

Livestock production dynamics, bird migration cycles, and the emergence of highly pathogenic avian influenza in East and Southeast Asia

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1.1 Introduction

The emergence of highly pathogenic avian influenza (HPAI) in Southeast Asia and its spread through the Eurasian continent has dramatic consequences. Direct impact in the affected countries includes disease and mortality of humans, poultry and wild birds infected by the H5N1 virus, disease control culls, and the interruption of local and international trade of poultry and poultry products, as well as the potential disruption of travel to and from affected countries. HPAI outbreaks have resulted in the death of 86 people (as of 2nd February 2006) (WHO 2006), and nearly 140 million domestic poultry have been destroyed most of which have been village level or backyard poultry, *i.e.* the subsector consisting of smallholder producers which are among the poorest strata in the rural societies (FAO 2005). A further concern is that the widespread circulation of the avian flu virus increases the chances of mutation into a form that could pass from human to human, which could result in a new human flu pandemic of unknown magnitude (Ferguson *et al.* 2004).

The extent of the current epidemic has no known precedent, as most previous primary outbreaks in poultry had relatively restricted distributions, and in the worst case, were contained within 1-3 years (Empres 2004). However, in contrast to several earlier unexpected epidemics, the gradual emergence of viruses of the type H5N1 in poultry populations in China has been well documented, at least in terms of virology (Cauthen *et al.* 2000; Li *et al.* 2004). These studies demonstrate that, following a phase of genetic diversification of H5N1 subtypes during 1999-2002, genotype Z emerged in 2002, and outperformed all other subtypes to cause the epidemic that started in 2004 (Li *et al.* 2004).

Disease emergence can generally be viewed as an evolutionary response to environmental changes, which may be related to anthropogenic factors such as changes in agricultural practices, urbanisation, climate change or globalisation (Daszak *et al.* 2001; Morse 1995; Schrag and Wiener 1995). For emerging diseases of livestock, changes in food preferences and agricultural practices are usually important factors determining the conditions in which zoonotic pathogens may evolve, spread, and eventually enter the human population (Webster 1998). Identifying the processes underlying the transformation of livestock production and its intensification are central to an understanding of the forces affecting livestock disease emergence (Slingenbergh *et al.* 2004).

Here, we aim to describe the agro-ecological conditions in which the virus H5N1 genotype Z emerged and spread in Asia, in an attempt to better identify the driving factors.

1.2 The natural ecology of avian influenza viruses

Our current understanding of the HPAI virus history is that a low pathogenic avian influenza (LPAI) is transferred from the wild bird genetic pool to domestic poultry, gains pathogenicity through a series of infection cycles until it becomes highly pathogenic (Alexander 2000). Wild birds are recognised as the natural reservoir of influenza A viruses, in particular avian influenza viruses (AI), and LPAI viruses have been recorded in most bird families (Stallknecht and Shane 1988). However, the prevalence and diversity of LPAI subtypes is not evenly distributed among bird families. Although LPAI viruses have been isolated in 12 bird orders, the large majority of isolations were reported in the orders Anseriformes (in particular in the family Anatidae: ducks, swans and geese) and Charadriiformes (shorebirds and relatives). Whilst a wide variety of LPAI virus subtypes have been sampled from Charadriiformes, sometimes with substantial prevalence (EFSA 2005; Stallknecht and Shane 1988), it is believed that they belong to a somewhat different genetic pool from those sampled in Anseriformes (Kawaoka *et al.* 1988).

It is generally assumed that species from the Anatidae family, and in particular the Anatinae sub-family (Delogu *et al.* 2003; Gilchrist 2005), represent a higher risk of transmission to domestic poultry because i) Anatidae harbour the highest diversity and prevalence of avian influenza viruses (EFSA 2005; Stallknecht and Shane 1988), ii) historical outbreaks of HPAI in poultry have been linked to LPAI strains circulating in ducks (e.g. Campitelli *et al.* 2004; Munster *et al.* 2005), iii) domestic ducks have shown to be able to excrete large amount of H5N1 virus while remaining relatively healthy (Hulse-Post *et al.* 2005), and iv) direct contacts especially between wild Anatidae and domestic wildfowl are believed to be more common than with other wild bird groups (Tracey *et al.* 2004).

Waterfowl migration cycles are a particularly important aspect of LPAI ecology because the persistence of LPAI viruses and its seasonal prevalence rely largely on the existence of immunologically naïve young birds. Siberia, and in particular the West Siberian Lowland (WSL; by far the largest wetland in the world, 2,745,000 km²), is the breeding area of many different migratory Anatidae species in the Palaearctic, where birds arrive during springtime, following different routes from Europe, Asia, and to a lesser extent for Anatidae, Africa (Fig. 1). The breeding season in these northern most regions of Eurasia is usually very brief, and migratory bird populations start migrating southward with their new-born juveniles to escape the first frosts in early autumn.

This results in the build up of pre-migration concentrations of many species of waterfowl in the south of the breeding areas, where maturation and moulting take place before the main southern migration actually starts. This is a critical stage in the LPAI virus transmission and redistribution process because the large concentrations of potential hosts increases the contact frequency and virus transmission between immunologically naïve individuals, which may undergo several subsequent infection episodes, shedding large quantities of the virus in their faeces, which in turn may infect other individuals (Halvorson *et al.* 1985; Stallknecht and Shane 1988). During the ensuing southern migration LPAI virus infection then declines as result of increased flock immunity and the dispersion of populations.

The possible persistence of AI viruses in cold water (Stallknecht *et al.* 1990) in the Arctic region and the transmission within populations during pre-migration concentrations is thus believed to lead to the large-scale redistribution of AI viruses along the different migration paths during these autumn migrations (Fig. 1). Furthermore, as the autumn migration involves juveniles, it is characterised by short flights and several stop-over sites along the way, which enhances the risk of AI virus transmission, when compared to the spring migration that involves much longer distance flights. There is thus a strong seasonality, both in the prevalence of LPAI viruses in the wild bird populations, and in the timing of the high risk period in a given location, which depends on its latitude position in relation to the migration routes.

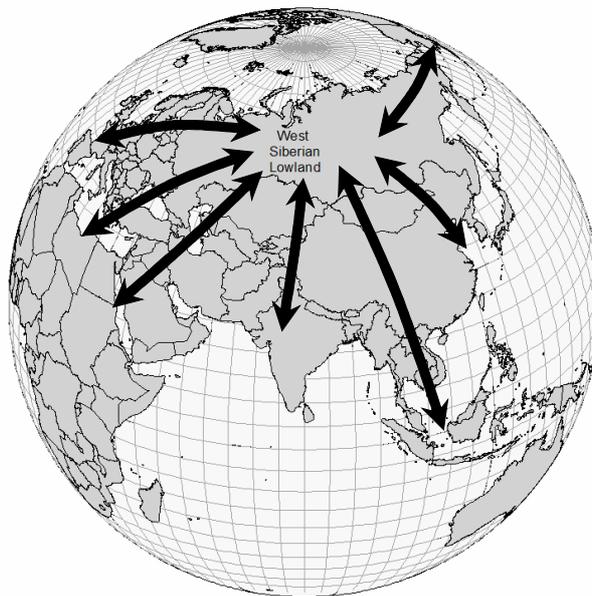


Fig. 1 Distribution of the main migratory flyways connected to breeding areas in Siberia for Anatidae species (the arrows are indicative of broad-scale direction of the flyways, not their actual distribution or extent).

Waterfowl migration routes are not fixed. Firstly, there are ample variations in migratory behaviour among Anatidae species, and even within populations. In general terms, the proportion of migratory species and the extent of migratory behaviour depend on the climatic conditions. In areas with harsh, cold climates most bird species migrate during the autumn to escape the frost. Areas further south, with more temperate or subtropical climates, show a proportionally higher number of resident species. This translates into a range of migratory behaviour of Anatidae (Newton and Dale 1997), from completely migratory species having distinct winter and summer habitats and undertaking long-distance migration (e.g. the smew *Mergus albellus*) to sedentary species resident in similar latitudes and moving comparatively short distances according to feed availability and/or regional climatic variations (e.g. the marbled teal *Marmaronetta angustirostris*). The intermediate situation is represented by partially migrating species, with a fraction of the population resident year-round at intermediate latitudes and another part of the

population migrating from north to south (e.g. the mallard *Anas platyrhynchos*). Secondly, though the distribution of bird populations during their migration and wintering is predictable at the broad scale (*i.e.* regular use of the “good” wetland habitats which are relatively static), it is highly dynamic at the finer scale. Local food availability, climate, or even changes in hunting patterns may affect the detailed distribution of populations, even within relatively short time frame.

In summary, consistent and reliable data demonstrate a circulation of AI viruses in the waterfowl reservoir, in particular Anatidae, which forms a coherent independent disease circulation system, with strong geographical seasonality linked to migratory patterns and variations in flock immunity. However, the diversity of migratory behaviour, the dynamic nature of bird distribution, and the variety of AI subtypes comprise a very complex and challenging epidemiological setting.

The waterfowl LPAI system is largely separated from the domestic poultry production systems, but historical outbreaks suggest the existence of scarce contact points in space and time between the two. These contact point allow introduction of LPAI into domestic poultry, and conversely occasional spill-over of HPAI into wild birds. During the H5N1 HPAI epidemic, both direct evidence, such as outbreaks in wild waterfowl, and indirect evidence, such as the general pattern of continental disease spread, strongly suggested that the wild bird and domestic poultry systems were in more frequent and closer contact than previously thought. Whilst it has long been recognised that the wild waterfowl system provides the genetic pool for most, if not all, HPAI virus emergence, this is the first time, that they are thought to have directly taken part in the spread of HPAI (rather than LPAI), though this remains a matter of considerable debate.

Whatever their role in the initial introduction of LPAI into domestic poultry production systems, or in the spread of the current H5N1 HPAI epidemic, wild birds probably played a minor role in the evolution processes that lead to the emergence of the HPAI H5N1 genotype Z in domestic poultry in Southern China, the origin of which is more likely to be found in changes in poultry production dynamics that have taken place in the region over the last two decades.

1.3 Livestock production dynamics in East and Southeast Asia

The persistence and emergence of infectious diseases depends largely on the size (Anderson and May 1991) and connectivity (Keeling 1999; May *et al.* 2001) of their host population. For ruminant livestock grazing in the open, this framework can be translated into a network of farms where connectivity is quantified by farm-to-adjacent-farm contagion and long-distance spread of the disease through animal movements (Gilbert *et al.* 2005). By contrast, monogastric animals (pigs and poultry) can be raised in enclosed, intensive or even industrial type units almost completely isolated from the outside world by strict biosecurity measures that largely exclude diseases borne by wind, insects or rodents, and also reduce the chance of infection from newly introduced animals or human visitors. On the other hand, the opportunities for transmission within such units are likely to be very high, because of the crowded conditions in which the animals are often kept. Production intensification is thus an important complementary epidemiological variable as it determines the degree of isolation of the animals from the outside world, the investment in disease control, and the level of animals’ susceptibility. In essence, the

chance of a disease spreading into an intensive production unit is minimised by its isolation, but once established, spread is likely to be very rapid.

In most OECD countries, intensification of the livestock sector has been a gradual process involving the majority of production units simultaneously (Slingenbergh *et al.* 2002). In developing countries, particularly in Asia, intensification occurs through the rapid establishment of specialised or industrial units around cities, in landscapes shared with high densities of smallholder producers raising animals in the open. Despite the very large number of individuals raised in industrial production units, they do not add substantially to the connectivity of the susceptible population because the possible microbial traffic to and from them is reduced to almost zero. At the other end of the production intensification spectrum, extensive systems are permanently exposed to prevailing disease agents, and thus contribute substantially to the susceptible connectivity, despite relatively low numbers of animals per unit. The highest risk of disease impact is to be expected where both types of production systems co-exist: extensive systems allowing virus circulation and persistence alongside large numbers of susceptible animals raised in specialised farms are likely to promote disease evolution (*e.g.* from LPAI to HPAI) and outbreaks. A key indicator of risk is thus to assess whether intensification results in an overall reduction of smallholders, or occurs in the context of an ever-increasing number of smallholders. If the latter, extensive units maintain virus circulation while the (semi-)intensive units may act both as local amplifier and as source of secondary spread through long distance jumps resulting from the trade and traffic associated with commercial broiler chains.

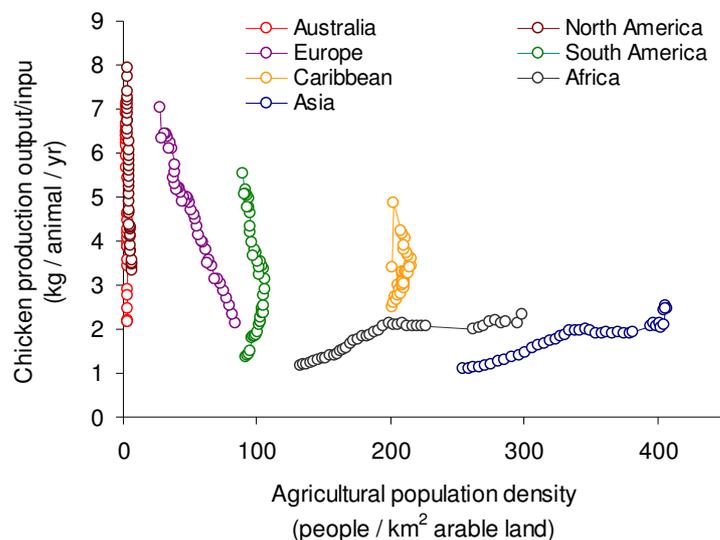


Figure 2. Changes in poultry meat production output/input and agricultural population density from 1961 to 2001, grouped by continent (FAO 2006).

The intensification of the poultry industry, including broiler production, entails raising productivity levels or output-input ratios, which are available as country level statistics (FAO 2006) (OI; kg chicken meat / parent stock animal / year). Continental trajectories of agricultural intensification for the 1961-2001 period can be illustrated in bi-variate

plots of consecutive annual values of agricultural human population density (Agpd) and chicken meat productivity level (Fig. 2). North-America and Australia have had a low and stable Agpd in 1961, since when they have steadily increased their productivity. This process may soon approach its physiological limits and impose a ceiling on output-input ratio. Europe, the Carribean and South-America have reduced their Agpd but increased intensification levels; whilst in Asia and Africa there have been very significant increases in Agpd with a relatively small rise in productivity. Though currently higher in Asia than in Africa, projections for Asia, unlike Africa, are that the density of agricultural people will start to decline in the decades ahead (Bruisma 2003). The trajectories along the intensification axis with a low (North-America, Australia) or decreasing (Europe, South America) agricultural population density are epidemiologically low risk, as extensive units openly exposed to pathogens are gradually replaced by more bio-secure production units, and the two types of system largely cease to coexist. In contrast, increases in productivity alongside increases in agricultural population density as currently observed in Asia can be associated to a higher risk of disease persistence and spread. Within East and Southeast Asia, the consistent continental patterns are not found in individual countries which show very diverse trajectories. The relatively low-risk transition which involves productivity increases alongside falls in agricultural population density is found only in Japan, South Korea and, to a lesser extent, Malaysia. Apart from Mongolia, where it has stayed unchanged, agricultural population density has increased in all other countries, alongside marked (Thailand, Myanmar, Philippines) or somewhat lesser productivity increases (Cambodia, Viet Nam, North Korea, China). These historical trends of intensification and smallholder density indicators suggest that, in several countries, continuing increases in human population and structural changes of the poultry production sector may have led to epidemiologically unstable paths of development which may enhance the chances of zoonotic disease emergence.

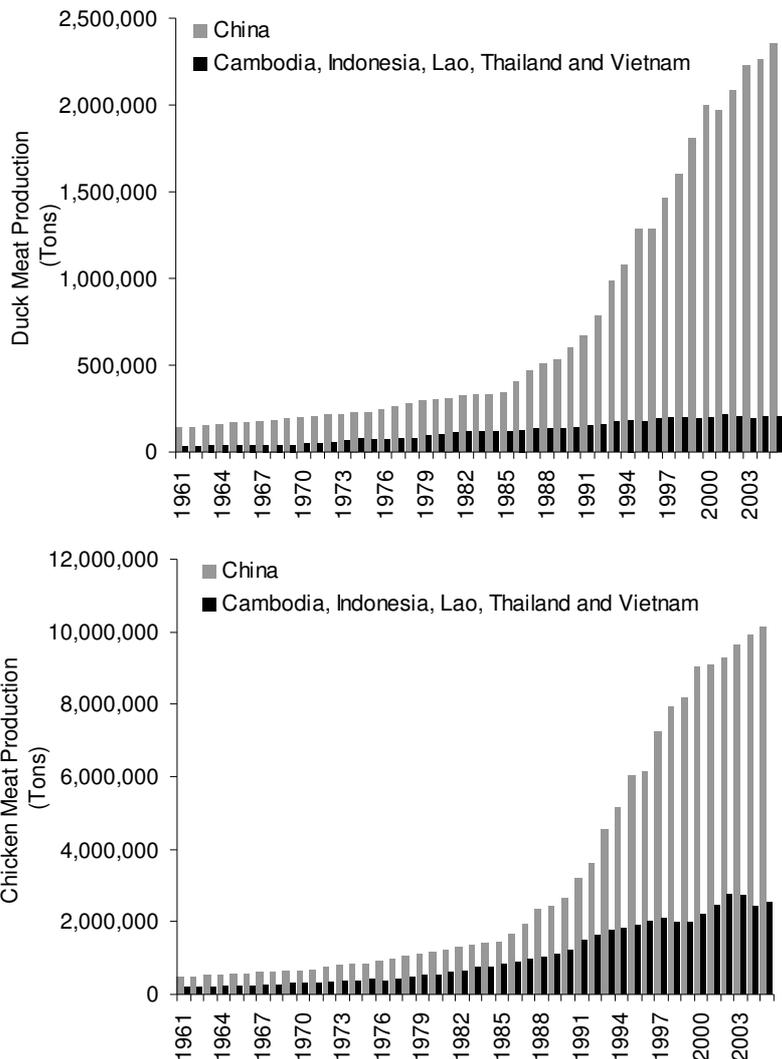


Fig. 3 Increase in Duck and Chicken meat production 1961-2005 (FAO 2006)

These variations in intensification patterns, which may have played a very significant role in the encroachment of HPAI in Asia, should not hide the fact that the major regional shift in terms of absolute levels of poultry production took place in China during the last 20 years (Fig. 3). The rise of production in China by far exceeds that of Cambodia, Indonesia, Lao, Thailand and Vietnam combined. In particular, the production of chicken and duck meat in China has increased by a factor of 6.9 and 6.8 respectively between 1985 and 2005. In comparison, the production of chicken and duck meat has multiplied only by 3.0 and 1.7 in the Mekong countries, Indonesia and Thailand during the same period. In Thailand, where the intensification of the poultry production has the fastest, chicken meat production has risen by a factor of 2.4 whilst duck meat production remained at a relatively low level of approximately 100,000 tons per year. It is thus clearly in China that the major shift in poultry production has taken place, with an unprecedented rapid rise in chicken and duck meat production, and where the highly pathogenic H5N1 subtype Z emerged since the late nineties (Li *et al.* 2004).

1.4 The agro-ecology of duck production: a key to understanding HPAI emergence, spread and persistence ?

Domesticated ducks are a key to understanding LPAI/HPAI transitions because they form the epidemiological link between the wild bird system and the poultry production systems. Firstly, ducks are the domestic poultry species most closely related to the wildfowl reservoir in immunological terms, and are thus the most prone to develop unnoticed sub-clinical LPAI infections. Secondly, they also constitute the domestic poultry species most often in contact with the wild fauna. Indeed, the typical agro-ecological setting of extensive duck meat and egg production implies free ranging flocks feeding in natural or irrigated wetlands or water bodies. These areas are also the natural habitat of many wildfowl species, where AI virus transmission can easily take place through water contamination. Thirdly, domestic ducks come into contact with the free ranging or backyard terrestrial poultry population on which HPAI has a much more deadly impact, and may spread rapidly to the more intensively reared birds, and onward through trade.

These two observations are well substantiated by field data on the persistence and spread of the HPAI H5N1 virus. Domestic ducks play an important and silent role in the persistence and spread of HPAI, as they can remain relatively healthy whilst excreting sufficient amounts of H5N1 virus to sustain transmission (Hulse-Post *et al.* 2005). Geospatial analysis of HPAI outbreak in Thailand (Fig. 4) corroborates these laboratory findings by demonstrating that the spatial distribution of HPAI outbreaks in chickens and ducks is strongly associated with that of free-grazing ducks (Gilbert *et al.* 2006). Free-grazing duck husbandry in Thailand and other Southeast Asian countries occurs extensively in the rural areas where multiple cropping in a year predominates (Gilbert 2005). Southeast Asia has a monsoon climate with distinct dry (autumn/winter) and wet (spring/summer) seasons. In order to meet the needs of an increasing population for food and fibre, irrigation infrastructure has been constructed to make it possible to cultivate second and/or third crops in the dry season (mostly in autumn/winter months). Multiple-cropping agricultural systems also provide essential food sources for large flocks of free-grazing ducks that move frequently from one harvested field to next, to feed on leftover rice grains, insects and snails as part of an integrated pest management strategy (*e.g.* Teo 2001). In other words, agricultural land use intensification (irrigated multiple cropping) provides new food resources and expanded habitats for domestic duck to contact and potentially be infected by migratory wildfowl during the autumn and winter. The significance of ducks in the persistence of HPAI is also suggested by the course of events in Cambodia and Laos. HPAI was quickly eradicated from these countries, where, like Vietnam, there is a dominance of small extensive chicken production units and backyard poultry), but there are much less large wetland with intensive rice production areas that support large domestic duck populations as there are in Thailand and Vietnam, where the disease tended to persist.

With domestic ducks being so central to the epidemiology of HPAI, the sharp rise of duck production in China is probably one major triggers that has promoted the evolution of H5N1 genotype Z in Southern China. In 2004, China reported that there were 9 avian influenza vaccine production plants in the country, and it seems probable they have been used to confront the influenza problem in poultry since the early nineties,

at the beginning of the sharp rise in poultry production (Fig. 3). However, avian influenza vaccines are much less effective in ducks than they are in chickens, and do not prevent the ducks from excreting viruses. It is tempting to speculate that these conditions may have contributed to the evolution of H5N1 genotypes to escape the pressure of vaccination, until a successful genotype candidate, initially very pathogenic also to ducks, emerged in 2002.

1.5 Remote sensing and environmental correlates of HPAI persistence and spread.

As mentioned previously, there is strong evidence that the persistence of HPAI in Asia relates to the free-grazing duck husbandry, which is associated with a number of factors that are amenable to assessment using remote sensing techniques, including rice production cycles, natural wetland distributions and temperature.

The spatial distribution and timing of duck and crop production in the autumn/winter seasons vary substantially in Southeast Asia, as it is affected by changes in the length and timing (starting and ending dates) of the dry season as well as by the location of markets and infrastructure and by the prevailing policy context. To date, risk assessments are largely based on agricultural census data that are often out-of-date and at coarse spatial resolution (e.g., at national or provincial levels) and temporal resolution (e.g., at annual scale). In recent years, however, substantial progress has been made in both satellite sensor capability and data analysis methods. For example, it is now possible to map and monitor paddy rice agriculture (Xiao *et al.* 2006; Xiao *et al.* 2005) and cropping intensity (Fig. 4) in Asia, using satellite images from the Moderate Resolution Imaging Spectroradiometer (MODIS) sensor onboard the NASA Terra satellite. The satellite-based algorithms can map and monitor crop intensity, crop calendar (planting and harvesting dates) and irrigation at fine spatial resolution (250-m to 500-m) in near-real time fashion, and the resultant geospatial datasets can therefore be used to assess where year-round availability of harvested rice fields may sustain free-grazing duck husbandry.

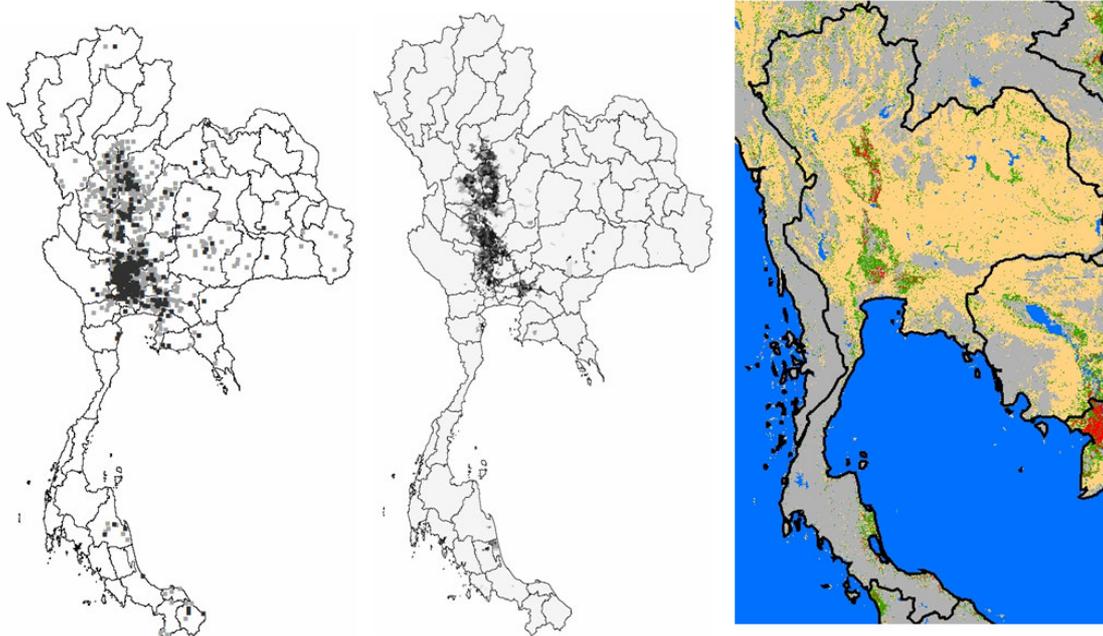


Fig. 4 Distribution of HPAI outbreaks (left; grey chicken outbreaks, dark grey duck outbreaks), free-grazing duck density (centre), and rice crop cultivation (yellow: one crop; green: 2 crops; red: three crops). Data derived from Gilbert *et al.* (2006) and Xiao *et al.* (2006).

The distribution of natural wetlands is also of critical importance as they represent potential contact points between wildfowl and aquatic domestic poultry. However, the spatial distribution of wetlands in Southeast Asia is strongly affected by the monsoon, *e.g.* some lakes like Tonle Sap Lake in Cambodia may seasonally double in surface area. Identifying the risk resulting from the overlap between water bird habitats and domestic poultry therefore requires mapping the distributions of both perennial and seasonal wetland distributions and capturing the period during which transient wetlands are flooded. Several studies have used satellite images to map wetland distribution at 1-km spatial resolution, *e.g.*, IGBP DIScover, GLC2000 and MODIS Land datasets (Friedl *et al.* 2006; Loveland and Belward 1997), but these algorithms are not well evaluated. A comprehensive Global Lakes and Wetlands Database (GLWD) was recently compiled and released (Lehner and Doll 2004), based on a number of global and regional databases and maps; the level-3 product is a 30-arcsecond resolution map of large and small lakes, reservoirs, rivers and wetlands. Human activity in Southeast Asia has created a large number of small water bodies for aquaculture (*e.g.*, fish and shrimp ponds), and there is a need to develop an updated dataset of wetlands at finer spatial resolution with additional information on seasonality of wetlands.

The seasonality in temperature distribution is a third important factor, as it affects the survival rate of AI virus in water bodies (Stallknecht *et al.* 1990), and is an important factor triggering waterfowl autumn migrations. Temperature is routinely monitored by a range of satellite sensors, and there are well established procedures for quantifying spatial, temporal and seasonal aspects of temperature at a range of resolutions, which could readily be incorporated into HPAI risk models.

1.6 Toward a better understanding of the wild birds / domestic poultry interface

As briefly discussed in the introduction to this book, transition phases involving major shifts in human and/or animal population number and structure have always resulted in epidemiologically instability, leading to the emergence and spread of new infectious diseases. The more we investigate infectious disease problem, the more we learn about the conditions favouring similar events. The rapid shift in poultry production in China most probably triggered the HPAI situation we face today, and we may yet discover novel extents of the H5N1 outbreak. We are still far from understanding the complex interplay between natural and anthropogenic factors that has contributed to the emergence, spread and persistence of H5N1 virus, but we are progressing. It is the authors' belief that the key to further progress lies at the interface between the natural history of AI viruses in wild waterfowl, and evolutionary forces taking place in the agricultural setting. Only a multi-disciplinary approach can adequately address these challenging issues.

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