



June 2007

## Industrial Livestock Production and Global Health Risks

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### 1. Abstract

Because of human and livestock population growth, changes in livestock production, the emergence of worldwide agro-food networks, and significant changes in personal mobility, human populations increasingly share a global commons of disease risk, among themselves and with domestic and wild animal species. To elucidate the linkage between livestock production and global public health, this paper draws upon recent experiences provided by different influenza A virus (IAV) incursions into domestic livestock populations, the most notable one being the ongoing HPAI H5N1 epidemic that originated in Asia, which now also affects Africa and which has led to outbreaks in the Near East and in Europe.

Livestock production has significantly changed over the past decades with industrial systems and their associated value chains being dominant in developed countries and becoming increasingly important in developing countries where traditional livestock production still provides an important source of income for a large share of the population. Industrial systems are characterized by large numbers of animals of similar genotype being raised, predominantly in confinement, for one purpose with rapid population turnover at a single site. This paper provides evidence suggesting that without commensurate private and public investments in bioexclusion and biocontainment measures these industrial systems can result in increased animal and public health risks.

Risks to animal and public health arising from livestock production are a local and global externality that may not be properly reflected in the costs of production and the authors argue that more equitable distribution of these costs requires well informed public intervention to shape

private incentives for the implementation of biosecurity so that livestock production aligns with public health interests.

## 2. Introduction

Recent emergence of contagious human diseases from animal populations, such as Nipah virus infection in 1999, SARS in 2002 and the current epidemic of highly pathogenic avian influenza (HPAI) caused by H5N1, from which nearly 200 people have died since 2004, have heightened public awareness of possible linkages between wild animal populations, livestock production and global public health. Because of human and livestock population growth, changes in livestock production, the emergence of worldwide agro-food networks, wild animal trade, and significant changes in personal mobility, human populations increasingly share a global commons of disease risk, among themselves and with other animal species.

It is, therefore, not surprising that three out of four emerging pathogens affecting humans over the past ten years have originated from animals or animal products (Taylor *et al.*, 2001). HPAI offers a recent example of how a new viral challenge has possibly emerged from wildlife, by first adapting to domestic livestock and then circulating within these populations with the risk of acquiring the ability to infect humans and of sustained human-to-human transmissibility. The case of HPAI also highlights how conditions of animal husbandry and the livestock supply chain can influence health risks for human populations worldwide. While individual countries have taken steps to contain outbreaks and to dissemination of HPAI, pathogens can move by unregulated and unrecognized pathways, such as on airborne dust, in animal wastes utilized in agriculture, in ballast water on ships, and in migrating wild animals. It is imperative to understand the formal and informal networks of exchange in order to develop evidence-based policies to anticipate and prevent emergence of novel zoonoses.

To elucidate the linkage between livestock production and the global commons of disease risk, we draw upon recent experiences provided by different influenza A virus (IAV) incursions into domestic livestock populations, the most notable one being the ongoing HPAI H5N1 epidemic that originated in Asia, which now also affects Africa and with outbreaks having been recorded in the Near East and in Europe.

This paper reviews changes in food animal production that have occurred over the past decade, and then summarizes the current understanding of the emergence of distinct influenza viruses. Direct and indirect evidence, drawn primarily from HPAI outbreaks in areas of high poultry density, is presented on aspects of biosecurity and biocontainment that are relevant to the transmission of influenza viruses in industrial poultry production systems. Incentives associated

with the management of animal and public health risks are discussed based on the evidence presented.

### **3. Changes in Food Animal Production**

As countries have become more affluent, demand for livestock-derived food has substantially increased, leading to a major transformation of global animal food production. The linkages between sub-sectors of the animal industry, such as feed manufacturers, breeding companies, livestock keepers and processors, as well as production practices have changed significantly over the past decades, with potentially serious consequences for disease risks. These changes include significant increases in livestock populations and densities, concentrated industrial food animal production, using fewer but more productive livestock breeds and lines, with, in the case of poultry and pigs, hybrid animals providing the end product, specialization in and vertical integration of stages of production (e.g. breeding, raising, finishing), and major changes in the design of animal housing facilities.

Industrial food animal production involves high throughput animal husbandry, in which thousands of animals of similar genotypes are raised for one purpose (such as pigs, layer hens, broiler chickens, ducks, turkeys) with rapid population turnover at one site under highly controlled conditions, often in confined housing, with nutrient dense, industrial feeds replacing access to forage crops. In the US, these facilities are known as animal feeding operations (AFOs). Concentrated animal feeding operations (CAFOs) are a type of AFO, which have a regulatory definition in the US as facilities that have animals stabled or confined for at least 45 days out of any 12 month period and holding at least 1,000 animal units (AUs) (1 AU = 1000 pounds body weight).

Globally, pig and poultry production are the fastest growing and industrializing livestock sub-sectors with annual production growth rates of 2.6 and 3.7 percent over the past decade (Table 1). As a consequence, in the industrialized countries, the vast majority of chickens and turkeys are now produced in houses in which between 15,000 and 50,000 birds are confined throughout their lifespan. Increasingly, pigs and cattle are also raised under similar conditions of confinement and high density. The trend towards industrialization of livestock production can also be observed in developing countries, where traditional systems are being replaced by intensive units at a rate of 4.3 percent of animal holding units per year, with much of that increase occurring in Asia, South America and North Africa (CAST, 1999). In developing countries a large proportion of industrial units are sited in or close to human population centres. Over the same time, the human population has grown by almost 700 million people, again, with

much of this growth occurring in the developing world and in particular affecting urban populations.

**Table 1:** Changes in global human population, pig and poultry inventories, and production and international trade of pig and poultry meat between 1996 and 2005.

	1996	2005	Annual growth (%)
<b>Human population</b>	5,762	6,451	1.1
<b>Inventory</b>			
Pigs (million)	859	963	1.1
Poultry (million)	14,949	18,428	2.1
<b>Production</b>			
Pig meat (thousand tons)	79,375	103,226	2.6
Poultry meat (thousand tons)	56,408	81,856	3.7
<b>International trade</b>			
Pig meat (thousand tons)	6,398	9,557	4.0
Poultry meat (thousand tons)	5,359	9,234	5.3

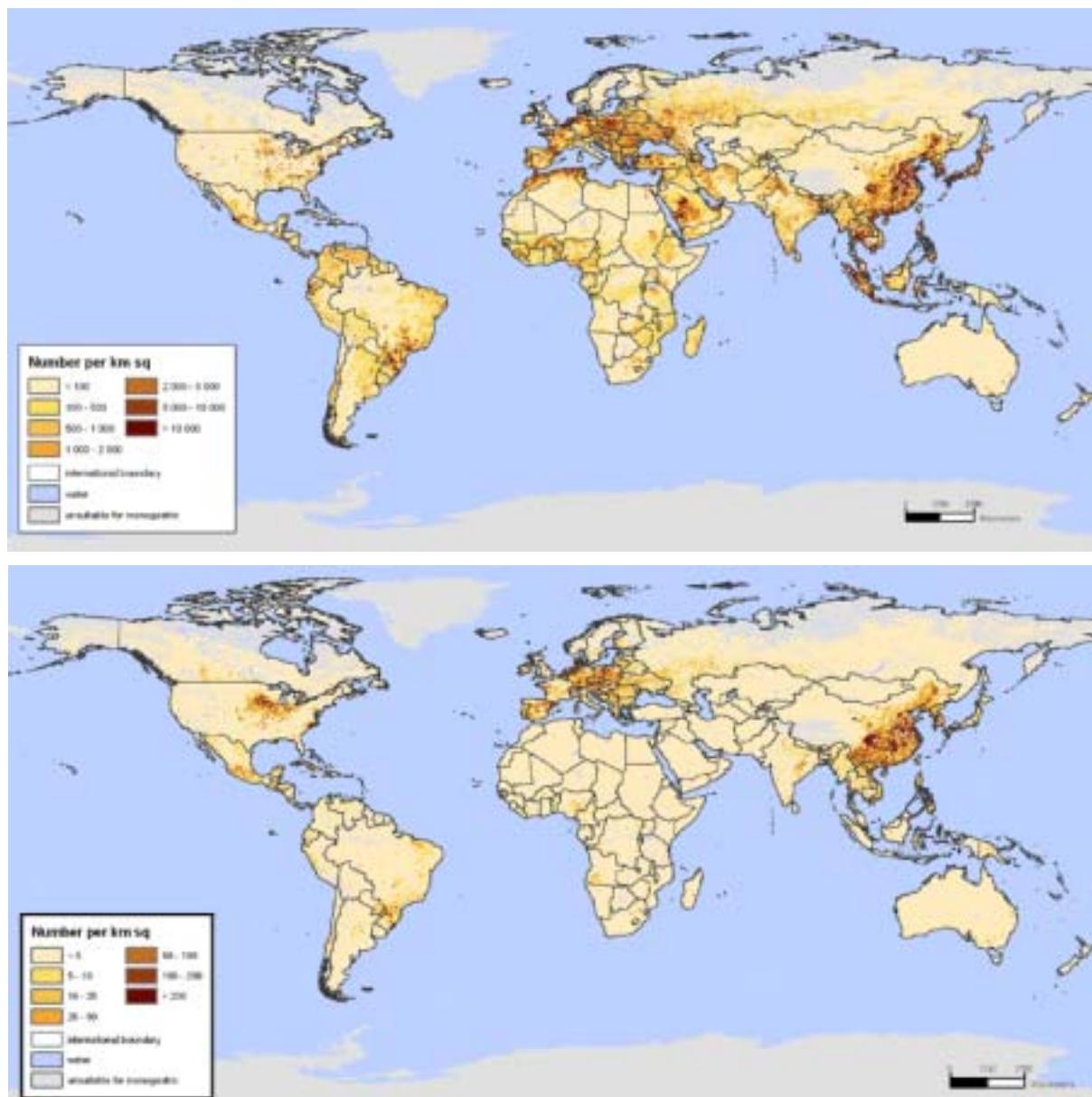
Source: FAOSTAT

Industrialization of food animal production has led to major increases in livestock productivity, which are to a large extent the result of genetic progress and the development of diets tailored to specific stages of production. For poultry and pigs, industrial production is organized in stages which separate primary breeders, multipliers and producers (often contract farmers). A small number of globally operating companies form the apex of the breeding pyramid. Different production stages are often undertaken at different sites, leading to significant movement of live animals, at times across national borders. In 2005, for example, more than 25 million live pigs, i.e. more than 2 million pigs per month, were traded internationally (FAOSTAT). In the US, there is a huge movement of unfinished animals, for example feeder pigs from the Carolinas to the Cornbelt. In 2001, 27 percent of pigs in the US were moved from one state to another (or more) (Hennessy, 2004). Investigations in relation to the recent HPAI outbreak in the UK revealed that links in poultry production within one enterprise between facilities located in the UK and in Hungary involved movement of hatching eggs, birds and poultry products four times before the final product reached retail (Lucas, 2007). Animal slaughter operations have also become concentrated, leading to larger average distances for transport to slaughter (Burrell, 2002; MLC, 2001).

The consolidation of poultry and pig production for reasons of competitive advantage has also affected the geography of food animal populations. Over the past 60 years, the geographic distribution of both pig and poultry production in the US, for example, has become more clustered, with poultry production now being highly concentrated in the southeastern states and pig production concentrated in some of these same states, as well as in the Midwest. Similar trends have occurred worldwide with pig and poultry populations increasingly concentrated in

particular locations which are often geographically coincident. An approximate overview of the global distribution of poultry and pig population densities is provided by Figure 1. With the geographical concentration of pig and poultry production, there has been an associated increase in global trade and movement of pig and poultry meat products, which over the past decade has increased at an average annual rate of 4.0 and 5.3 percent, respectively (Table 1). Although trade can be considered safe when conducted in line with OIE regulations, poultry trade has been implicated in the cross-border spread of H5N1 in Asia and Africa (Kilpatrick *et al.*, 2006).

**Figure 1:** Global poultry (top) and swine (bottom) distributions.



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Industrial pig and poultry production with its geographic intensity and being coincident for the two species, and with the regular movement of animals between production stages provides significant opportunities for interactions between large populations of confined poultry and / or

pigs and thus has potential consequences for the development and transmission of some zoonotic disease agents. The proximity of thousands of confined animals increases the likelihood of transfer of pathogens within and between these populations, with consequent impacts on rates of pathogen evolution. Furthermore, animals held in confinement produce large amounts of waste, which need to be disposed of. Much of this waste, which may contain large quantities of pathogens, is disposed of on land, posing an infection risk for wild mammals or avians. Poultry house waste is also utilized in aquaculture, a form of food animal production, which results in the creation of artificial wetlands and thereby increases direct opportunities for contact with wild avians.

## 4. Emergence of Novel Influenza A Viruses

Evidence suggests that non-domesticated aquatic birds are the primary reservoir of influenza A viruses (IAVs) and probably all IAVs of mammals have ancestral links to avian lineages (Webby and Webster, 2001). An important feature of IAVs is their capacity to undergo molecular transformation and to adapt to new host populations<sup>1</sup> and thereby acquire the potential to cause major disease outbreaks. One way of classifying IAVs into sub-types is on the basis of their haemagglutinin (HA) and neuraminidase (NA) antigens. Known hosts for different IAV HA and NA types are presented in Table 2.

**Table 2:** Known hosts for different HA and NA influenza A virus subtypes.

Host	Role in epidemiology	HA Subtype	NA Subtype
Waterfowl	Reservoir	All 16 subtypes	All 9 subtypes
Domestic ducks	Reservoir	Wide range <sup>a</sup>	Wide range <sup>a</sup>
Humans	Reservoir Spillover	H1, H2, H3, H5, H7	N1, N2, N3, N7
Pigs	Reservoir Spillover	H1, H3, H4, H9	N1, N2
Horse	Reservoir	H3, H7	N7, N8
Cattle	Reservoir	H3	N2
Cat, Tiger	Spillover	H5	N1
Whale	Reservoir	H3, H13	N2, N9
Seal	Reservoir	H4, H7	N7
Chicken & Turkey	Reservoir Spillover	H9 H1, H5, H6, H7	N1, N2, N3, N7, N9

Source: Adapted from Webster et al., 2006; and Li et al., 2003

<sup>1</sup> Two distinct genetic processes underlie antigenic transformation of IAVs: antigenic drift and antigenic shift. Molecular changes result from point mutations in the viral haemagglutinin (HA) and neuraminidase (NA) glycoproteins. Antigenic changes occur in conjunction with the selection pressure applied by the host immune response. Less frequent, but of potentially far greater impact is the process of antigenic shift, which can result when a single cell is infected by two distinct IAVs giving rise to progeny viruses containing genetic material from both parental viruses. This reassortment can completely change the molecular profile of IAVs and thereby facilitate virus spread through a host population, potentially giving rise to major epidemics.

Another criterion for classifying IAVs is their pathogenicity, i.e. their ability to cause disease in experimentally inoculated chickens. Thus virulent viruses leading to severe disease and high levels of mortality are classified as highly pathogenic AI (HPAI) while viruses causing much milder disease (primarily mild respiratory disease, depression and reduction in egg production in laying birds) are classified as low pathogenicity AI (LPAI).

To date, only IAVs of the H5 and H7 subtype have been shown to cause HPAI, but not all H5 and N7 IAVs are highly pathogenic. Current evidence suggests that HPAI viruses are not endemic in wild bird populations and only arise as a result of molecular changes from low pathogenicity IAVs (LPAI) that occur after introduction into domestic poultry from wild birds (Capua and Alexander, 2004), although one outbreak of HPAI H5N3 that could not be linked to domestic poultry has been recorded in terns in South Africa in 1961.

Evidence suggests that introduction of LPAI viruses into domestic poultry populations usually occurs as a result of direct or indirect contact with wild waterfowl or domestic ducks. Various incursions of LPAI virus into domestic poultry have been reported over the past decade, mostly in North America and Europe, but also in Mexico, Chile and Pakistan, details of which have been compiled by Capua and Alexander (2004). In Mexico, 1994, a LPAI H5N2 virus mutated into a HPAI virus and spread to Guatemala in 2000 and to El Salvador in 2001, presumably via trade (*ibid*). LPAI H5N2 is now established in domestic chicken populations in Central America. In both, the 2003 H7N7 HPAI epidemic in the Netherlands (Stegeman *et al.*, 2004) and the 2004 H7N3 HPAI epidemic in British Columbia, Canada (Power, 2005), it appears that LPAI infections in poultry preceded the emergence of HPAI in different poultry houses on the same commercial farms. In Italy, the 1999/2000 H7N1 HPAI epidemic was preceded by 199 reported outbreaks of LPAI H7N1 in the same region. On the other hand, between the mid-1990s and 2004 H7N2 LPAI virus appears to have been endemic in parts of the US, linked to live poultry markets, without conversion to an HPAI virus.

Overall, over the past 10 years reports of HPAI have increased dramatically with ten distinct minor or major epidemics reported worldwide since 1997 while 14 outbreaks have been recorded over the preceding 40 years. It is however important to acknowledge the limits in detection and reporting of HPAI and LPAI outbreaks when attempting to interpret this apparent increase in disease incidence.

In addition to the apparent increase in outbreaks caused by H5 and H7 LPAI and HPAI viruses, H9N2 LPAI virus has also spread through domestic poultry populations in the 1990s and become endemic in commercial poultry in China, the Middle East and elsewhere. H9N3 outbreaks are said to have occurred in China in 1994 (Yingjie, 1998, quoted in Capua and Alexander, 2004).

Pigs may potentially assume an important role in the emergence of novel IAVs as they can be infected by either avian or human viruses (Kida *et al.*, 1994; Schulz *et al.*, 1991). Gilchrist *et al.* (2007) note the proximity of concentrated poultry and swine operations as a source of disease risk from IAVs although so far there have only been reports of AI viruses from poultry in pigs and not vice-versa. Classical H1N1 swine influenza viruses are very similar to the virus implicated in the 1918 – 1919 human influenza pandemic and circulate predominantly in the US and Asia. H3N2 viruses of human origin have been isolated from pigs in Europe and the Americas shortly after their emergence in humans (Webby and Webster, 2001) and are now endemic in pigs in southern China (Peiris *et al.*, 2001), where they co-circulate with H9N2 viruses with the potential of reassortment with H5N1.<sup>2</sup> In the USA, outbreaks of respiratory disease in swine herds have been caused by IAVs which arose from reassortment of human H3N2, classic swine H1N1 and avian viral genes (Zhou *et al.*, 1999)

Thus, it appears that IAVs are now fairly widespread in commercial poultry (and to a lesser extent pig) populations and that highly pathogenic strains are emerging or being detected with growing frequency. This may be due to the substantial increase in poultry numbers (25 percent) over the last decade and / or to changes in poultry production, as well as to enhanced diagnostic capacities and better disease reporting and / or to changes in poultry production (Capua and Alexander, 2006). Although the specific role of CAFOs in the emergence of novel diseases is not well understood, the US Council for Agriculture, Science and Technology (CAST, 2005) warns that a major consequence of modern industrial livestock production systems is that they potentially allow the rapid selection and amplification of pathogens.

## 5. Biosecurity and Disease Transmission in Industrial Systems

Biosecurity has been broadly defined as any practice or system that prevents the spread of infectious agents from infected to susceptible animals, or prevents the introduction of infected animals into a herd, region, or country in which the infection has not yet occurred (Radostits, 2001). More specifically, farm biosecurity combines ‘bioexclusion’, i.e. measures for preventing a pathogen from being introduced to a herd/flock, and ‘biocontainment’, which addresses events after introduction, i.e. the ability for a pathogen to spread amongst animal groups within a farm or of being released from the farm (Dargatz *et al.*, 2002). The majority of farms devote most resources to bioexclusion although large multiunit farms also invest in biocontainment to prevent spread to other units.

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<sup>2</sup> For instance, in 1999, IAV subtype H9N2, was isolated from two girls in Hong Kong, who recovered from influenza-like illnesses (Peiris *et al.*, 1999).

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Disease transmission between farms depends on the combination of individual bioexclusion practices and biocontainment measures. The importance of the latter is largely determined by the magnitude and direction of resource (and waste) flows across and between farm populations. In the livestock sector, these flows can be complex because of specialization at different stages of animal production and processing and intricate formal and informal market chains. Large scale production at all stages is highly concentrated, with small numbers of large, intensive facilities and even fewer responsible enterprises. Larger facilities are often assumed to implement more advanced biosecurity measures, but the intensity of their operations also poses higher risks for infection and pathogen propagation. Over one cycle of 10,000 broilers for example, around 42 tons of feed and 100,000 l of water have to be supplied to the birds, and unless stringent measures are taken these remain potential routes of introduction, while around 20 tons of waste will be produced requiring disposal.

The design and operational requirements of large scale poultry and swine houses also result in compromises of biosecurity. Because confinement of thousands of animals requires controls to reduce heat and regulate humidity, poultry and swine houses are ventilated with high volume fans that result in considerable movement of materials into the external environment (Jones *et al.*, 2005) and dust emissions, visible (particles >10 microns) and invisible (particles <10 microns), from poultry barns housing thousands of birds can be substantial. Measurement of aerosol emissions from a broiler operation revealed a million fold elevated concentration of aerosolized invisible dust near a poultry barn fan as compared to outdoor air in a semi-rural area (Power, 2005). These particles have the potential to remain suspended in the air for up to several days, and, depending on prevailing winds, poultry barn dust could be found several kilometers from its source. Although little is known about the survival of IAVs on dust particles, high concentrations of infectious AI virus have been detected in air samples from an infected barn while low levels of virus were detected in one of nine samples some 800 m from an infected barn. However, it was not determined if this sample of virus was infectious (Power, 2005).

Other pathogens have been shown to readily move in and out of poultry and swine houses. Pathogen entry was demonstrated in a recent study of *Campylobacter*-free broiler flocks, housed in sanitized facilities, using standard biosecurity measures, and fed *Campylobacter*-free feed and water. Seven out of ten flocks became colonized with *Campylobacter* by the time of slaughter and two flocks were colonized by *Campylobacter* strains genetically indistinguishable from strains isolated from puddles outside of the facility prior to flock placement (Bull *et al.*, 2006). Although the route of entry was not determined, this study clearly shows that some pathogens in the immediate environment of a poultry facility have a high chance to overcome standard bioexclusion measures. Contaminated air exiting the house via ventilation systems becomes a source of *Campylobacter* to the external environment and microbes may be carried some distance by wind and surface water transport. *Campylobacter* strains with identical DNA

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fingerprints to those colonizing broilers have been measured in air up to 30 m downwind of broiler facilities housing colonized flocks (Lee *et al.*, 2002).

Insects are another means for pathogen entry to and exit from poultry houses. Research carried out during an HPAI outbreak in Kyoto, Japan in 2004, found that flies caught in proximity to broiler facilities where the outbreak took place, carried the same strains of H5N1 influenza virus as found in chickens of an infected poultry farm (Sawabe *et al.*, 2004). A study in Denmark found that as many as 30,000 flies may enter a broiler facility during a single flock rotation in the summer months (Hald *et al.*, 2004).

Evidence that bioexclusion measures of (at least some) large-scale industrial poultry operations are not impenetrable by IAVs is provided by reviewing the HPAI H5N1 outbreaks reported to OIE ([www.oie.int](http://www.oie.int)). HPAI H5N1 for instance has been reported to have caused outbreaks in large-scale industrial poultry units with supposedly high biosecurity standards in South Korea (a 300,000 bird unit), Russia (two 200,000 bird units) and Nigeria (a 50,000 bird unit) in 2006, and in the UK (a 160,000 turkey unit) in 2007. Moreover, large(r) industrial-type flocks appear to be overrepresented in the list of HPAI H5N1 outbreaks reported to OIE vis-à-vis outbreaks in backyard / village flocks in relation to their respective shares of total national flocks. Around 40 percent of the HPAI H5N1 outbreaks in domestic poultry reported to OIE between late 2005 and early 2007 occurred in poultry units of 10,000 birds or more (more than 25 percent occurred in units of more than 10,000 birds), while, even in many OECD countries, e.g. Germany, France, UK and Belgium, less than 10 percent of flocks consist of more than 10,000 birds. It is likely that some of this overrepresentation of large industrial-type flocks in reported outbreaks is due to ascertainment bias because outbreaks are more likely to be detected and reported in large-scale operations than in backyard systems<sup>3</sup>. Nevertheless, it demonstrates that, whatever the source of the virus (wild avians, backyard poultry, other commercial units), bioexclusion measures implemented by some large-scale industrial poultry units, including those in industrialized countries, may be insufficient to protect against H5N1 incursion when challenged.

This empirical evidence of sub-optimal biosecurity of a proportion of commercial operations is substantiated by direct observations and points to a need for greater oversight and or regulation of biosecurity of industrial poultry production. For instance, Power (2005) reports that more than three quarters of commercial broiler and table egg farms in Fraser Valley, Canada, had indicated in a survey that they did not provide disinfection footbaths nor required a change of clothes / coveralls by employees on entering their barns. In Maryland, US, Price *et al.* (2007) found that

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<sup>3</sup> But note that assuming a lag of 8 to 10 days between infection of a flock and notable increase in mortality and a 45-day cycle for broilers, between 15 and 20 percent of infections of broiler flocks are expected to go undetected.

most poultry workers are provided little or no protective clothing or opportunities for personal hygiene or decontamination on site, and that they take their clothes home for washing.

Once IAVs have entered industrial production facilities they can be transferred between operations by contaminated shipping containers and trucks. Given that a gram of infected faeces can contain as many as ten billion infectious virus particles, a small amount of contaminated faecal material or litter adhering to boots, clothing or equipment may be sufficient to transmit virus from an infected to a susceptible flock (Power, 2005). Biocontainment of IAV, once poultry are infected thus poses a substantial challenge, even in countries with advanced animal-health services and depends on early detection of outbreaks and action before the virus has spread widely in infected premises.

## 6. HPAI Epidemics in Densely Populated Poultry Production Areas

The 1999-2000 H7N1 epidemic in northern Italy, the 2003 H7N7 epidemic in the Netherlands and the 2004 H7N3 epidemic in Fraser Valley (British Columbia, Canada) highlight the difficulties faced by animal health authorities when HPAI infects flocks in densely populated poultry production areas (DPPAs). Table 3 provides a summary of these three epidemics.

**Table 3:** Summary of HPAI outbreaks in densely populated poultry production areas.

	Italy <sup>1</sup> 1999 – 2000		Netherlands 2003		Canada 2004	
Farm type	Industrial	Backyard / hobby	Industrial	Backyard / hobby	Industrial	Backyard / hobby
Farms in the affected area	3,271	na	1,362	17,431	app. 800	533
Farms declared infected	382	10	233	22	42	11
Infection risk	12%	na	17%	0.1%	app 5%	2%
Farms depopulated	all in 5,500 km <sup>2</sup>		1,255	17,421	410	533
Proportion farms depopulated	100%		92%	100%	app 50%	100%
Birds culled	app 16 million		app 30 million		13.6 million	17,977

<sup>1</sup> Figures are for Veneto and Lombardia, the hardest hit provinces, source: Capua pers. comm..

In all three epidemics animal health authorities noted the high density of poultry farms with frequent contact between farms by trucks and surprisingly low levels of biosecurity practiced by some operators as having been associated with the considerable spread of virus (Capua *et al.*, 2002; Stegeman *et al.*, 2004; Power 2005). Retrospective analysis of between-flock transmission in two distinct outbreak areas in the case of the Netherlands and of an H7N3 LPAI epidemic in Italy in 2003-2004 estimated reproduction ratios ( $R_h$ , the average number of

secondary infections caused by 1 infectious flock) of 6.5, 3.1 and 2.9 respectively (Stegeman *et al.*, 2004; Capua and Marangon, *in press*) prior to the implementation of control measures. This clearly indicates that standard bioexclusion and biocontainment measures in a number of the predominantly industrial flocks were insufficient to prevent disease spread, and that disease detection or reporting was delayed. For caged layers, for example, Capua and Alexander (2006b) cite a ‘flock incubation period’ of up to 18 days, which, in areas with intense between-farm traffic, provides sufficient time extensive movement of the virus.

Control of the three epidemics was only achieved through massive depopulation of commercial and backyard / hobby flocks (vaccination was not applied). Retrospective analysis of the Dutch outbreak also revealed that between-flock transmission continued even after the implementation of strict movement controls in the affected areas. The authors conclude that containment of the epidemic was more likely to be the result of the depletion of susceptible flocks by depopulation than the reduction of the transmission rate through biocontainment measures (Stegeman *et al.*, 2004).

The lower probability of infection of backyard / hobby flocks compared to that of industrial flocks in the Dutch and Canadian epidemics, in which samples were collected from backyard / hobby flocks in the vicinity of infected industrial flocks, is consistent with findings from the HPAI epidemic in Thailand in 2004 and the 2002 outbreak of Newcastle disease in Denmark (Otte *et al.*, 2007) and suggests that commercial transactions are an important route for disease transmission between industrial farms.

## 7. The Animal:Human Interface

Over the past 100 years, the sudden emergence of antigenetically different strains of IAVs transmissible among humans leading to human influenza pandemics has occurred in 1918 (H1N1, Spanish flu), 1957 (H2N2, Asian flu), and 1968 (H3N2, Hong Kong flu) (Webby and Webster, 2001). Studies on these pandemic viruses have shown that all three contained an avian component (Capua and Alexander, 2006b).

A number of studies demonstrate that IAVs from animals can move across the animal:human interface in the context of food animal production and processing, and therefore, livestock keepers and people otherwise in close contact with live animals are the most likely group to act as ‘bridge’ for IAVs between livestock and human communities at large (Saenz *et al.*, 2006), should an IAV acquire the capability of sustained human-to-human transmission.

Myers *et al.* (2006), for example, report that swine farmers had higher titres of H1N1 and H1N2 antibodies and greatly elevated risks of seropositivity to these two influenza A viruses (35.3 and

13.8 odds ratios respectively), as compared to community referents. A comprehensive study of the outcome of exposure to H5N1 has been conducted in Hong Kong during the 1997 outbreak (Bridges *et al.*, 2002). In this study, 1,525 poultry workers and 293 government workers involved in culling activities and disease investigations were assessed for risk factors for seropositivity. Only occupational tasks involving contact with live poultry were associated with increased risks of seropositivity, and the probability of carrying H5 antibodies increased with increased numbers of such occupational contacts from around 3 percent at the low end to nearly 10 percent at the high end. A study in Italy found anti-H7 antibodies in 3.8 percent of serum samples from poultry workers during the period in 2003 when LPAI H7N3 was circulating (Puzelli *et al.*, 2005). A study of H7N7 infection among persons reporting influenza-like symptoms was conducted in the Netherlands in association with the 2003 H7N7 HPAI epidemic (Koopmans *et al.*, 2004). H7 virus was detected by PCR in ocular swabs of 86 of 453 persons (18.9 percent) calling into the health department. The highest detection rates were found in poultry cullers (41.2 percent), followed by veterinarians (26.3 percent) and farmers and their family members (14.7 percent).

Fortunately, thus far, the recent HPAI viruses do not easily infect humans, have not acquired sustained human-to-human transmissibility and only the Asian HPAI H5N1 appears to have a high case fatality in infected humans. Increased exposure of humans to avian IAVs undoubtedly increases the likelihood that avian and human influenza viruses infect the same individual, which could facilitate the emergence of a ‘novel’ virus, but the molecular changes required for efficient transmission of IAVs among humans remain poorly understood. Thus, in a ferret model (used to investigate the transmissibility of human influenza viruses) two H5N1 avian-human reassortant viruses and one H3N2 human-avian reassortant virus exhibited reduced replication efficiency and no transmission, suggesting that H5N1 viruses may require further adaptive steps in order to develop pandemic potential (Maines *et al.*, 2006), the likelihood of which remains unknown.

## **8. Management of Animal and Public Health Risks**

Animal and public health risks have a complex relationship with economic incentives. Some responses to market and regulatory signals elevate infection risk, including the scope and term of disease incubation, while others reduce risk levels. Generally speaking, incentives for risk reduction are associated with a ‘virtuous cycle’ of product quality, reputation, and profit. Behaviours that increase risk usually arise from uncertainty, loss aversion, or illicit profit incentives.

Although the effects of HPAI primarily become evident in domestic poultry, disease outbreaks have repercussions that go far beyond primary producers. These repercussions are to a large extent a result of public and private responses to the (real or perceived) risk of the disease and

its potential effects rather than to the actual, direct on-farm impact. Thus, any control programme needs to take into account this plurality of stakeholder reactions and interests as well as their potential to contribute to, and their incentives to undermine control programmes. It must be recognized that some individuals and enterprises may actually gain from an animal disease outbreak affecting others.

Disease risk can be considered as the outcome of an initial process of infection, followed by within farm / flock transmission, exposure of other actors in the production process, and reaction. The magnitude of each of these processes can be positively or negatively affected by economic incentives and policy interventions. For example, the risk posed by an infectious disease related to food animal production may be influenced by:

- Providing incentives and introducing regulations to promote adoption of practices that reduce the probability of initial outbreaks (e.g. bioexclusion measures);
- Introduction of incentives and standards that facilitate early detection, on-farm containment, and eradication;
- Establishing incentives and standards to reduce release from farms and other routes of exposure of others (e.g. biocontainment measures); and
- Developing strategies to mitigate disease impact, for example through emergency or preventive vaccination in high risk areas.

It would seem logical that ‘private’ decision makers will primarily focus on bioexclusion and less so on on-farm biocontainment, since the latter is only relevant once the pathogen has been introduced into their facilities, and as they are likely to believe that their bioexclusion measures are sufficient to prevent that from happening.

A critical issue of incentives and disincentives relates to early detection of disease incursion. The importance of early detection cannot be overstated as the magnitude of disease epidemics is exponentially related to the time elapsed between pathogen introduction and implementation of control measures. Timely reaction heavily relies on early detection and disclosure by those in daily contact with livestock, however current disease control policy tends to encourage individual behaviour along the old adage ‘shoot, shovel and shut up’. Incentive systems need to be devised that encourage ‘good behaviour’ while penalizing ‘bad behaviour’. A dilemma in the latter will be that the required disincentives may run counter to the need for incentives for early disclosure. Compensation schemes that offer equal compensation for lost animals, irrespective of timing of disclosure fail to create an incentive consistent with the policy objective of early reaction (Graming *et al.*, 2006). Likewise, depopulation of entire premises in the event of selected pathogen entry into a poultry house, for example, does not offer an incentive for

reporting the latter or for major investments in within-farm biocontainment (let alone between-farm biocontainment).

Compensation for depopulation usually only covers (partial) costs to producers that are directly affected by the depopulation measures, while the other costs of disease control measures, such as movement restrictions, on other market participants are not normally covered. Unless an appropriate balance is struck between the control and compensation systems, farmers in a quarantined area may have an incentive to introduce disease onto farms with consequential depopulation and partial compensation rather than to suffer the indirect impacts of disease control measures.

As it can be more profitable to raise or move animals for ‘finishing’ to locations where animal feed is abundant, e.g. close to feed mills, than to continuously move feed over large distances, areas of high livestock density have emerged in a number of regions worldwide. Semi-vertical integration of production processes, where a large company supplies young stock and feed, while farmers provide animal housing and labour, has often not been accompanied by systematic spatial planning of the units in the system. Although spatial concentration is convenient from an organizational point of view, as illustrated in the case of the HPAI outbreaks in DPPAs, it has serious drawbacks for the control of epidemic diseases. In the European Union (EU), location-specific disease risks, as for example determined by concentration of production units or proximity to wildlife reservoirs, are not factored into the cost of production because the current tax-financed system of disease outbreak response acts as a free insurance of last resort, and thereby results in the generation of avoidable amounts of ‘risky’ production (Jansson *et al.*, 2006). The same authors show that although moving to risk-based compulsory insurance for FMD, financed by the livestock sector, would not result in major relocation of dairy production within the EU, it would lead to a fairer distribution of disease control costs between member countries and between consumers and producers. Location of poultry and pig production, which does not rely on the availability of grazing land, might however shift in response to a risk-based insurance system.

The benefits of freedom from highly contagious diseases are shared by all market participants, i.e. non-exclusive, and therefore have similarities with common property resources. But as achievement and maintenance of disease freedom is heavily dependent on individual behaviour, livestock keepers may become locked into a ‘Nash equilibrium’ in which no one has anything to gain by unilateral action. Public intervention is required to align individual and societal interests, but to do so successfully requires detailed understanding of the individual incentives of market participants and of the full set of consequences of potential interventions.

## 9. Conclusions

Intensification of food animal production is an entrepreneurial response to the increasing demand for food of animal origin, at times supported by public investment. Satisfying current global demand for poultry meat by traditional systems would require a dramatic expansion of the poultry population as meat offtake per bird per year in traditional systems is about one tenth that of industrial systems (a similar ratio would hold for egg production). Therefore, from the point of view of meeting the growth in demand, the world has to depend upon some of the technologies of large scale industrial type production. However, as CAST (2005) states “the cost of the increased production efficiency of these industrial systems is the necessity for heightened biosecurity and improved surveillance to safeguard global public health.” Hennessy *et al.* (2004) have shown that the risk of infectious disease can create decreasing returns to scale, when technology is otherwise increasing returns to scale. The same holds true for waste disposal. Thus, once these externalities are factored into the production costs of industrial systems, the economically optimum size and siting of operations may change.

Concentration of food animal production and the unregulated ‘evolution’ of densely populated livestock production areas not only result in major environmental burdens, but also generate significant animal and public health risks. Recent experience has shown that disease containment in these areas is extremely difficult, and in the case of outbreaks can result in the ethically rather questionable destruction of millions of healthy birds. An unrecognized aspect of industrial food animal production concerns worker exposures (Price *et al.*, 2007) to zoonotic diseases. Saenz *et al.* (2006), using mathematical transmission models, show that when CAFO workers comprise more than 15 percent of a community they may act as IAV amplifiers for the community as a whole.

Although understandably H5N1 is currently of major global concern, IAVs in general in poultry and swine, kept whichever way, should be closely monitored internationally as human exposure to ‘silently’ circulating IAV is just as likely (or unlikely) to lead to emergence of a potentially pandemic strain as exposure to HPAI.

The trend towards division of labour (within and between countries) for different stages of food production and processing increases the risk of pathogen transfer over large distances even if production facilities are not highly concentrated. An example of this effect is the Longtown livestock market during the 2001 foot-and-mouth disease epidemic in Great Britain which acted as a source of infection for many different herds and flocks, and thereby resulted in the spread of infection to several geographically dispersed areas in the country (Gibbens and Wilesmith, 2002). The risk of pathogen transfer via animal movements could be significantly reduced by enforcement of minimum time intervals between movement of animals onto and off farms

While the role of industrial food animal production in the emergence of drug resistant bacteria is beyond doubt, its role in the emergence of novel virus strains requires further investigation. As all parasites, viruses face a life-history trade-off between persistence, i.e. host survival, and fecundity, i.e. host exploitation (Galvani, 2003). Maximising fecundity may lead to an increase in virulence and in a number of avian influenza outbreaks, highly pathogenic viruses have indeed emerged after multiplication in large flocks of chickens. However, as HPAI viruses have occasionally been reported before the development of large-scale industrial poultry production, the latter are not a pre-requisite for the emergence of virulent strains.

Policy makers in both developing and developed countries appear to accept that large-scale industrial farms have higher standards and self-discipline in biosecurity, while smallholders need more rigorous public oversight. The realities of animal health, economic incentives, and the public interest in disease prevention are far too complex for simple rules of thumb like this to be optimal for society. Only a comprehensive, evidence-based approach to risk management can sustain a safe food supply. Although it is in the self-interest of individuals to enhance their bioexclusion measures, biocontainment has a strong collective action component requiring public intervention. Thus, at least initially, it might be more cost-effective for public authorities to ensure that the small share of large industrial operations, which is responsible for a large share of resource, product and waste flows implements high biosecurity standards.

Given the proven difficulties of containing the spread of HPAI in areas of high flock density, the wisdom of creating poultry production zones, as envisaged by some governments, seems at least questionable unless these are properly planned and adequate land is provided to allow appropriate dispersal of units. To be effective, such zones would require careful planning of all aspects of food animal production following the principles of 'industrial ecology', which focuses on closing cyclical processes and reducing transfers. Development of such solutions requires a 10 to 20 year time horizon and institutionalized collaboration between a large number of stakeholders (de Wilt *et al.*, 2000). Shorter term health risk-based decisions on siting of industrial production units should be based on application of tools akin to those developed to assess the cumulative impacts of multiple CAFO facilities in a watershed subunit as described by Osowski *et al.* (2001).

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## 11. Disclaimer, Acknowledgements & Contacts

PPLPI Research Reports have not been subject to independent peer review and constitute views of the authors only. This paper has significantly benefited from insightful comments provided by Les Sims, Mo Salman and Martin Upton. The authors would also like to acknowledge the responsiveness to requests for information on HPAI outbreaks in Italy and Canada by Ilaria Capua and colleagues of the Istituto Zooprofilattico Sperimentale delle Venezie and of Susan Wilson of the Canadian Food Inspection Agency. For comments and / or additional information, please contact:

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