds, particularly waterfowl, are traded informally in small markets, mainly for local consumption, in several countries of the region.

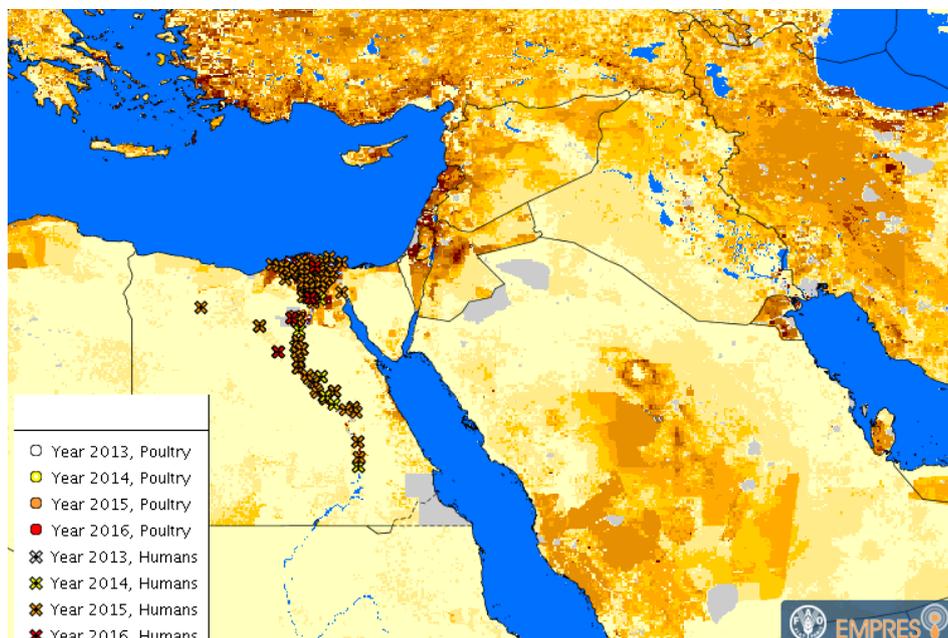
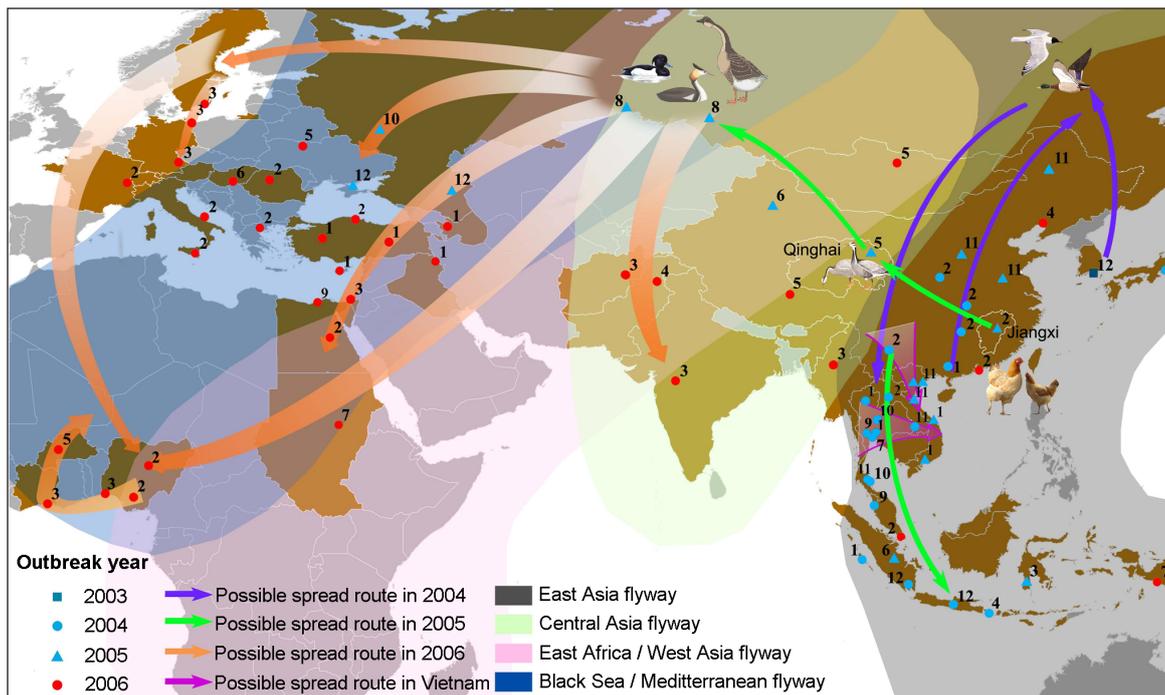


Figure 13. H5N1 HPAI events reported in humans, poultry and wild birds in the Middle East from 2013 to 2016, overlaid on poultry population density.

Figure 14. Waterfowl flyways, H5N1 HPAI outbreaks and possible spread routes in 2004–2006.



Central Africa

H5N1 Highly pathogenic avian influenza

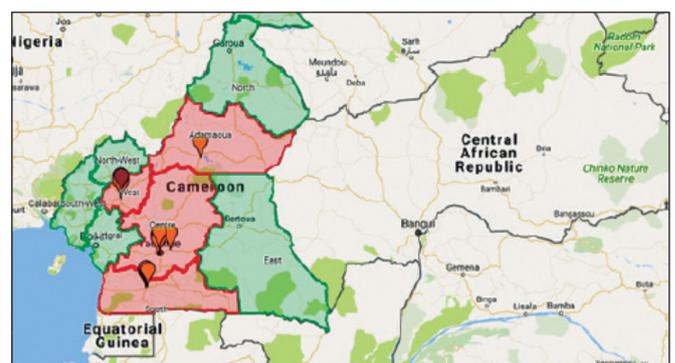
Following H5N1 HPAI outbreaks in Cameroon in May and September 2016 (Figure 15), a FAO assessment (<http://www.fao.org/3/a-i6348e.pdf>) evaluated the risks of the virus entering into neighbouring countries, bearing in mind that Nigeria has been affected by H5N1 HPAI outbreaks in poultry since December 2014, and circulation of the virus is considered to be endemic there. The likelihood of introduction of H5N1 HPAI from Cameroon into previously unaffected countries in the Central African Region was considered:

- through **live adult poultry trade**:
 - negligible through legal trade with Equatorial Guinea and Gabon;
 - low through legal trade with the Central African Republic, Chad and the Congo;
 - moderate through illegal trade with neighbouring countries, especially with Chad.
- very low through **wild bird migration**.
- through **fomites**:
 - moderate for Chad, due to informal commerce with Cameroon;
 - low for Congo, Equatorial Guinea and Gabon; very low for the Central African Republic.

Considering the different regions in Cameroon, the likelihood of H5N1 HPAI spreading into unaffected areas was considered:

- high for the Littoral Region due to infection in neighbouring regions and significant poultry activities;
- moderate for the Far North Region that has elevated poultry density and shares a border with Nigeria, where virus circulation is high;
- low for the East, North, Northwest and Southwest regions.

Figure 15. Geographical distribution of H5N1 HPAI outbreaks in Cameroon observed between 20 May and 29 August 2016 – Risk Assessment H5N1 HPAI.



Trade-related activities (legal and illegal) involving live poultry and derived products were considered the principal risk factors for local and cross-border spread of HPAI, together with the possible contribution of fomites (e.g. non-disinfected trucks).

The importance of live animal trade and the role of live bird markets in AI transmission and amplification have also been assessed in Nigeria in recently published papers (Fasanmi *et al.*, 2016; Okpukpara, 2016) showing that poor biosecurity conditions in LBMs were significant risk factors.

East Africa

H5N8 Highly pathogenic avian influenza

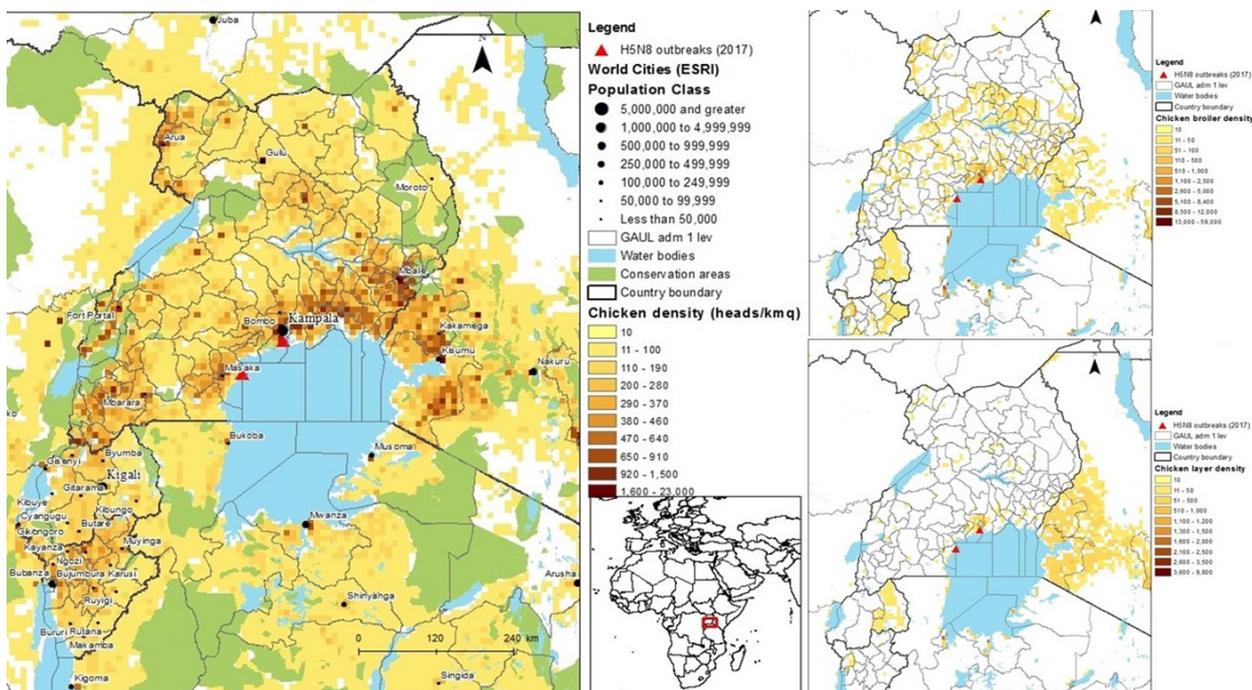
In December 2016 an episode of massive mortality in wild birds (white-winged terns – *Chlidonias leucopterus*) along the shores of Lake Victoria was observed and reported from Uganda in January 2017. The virus responsible was characterized as H5N8 HPAI. The infection spread from wild to domestic birds in villages and districts close to the lake's shores (Figure 16).

Uganda hosts important breeding, wintering and transit areas for wild birds, being a major stopover along the East Asian-East African flyway. The region where the outbreak was reported is considered a shelter for 240 000 birds, including 100 migratory waterbird species, of which 82 are Palearctic and 17 Afro-tropical migrants. The Ugandan shores of Lake Victoria number five Ramsar sites (sites listed under the Ramsar Convention on internationally important wetlands) (Figure 17), and one of them, Lutembe Bay, may be home to 50 000 birds during the month of January. The numbers of waterbird species and individuals fluctuate depending on the season, with the largest number of waterbirds present

from December to March. Palearctic wintering gulls, terns, white-winged terns and waders represent 70 percent of the population (NatureUganda, 2014). Among the regularly observed migratory birds in the region, eight species are considered as representing a high risk for the spread of influenza viruses. They include the tufted duck (*Anthia Fuligula*), the long-tailed cormorant (*Microcarbo africanus*), the northern shoveller (*Anas clypeata*), the garganey (*Anas querquedula*), the black-headed gull (*Chirocephalus red-buds*) and the Eurasian wigeon (*Anas penelope*).

The migratory flyways of the white-winged terns largely overlap the zones involved in the H5N8 outbreak during the summer and autumn of 2016 (Figure 18), thus raising the hypothesis that they played a role in the introduction of H5N8 HPAI into Uganda. Alternative theories are also advanced, however, including the involvement of other wild bird species, such those belonging to Anatidae.

Figure 16. Geographical localization of H5N8 events in Uganda and chicken density (heads/km²) in the region – Risk Assessment H5N8.



Uganda has two rainy seasons: from March to May and from September to December (UNMA 2016). Migrating wild birds, including waterfowl, arrive in the Ugandan wintering areas in October/November, during the rainy season, when the availability of food should be greatest.

But, since October 2016, below-average and erratic rainfall has affected most of Uganda, Rwanda, Kenya, Tanzania and Democratic Republic of the Congo, resulting in strong moisture deficits, degraded ground conditions and drought (Figure 19). The situation appears to be associated with the weak La Niña conditions over the equatorial eastern Pacific Ocean. Rainfall anomalies influence phenology and forage availability for wildlife, thus affecting migration routes, wintering areas, and departure timing for migratory wild bird species (Gaidet *et al.*, 2008; Hurlbert and Liang, 2012). Just as cold spells in temperate regions (Reperant *et al.*, 2010), droughts in tropical areas may determine higher concentrations of wild bird species in critical available hotspots, increasing competition for food and shelter and the risk of dis-

ease transmission. The current and persistent droughts around Lake Victoria where H5N8 was reported may have triggered precisely that scenario. Drought may also have made less food available, thus increasing the vulnerability of the wild bird migratory and resident species to diseases.

A rapid risk assessment was performed by FAO's Global Surveillance and Early Warning System (GLEWS) with the involvement of international experts. The experts considered that H5N8 HPAI spread from Uganda to Kenya was **likely** (66%–90% chance), while spread to the Republic of Tanzania and Rwanda was considered as **likely as not** (33%–66% chance). The uncertainty for these estimates was deemed high.

Spread of H5N8 HPAI within Uganda was estimated as **likely** with a medium level of uncertainty. Further spread in Uganda's poultry system was considered more likely to affect backyard than commercial poultry, given that Uganda's live bird market system is characterized by poor biosecurity (Kirunda *et al.*, 2014).

Rift Valley fever in East Africa

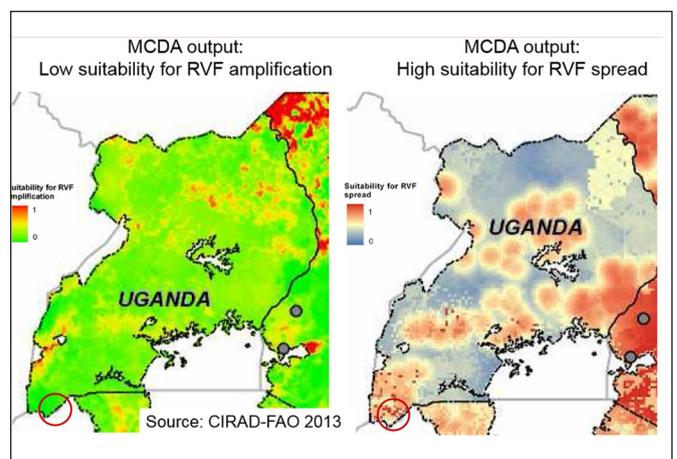
In early March 2016, Uganda declared its first outbreak of Rift Valley fever, with two human cases in the southwestern Kabale district. The patients had been in close contact with livestock. Successively, one goat was found positive in testing. No previous outbreaks had been reported in the country, but the presence, discovered in previous studies, of antibodies to RVF in domestic animals suggested RVF virus circulation in the country.

Outbreaks of RVF are closely associated with periods of heavy rain and prolonged flooding, which increase habitat suitability for vector populations. The role of vector-borne transmission in the Kabale outbreak was considered low, however. Despite the strong 2015–2016 El Niño phenomenon and associated abnormal rainfall in East Africa, no substantial climatic anomalies were observed in the Kabale area during the 2016 event. In fact, Normalized Difference Vegetation Index (NDVI) values were generally lower than, or equal, to the average in the area between September 2015 and February 2016. In addition, because of its physical and environmental characteristics, the area lies outside the RVF vector suitability map produced by NASA (Anyamba *et al.*, 2009). Consequently, this area is not identified by climate-based models as at risk of RVF vector amplification (FAO, OIE, WHO 2015).

Kabale has relatively low livestock densities compared to neighbouring counties and districts. Nevertheless, the district is an important commercial centre, with six animal markets – a situation associated with a higher risk of RVF spread due to significant

livestock movements both domestically and across international borders. According to a FAO Multi-Criteria Decision Analysis (MCDA) model (Tran *et al.*, 2016), and in line with the socio-economic and ecological environments in Kabale district, the outbreak area was identified as poorly suitable for RVF amplification but highly suitable for RVF spread (**Figure 20**). No other outbreaks of RVF were detected in Uganda and none in neighbouring countries.

Figure 20. MCDA maps for RVF amplification (left) and spread (right) in Uganda – Risk Assessment RVF. Kabale district is in the red circle.



West Africa

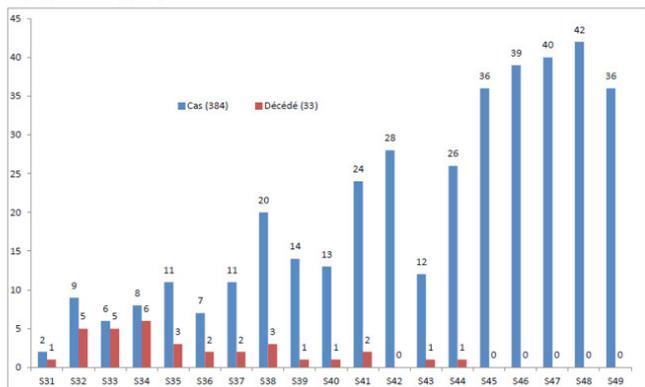
Rift Valley fever

Since August 2016, there have been 384 human cases of RVF and 33 deaths notified in Niger, in Tahoua department and Keita district, Tahoua region. Of the cases, more than a third were herders (Figure 21).

Few data are available on previous occurrences of RVF in Niger. A paper published in 1995 (Mariner *et al.*, 1995) reported the detection of RVF neutralizing antibodies in camels sampled between 1984 and 1988, in Agadez Department in the north of the country. Of the 141 animals tested, 67 were found serologically positive. Another serosurvey of 557 sheep and 643 goats in 1986 indicated that 2.8% of the animals tested had RVF virus antibodies (Akakpo *et al.*, 1991). Two major drivers for the occurrence of RVF in Niger were considered: the introduction of large numbers of ruminants in September 2016, and precipitation from January to mid-September 2016.

Figure 21. RVF human cases in Niger by week of onset and by district of occurrence, August-December 2016 (WHO, Situation report, 14/12/2016).

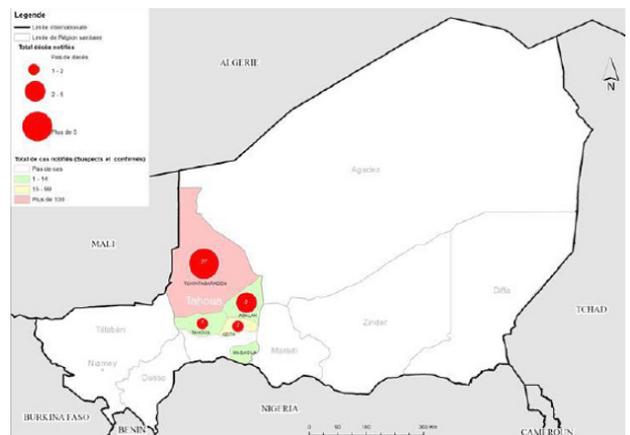
Graphique N2 Répartition hebdomadaire des cas (suspects et confirmés) et décès de Fièvre de la vallée de Rift de la semaine 31 à la semaine 49 de 2016 (Région de Tahoua), au Niger



patterns, significantly increases the risk of transboundary spread of the disease (Figure 22).

In addition, NDVI time-series data recorded between 2000 and 2016 for the RVF-affected area showed suitable environmental conditions for RVF vector amplification. From January to mid-September 2016, total precipitation in Tahoua region was 355 mm, about 80 mm more than the overall average (mean = 274 mm) for the area and the 16-year time period. Peaks in rainfall occurred in April (which is usually a dry month in the area), late May, July and late August 2016. In mid-August, precipitation was lower than average, while June also registered a dry spell. In semi-arid areas of Senegal and Mauritania, dry spells positively influence the dynamics of *Aedes* mosquitoes (*Aedes spp.*) by favouring the development of a second population in the wet season. This coincides with the proliferation of *Culex* mosquitoes (*Culex spp.*), increasing the risk of RVF insect transmission to livestock (Figure 23).

A rapid risk assessment performed in October 2016 by FAO's GLEWS unit (<http://www.fao.org/ag/againfo/programmes/en/>



As regards ruminants introduction, nomadic stockbreeders from Niger and neighbouring countries held a major annual gathering, the Cure Salée festival, from 23 to 25 September 2016. During the event, herds are brought towards the city of Ingall in the central part of Niger, around 120 km west of Agadez, to graze on the salty pastures of the lazra plain ahead of the dry season. Around 2 million cattle and an even greater number of small ruminants are thought to participate. At the end of the rainy season, following known migration patterns, the region's nomadic human population and their herds move on to other sub-Saharan countries, where irrigation systems and pastures along the Niger River may still be available. The ongoing RVF outbreak, along with the high concentration of animals in the area and likely transhumance

[empres/news_031116.html](http://www.fao.org/ag/againfo/programmes/en/empres/news_031116.html)) highlighted how the RVF infection in Niger posed a **medium** risk (a mean score of 5.75 out of ten) to the country's public health and a **medium-high** risk (a mean score of 6.5) to animal health. The experts consulted during the risk assessment considered RVF **likely/very likely** (66%–99% chance) of occurring in neighbouring Mali during the same vector season, whereas the occurrence of the disease in other neighbouring countries – Burkina Faso, Benin and Nigeria – was considered less probable, between **unlikely** (10%–30% chance) and **likely as not** (33%–66% chance). The experts consulted took the view that RVF is unlikely to spread into the North African countries of Morocco, Algeria and Libya in the next three to five years. Animal movements and trade, as well as the changes in

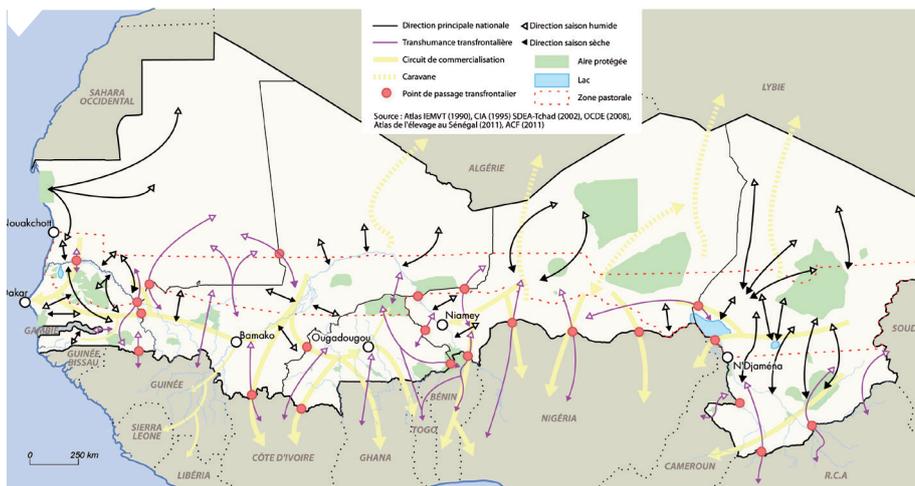
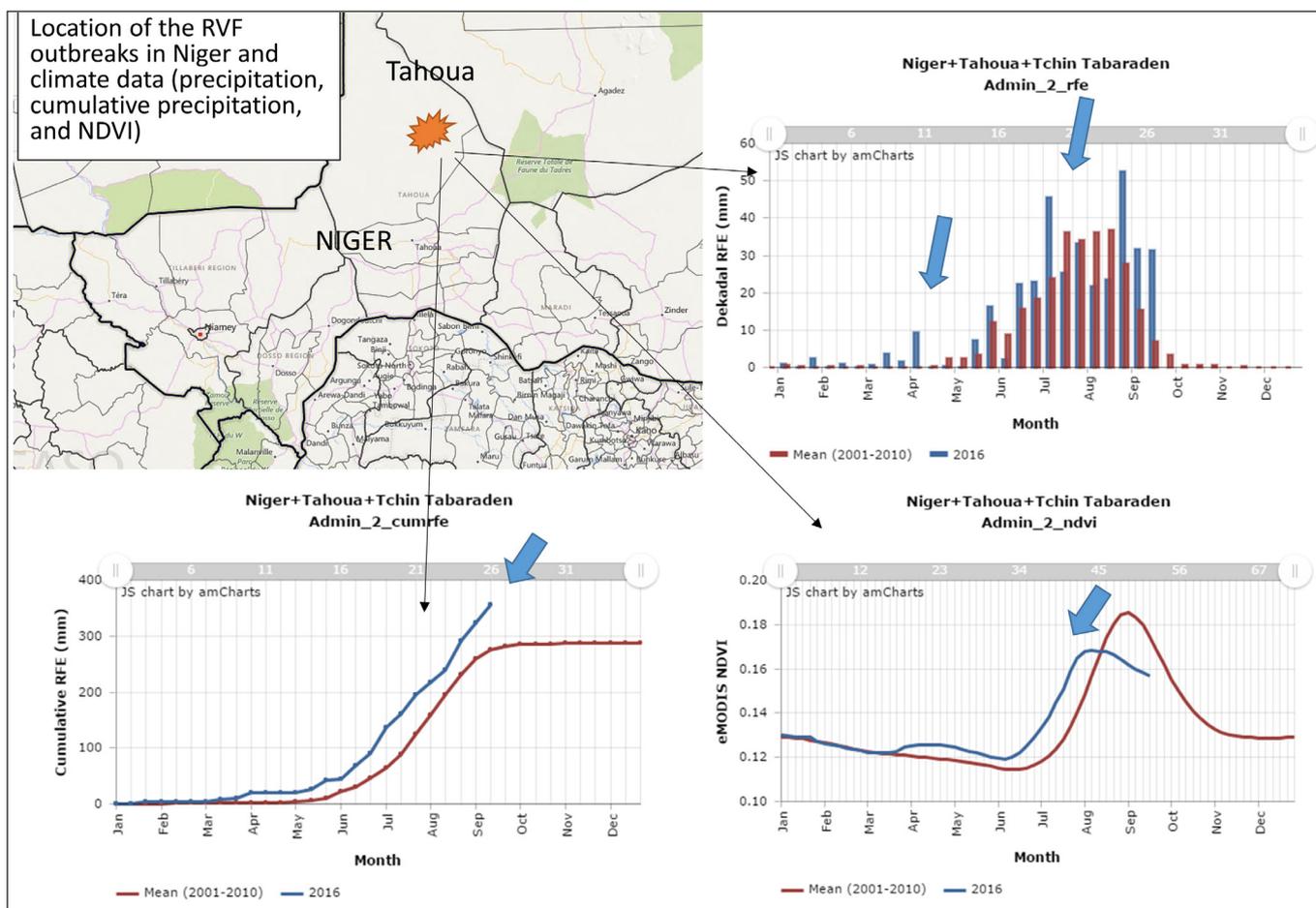


Figure 22. Map of the main transhumance routes (source: FAO, CIRAD, 2012) – Risk Assessment RVF.

Figure 23. Results of precipitation, cumulative precipitation and NDVI recorded between 2000 and 2016 in the area affected by RVF. The blue arrows in the charts indicate precipitation and NDVI anomalies during 2016 (blue) as compared to the average period (red) – Risk Assessment RVF.



weather conditions, were considered the main risk factors in RVF (re)occurring in West Africa, and spreading to unaffected areas.

close to the border with Niger. Animals were sampled from 22 to 29 October 2016, thus indicating that the infection and exposure probably occurred at the latest in August.

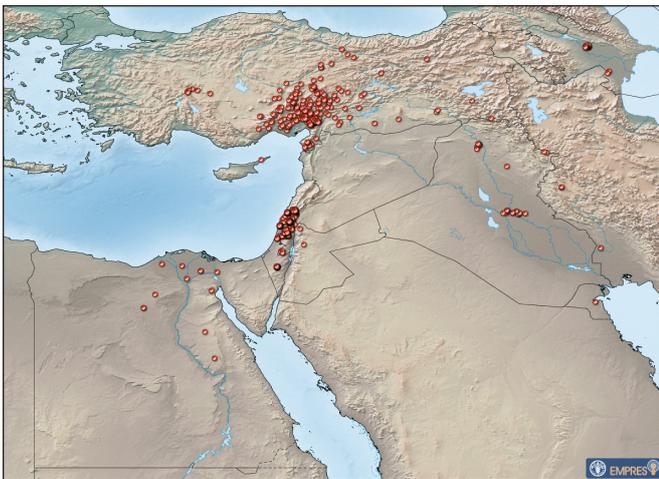
FAO's October predictions were confirmed in January 2017 with notification by Mali of the first RVF outbreak in small ruminants

Europe

Lumpy skin disease

Until 2014, lumpy skin disease was confined to the Middle East and Turkey, but then spread rapidly to Europe. The main factors behind this sudden expansion are considered the presence in the area of uncontrolled cross-border movements of animals, exacerbated by the civil war in Syrian Arab Republic. In addition, another effect of the war, the disruption of veterinary controls in the region, has facilitated the reappearance and spread of animal diseases such as LSD (Figure 24).

Figure 24. LSD outbreaks, 2010-2014



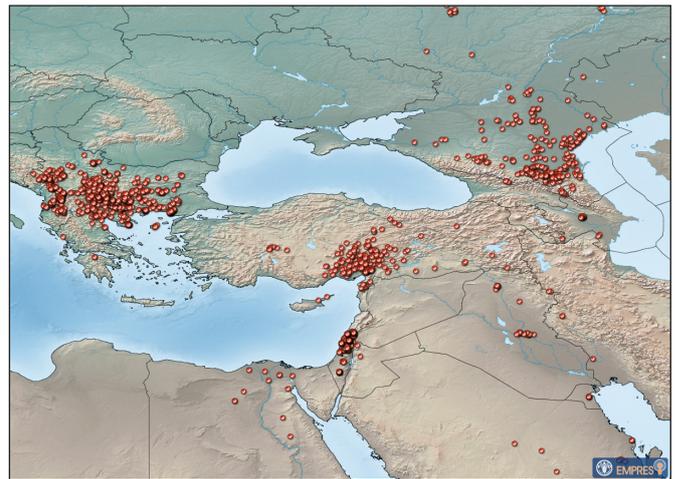
In August 2015, LSD was reported in Greece for the first time and, in 2016, it swept through southeast Europe, entering Bulgaria, Kosovo, the Former Yugoslav Republic of Macedonia, Serbia and Albania, with further outbreaks reported in the Russian Federation and Georgia (Figure 25).

With the exception of the Russian Federation and Georgia, the control policy applied centred on the vaccination of susceptible animals wherever the disease was found.

The main possible pathways for LSD introduction into free areas from affected regions in Greece are seen as movements of

infected animals and vectors. Spread of LSD in Greece was mitigated by the vaccination of susceptible animals and restrictions on animal movement in affected areas.

Figure 25. LSD outbreaks, 2010-2016



A risk assessment performed by the European Food Safety Authority concluded that vaccination had a greater impact in reducing LSD virus (LSDV) spread than stamping out herds, even considering low vaccination effectiveness (40 percent). However, independently of any stamping-out interventions, vaccination measures were considered most effective in reducing LSDV spread if protection had already been developed at the time of virus entry and was followed by vaccination after virus entry. The assessment stressed the importance of vaccinating susceptible cattle populations in regions at risk of LSDV introduction prior to any virus incursion (EFSA, 2016).

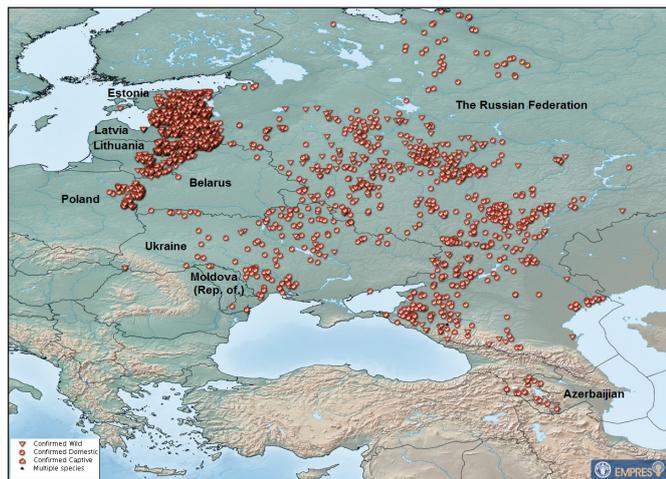
The results of the assessment supported the decision taken by Croatian veterinary authorities to preventively vaccinate the entire cattle population to minimize the risk of LSDV introduction and spread from nearby infected zones.

African swine fever

In January and February 2014, African swine fever spread across Lithuania, Poland, the Russian Federation and Ukraine. The virus then moved into Estonia in September the same year, and an incursion was reported in Republic of Moldova in September 2016 (Figure 26).

The disease is endemic in most countries of sub-Saharan Africa including Madagascar. According to the OIE, in 2016 outbreaks were reported in Burundi, Kenya and South Africa.

Regarding the situation in Eastern Europe, ASF is circulating endemically in wild boar populations, with seasonal fluctuations linked to wild boar ecology. No incursion into new countries has been observed since September 2016, although new areas were affected in Ukraine. Informal and uncontrolled animal movements, and poor biosecurity conditions in pig farms, were considered the main drivers behind the disease's entry into farms and territories.

Figure 26. ASF outbreaks, 2010-2016

In addition, the crucial role of wild boar populations in the maintenance and spread of the infection can significantly hamper eradication efforts. Strategies using conventional wild boar management approaches – bans on feeding them and targeted hunting of reproductive females – were found to become effective only over multiple generations of animals (Lange, 2015). ASF virus can survive in extreme environmental conditions in winter, especially in the carcasses of dead wild boar.

Anthrax

Anthrax spores can persist in the soil under extreme environmental and climatic conditions for long periods of time and transmit the disease when the situation is favourable. Factors associated with the activation of soil foci can be both natural (e.g. a prolonged hot, dry period preceded by heavy rains, or rains which end a long dry period, landslides, dust storms); and anthropogenic (e.g. agricultural encroachment into pastoral areas; land excavation such as irrigation, canal digging, road or house building; high livestock density, grazing and movements such as transhumance and trade). The above factors determine the contamination of the upper soil surface with spores, thus increasing the likelihood of infected soil ingestion by ruminants.

A large outbreak of anthrax was reported in Siberia (Russian Federation) in July 2016, affecting reindeer and humans. The previous outbreak reported in this region had occurred some 75 years before, in 1941. The current outbreak is suspected of being associated with climate change and the abnormally warm temperatures observed in 2016, which may have substantially reduced snow cover and permafrost in the area.

The average annual change in snow cover in the outbreak area is shown in **Figure 27**. From January to April, 100 percent of the area is generally covered by snow, which then starts melting in May and disappears around June. During the summer season, the area is generally covered by grass, becoming an important food resource for wild and domestic animals and herders. From September onward, the snow starts covering the area again and by December/January there is 100 percent cover.

However, over the past two decades substantial climatic changes have been observed in northern Siberia, including the study area. Water ice in the Arctic Ocean and snow cover in the outbreak area significantly decreased during the period 1999–2016. **Figure 28** shows the change in ice and snow cover during May 1999, 2006 and 2016, as well as July 1999, 2006 and 2016. It can be noted that snow and ice cover significantly decrease during the period. Ocean warming with a resulting decrease of ice cover in the Arctic Ocean is a main determinant of permafrost melting.

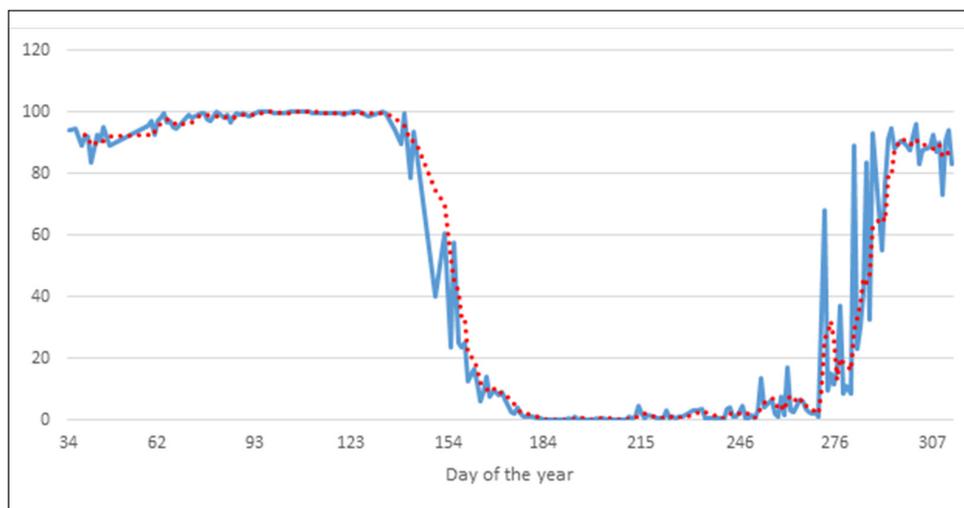


Figure 27. Mean Fractional Snow Cover (blue line) and its moving average (red dots) during the period 2001-2006 for the study area.

Figure 28. Snow Cover (white) and water ice (yellow) in 1999, 2006 and 2016 during May (upper) and July (lower). Source: NOAA. The study area is highlighted by the red circle.

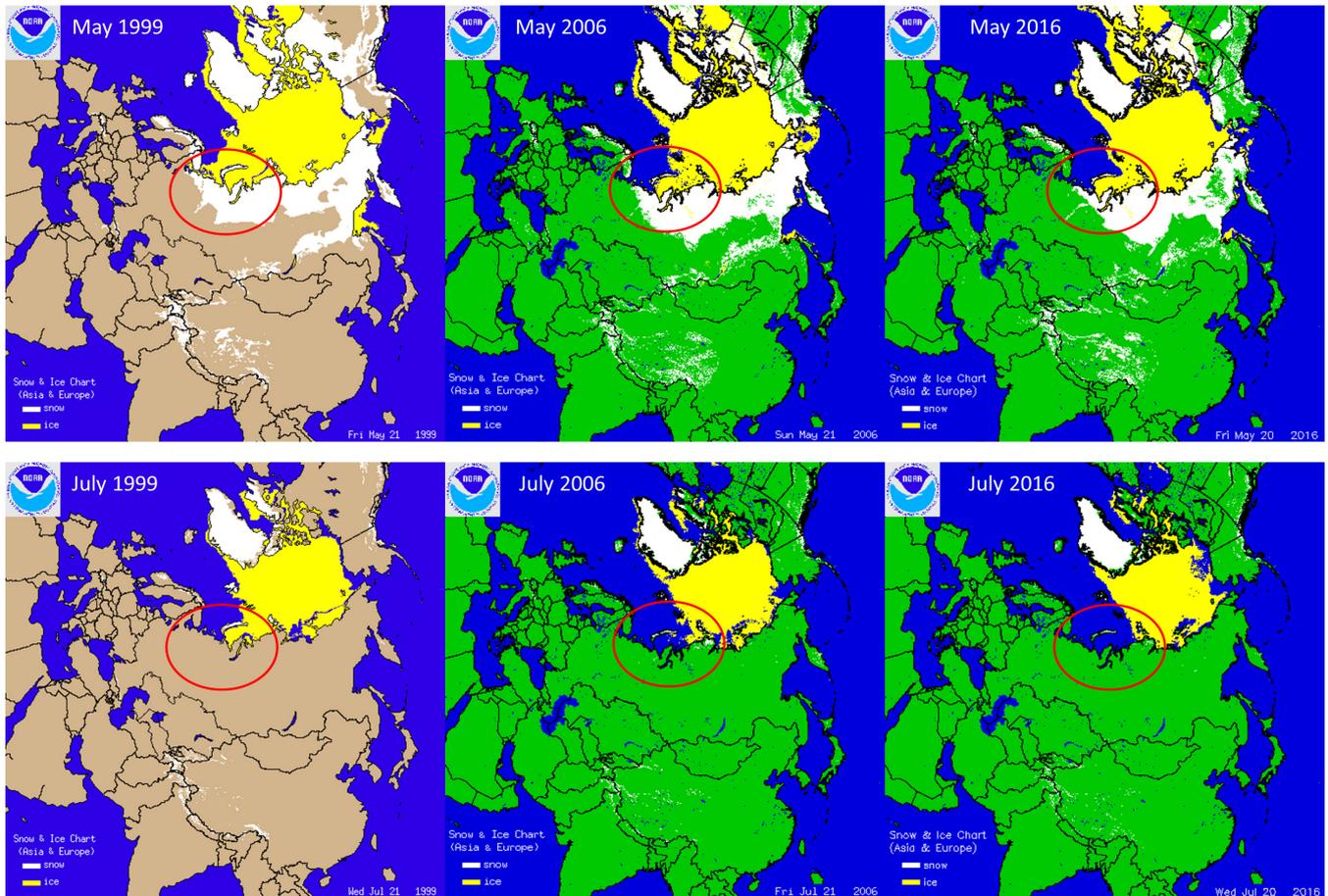
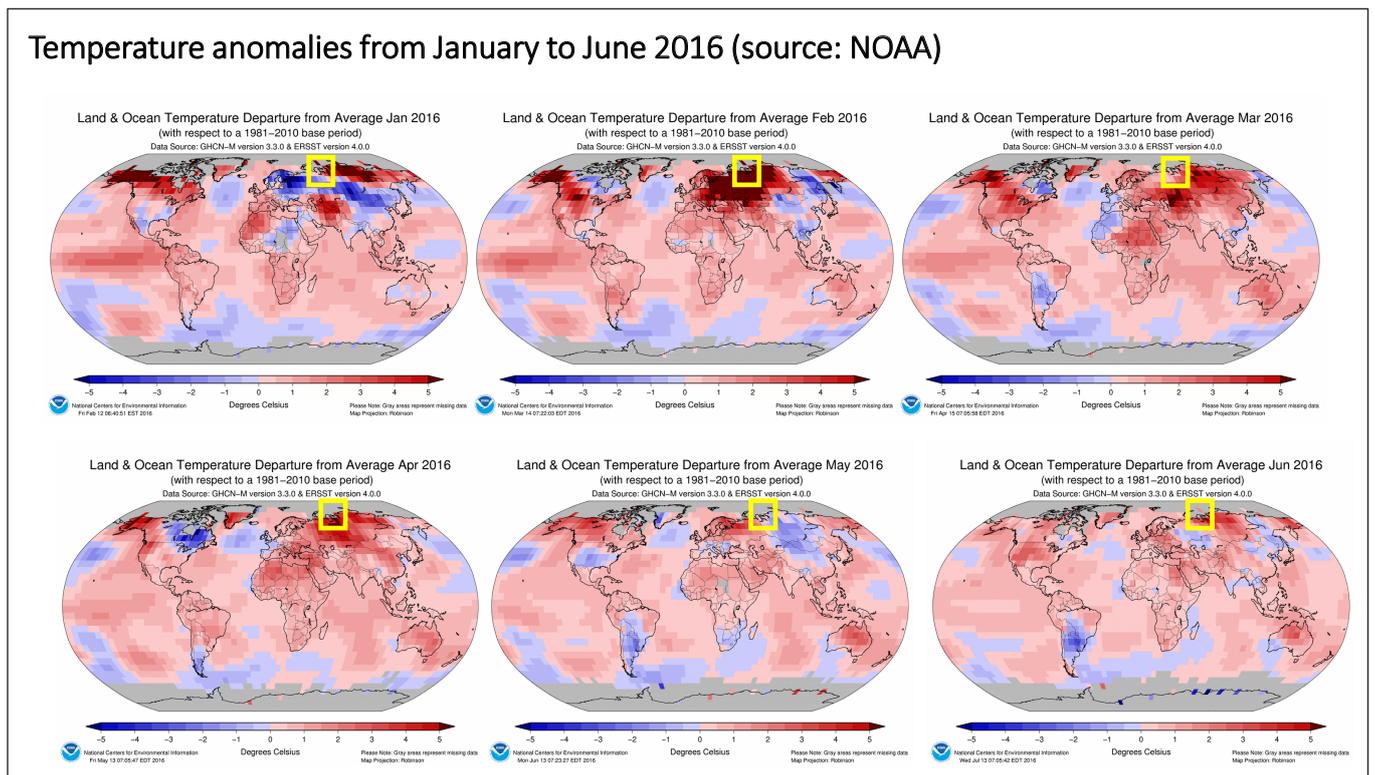


Figure 29. Global land Surface Temperature Anomalies in 2016 from January (upper left) to June (bottom right). The study area is highlighted by the yellow box.

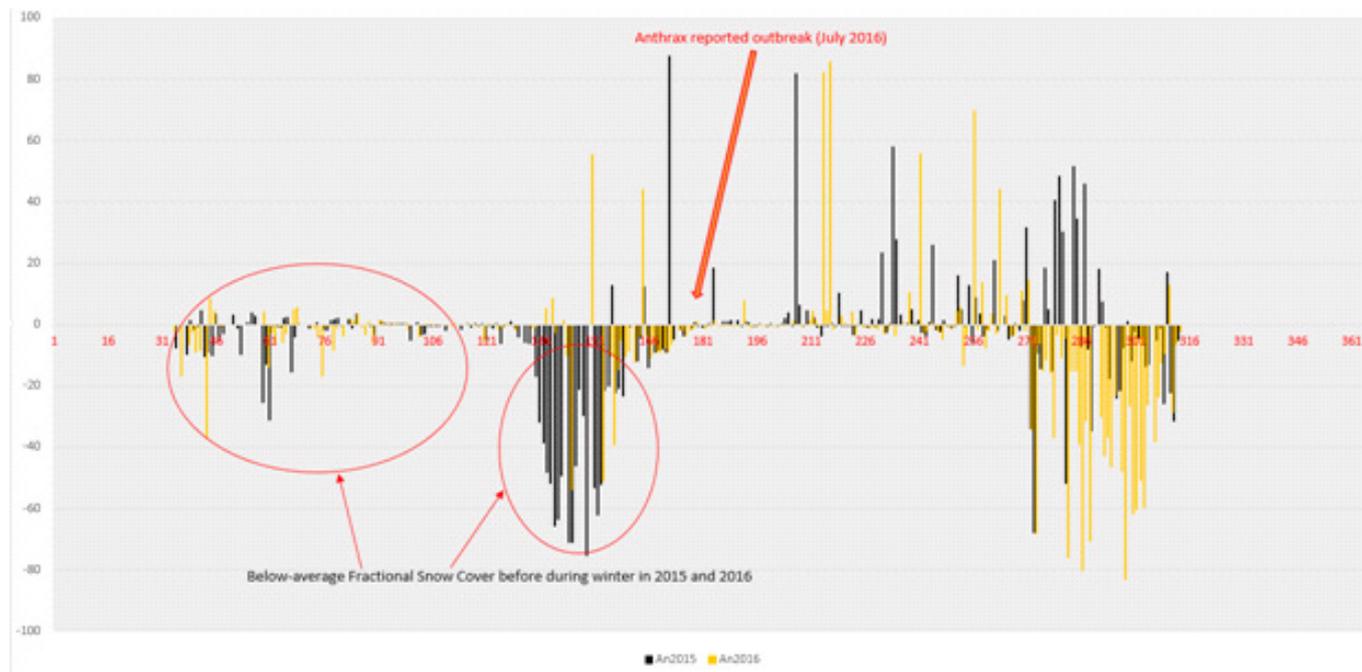


As shown in **Figure 29**, land surface temperature was well above average in the study area during the winter season of 2016, particularly in February.

FAO also analysed the daily Fractional Snow Cover (percentage of snow cover; MODIS, 500 x 500 m) from 2001 and 2016, using Google Earth Engine. The results showed that in 2015 and 2016 (years significantly influenced by strong El Niño conditions),

the snow cover during the winter season was lower than average. In particular, the melting phase started well before normal (20 days) and reached zero coverage in a relatively shorter period of time (around 10-15 days versus 30-40 days) (**Figure 30**). This may have contributed to the melting of permafrost in the study area, which could have resulted in soil disturbances bringing anthrax spores to the soil surface.

Figure 30. Fractional Snow Cover change in 2015, 2016 and average (Short Term Mean: 2001-2006).



Annex

Notified outbreaks of main emerging diseases

| SUBREGION* | ANIMAL SPECIES | DATE OF ONSET | DATE FIRST REPORTING | NO. OF OUTBREAKS ** | NO. OF INDIVIDUALS | | |
|---|------------------|---------------|----------------------|---------------------|--------------------|--------|--------|
| | | | | | AT RISK | CASES | DEATHS |
| African swine fever | | | | | | | |
| Eastern Europe | Wild boar | 01/01/2016 | 11/01/2016 | 1048 | N/D | 1706 | 1343 |
| Eastern Europe | Swine | 25/01/2016 | 29/01/2016 | 340 | 253319 | 2905 | 2215 |
| Highly pathogenic avian influenza - H5N1 | | | | | | | |
| Northern Africa | Domestic poultry | 04/01/2016 | 05/01/2016 | 157 | N/D | 177215 | 0 |
| Northern Africa | Humans | 25/02/2016 | 07/03/2016 | 10 | -- | 10 | 4 |
| Central Africa | Domestic poultry | 20/05/2016 | 24/05/2016 | 18 | 101577 | 24668 | 24668 |
| Western Africa | Domestic poultry | 02/01/2016 | 04/01/2016 | 264 | 1806326 | 274980 | 280675 |
| Western Africa | Wild birds | 02/01/2016 | 04/01/2016 | 3 | 15450 | 376 | 376 |
| Eastern Asia | Domestic poultry | 11/01/2016 | 22/01/2016 | 9 | N/D | 5880 | 5617 |
| Southern Asia | Wild birds | 19/12/2016 | 27/12/2016 | 1 | N/D | 23 | 23 |
| Southern Asia | Domestic poultry | 07/01/2016 | 19/01/2016 | 7 | 160080 | 10085 | 10085 |
| Southeastern Asia | Domestic poultry | 02/01/2016 | 02/01/2016 | 276 | N/D | 34863 | 122127 |
| Western Asia | Domestic poultry | 25/01/2016 | 25/04/2016 | 17 | 3061535 | 565448 | 565448 |
| Central Europe | Domestic poultry | 04/01/2016 | 12/01/2016 | 6 | 61050 | 1480 | 1480 |
| Highly pathogenic avian influenza - H5N6 | | | | | | | |
| Eastern Asia | Humans | 01/01/2016 | 07/01/2016 | 9 | -- | 9 | 1 |
| Eastern Asia | Wild birds | 28/10/2016 | 28/10/2016 | 8 | N/D | 10 | 3 |
| Eastern Asia | Domestic poultry | 09/01/2016 | 18/01/2016 | 95 | 1679362 | 98044 | 74247 |
| Southeastern Asia | Domestic poultry | 06/01/2016 | 11/01/2016 | 9 | 13630 | 4424 | 9773 |

* Subregion as defined by the UN Statistical Division (<https://unstats.un.org/unsd/methodology/m49/>)

** Number of individual cases for humans

Source: OIE WAHIS

(cont.)

| SUBREGION* | ANIMAL SPECIES | DATE OF ONSET | DATE FIRST REPORTING | NO. OF OUTBREAKS** | NO. OF INDIVIDUALS | | |
|---|------------------|---------------|----------------------|--------------------|--------------------|--------|--------|
| | | | | | AT RISK | CASES | DEATHS |
| Highly pathogenic avian influenza - H5N8 | | | | | | | |
| Northern Africa | Wild birds | 24/11/2016 | 30/11/2016 | 2 | N/D | 32 | 32 |
| Northern Africa | Domestic poultry | 29/12/2016 | 02/01/2017 | 1 | 190 | 89 | 60 |
| Western Africa | Domestic poultry | 19/11/2016 | 17/12/2016 | 1 | 250 | 15 | 15 |
| Eastern Asia | Wild birds | 12/12/2016 | 19/12/2016 | 3 | N/D | 21 | 21 |
| Eastern Asia | Domestic poultry | 30/01/2016 | 22/02/2016 | 20 | 44500 | 12610 | 12648 |
| Southern Asia | Wild birds | 14/10/2016 | 19/01/2017 | 9 | N/D | 204 | 204 |
| Southern Asia | Domestic poultry | nd | 19/10/2016 | 36 | 1447986 | 249938 | 75328 |
| Western Asia | Wild birds | 24/12/2016 | 25/12/2016 | 10 | N/D | 18 | 18 |
| Western Asia | Domestic poultry | 09/11/2016 | 13/11/2016 | 13 | 198900 | 26800 | 21100 |
| Eastern Europe | Wild birds | 09/06/2016 | 17/06/2016 | 17 | N/D | 55 | 37 |
| Eastern Europe | Domestic poultry | Unknown | 18/11/2016 | 268 | 2676988 | 224057 | 44416 |
| Northern Europe | Wild birds | 30/12/2016 | 09/01/2017 | 71 | N/D | 125 | 114 |
| Northern Europe | Domestic poultry | 19/11/2016 | 21/11/2016 | 7 | 153282 | 42265 | 480 |
| Southern Europe | Wild birds | 30/10/2016 | 10/11/2016 | 11 | N/D | 32 | 31 |
| Southern Europe | Domestic poultry | 10/12/2016 | 15/12/2016 | 4 | 278 | 21 | 16 |
| Western Europe | Wild birds | nd | 11/11/2016 | 229 | N/D | 867 | 866 |
| Western Europe | Domestic poultry | nd | 18/11/2016 | 139 | 927497 | 53796 | 20009 |
| Lumpy skin disease | | | | | | | |
| Eastern Europe | Cattle | 14/04/2016 | 14/04/2016 | 448 | 138509 | 7023 | 319 |
| Southern Europe | Cattle | 04/04/2016 | 15/04/2016 | 792 | 14765 | 1370 | 104 |
| Rift Valley fever | | | | | | | |
| Western Africa | Humans | nd | 30/08/2016 | 384 | -- | 384 | 33 |

* Subregion as defined by the UN Statistical Division (<https://unstats.un.org/unsd/methodology/m49/>)

** Number of individual cases for humans

Source: OIE WAHIS

Number of countries declaring the presence of emerging zoonotic and livestock diseases in the first semester of 2016

| Subregion | African swine fever | Lumpy skin disease | Peste des petits ruminants | Rift Valley fever |
|---------------------|---------------------|--------------------|----------------------------|-------------------|
| Western Asia | | 5 | 5 | |
| Central Asia | | 1 | | |
| Southern Asia | | 1 | 4 | |
| Total Asia | 0 | 7 | 9 | 0 |
| Northern Africa | | 1 | 3 | |
| Middle Africa | 4 | 2 | 3 | |
| Western Africa | 6 | 6 | 10 | 4 |
| Eastern Africa | 4 | 9 | 6 | 2 |
| Southern Africa | 2 | 4 | | |
| Total Africa | 16 | 22 | 22 | 6 |
| Eastern Europe | 4 | 2 | | |
| Northern Europe | 3 | | | |
| Southern Europe | 1 | 2 | | |
| Total Europe | 8 | 4 | 0 | 0 |

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