

28 April 2009

FAO
Viale delle Terme de Caracalla
Roma 00100
ITALY

Dear (FAO),

Mexico influenza: call for a thorough investigation

In view of the serious global public health risks posed by the recent outbreak of H1N1 influenza, Compassion in World Farming urges the United Nations' Food and Agriculture Organisation and the World Organisation for Animal Health to undertake a full investigation into the role of industrial intensive pig production operations in the emergence of the current highly pathogenic influenza epidemic in Mexico. The investigation should definitively determine the cause of the outbreak and identify the risk of further emergence of highly pathogenic influenza strains from intensive farming practices.

Role of industrial production in emergence and transmission of disease

Compassion is calling for this investigation as there is strong scientific evidence that intensive farming of pigs has a significant potential role in the development of highly pathogenic influenza.

The FAO's own 2007 report on *Industrial Livestock Production and Global Health Risks* shows that industrial livestock production plays an important part in the emergence of highly pathogenic influenza and other diseases. The paper notes that "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**" (emphasis added). The report also refers to the US Council for Agriculture, Science and Technology which has warned that a major consequence of modern industrial livestock production systems is that they potentially allow the rapid selection and amplification of pathogens.

(http://www.fao.org/ag/AGInfo/projects/en/ppipi/docarc/rep-hpai_industrialisationrisks.pdf)

Intensive pig farms provide the optimum conditions for viral mutation and transmission, with thousands of pigs crowded together in a closed, warm and dusty environment, highly conducive to the transmission of a contagious disease. The risks arising from disposal of large quantities of excreta and other waste from an infected premises is also significantly increased in farms with large pig populations - particularly where slurry lagoons are accessible to external vectors such as wild animals, birds and flies or where the waste disposal may contaminate local water courses.

Selecting generation after generation of pigs for faster growth rates and higher meat yields has left the animals' immune systems less able to cope with infections; this, together with the high degree of genetic uniformity in the population, facilitates spread of the virus.

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Once a low pathogen influenza virus enters an intensive pig farm it has the optimum conditions for rapid mutation into a highly pathogenic strain. The virus continuously accumulates mutations as it reproduces. The more animals that are kept together in a confined space, the higher the virus load generated and consequently, the faster changes in the virus can occur. In time, the result can be the emergence of a highly virulent strain of the virus.

The evidence indicates that once a new and highly virulent strain of influenza has emerged, it can be spread in various ways including movement of pigs and pig products, associated vehicles and people. When assessing another influenza, H5N1 highly pathogenic avian influenza (HPAI), many experts view the global trade in poultry and poultry products as the major cause of the spread of this HPAI. An editorial in *The Lancet* in April 2006 stressed that the movement of poultry and poultry products or infected material from poultry farms such as animal feed and manure is far more likely to be perpetuating the spread of the virus than wild birds. Indeed, the geographical spread of the disease does not correlate with bird migratory routes and seasons; instead the pattern of outbreaks follows major road and rail routes.

The myth of biosecurity

Doubt is cast by the FAO's report on the ability of biosecurity measures to effectively keep pathogens out of industrial livestock units ('bioexclusion') and, once they have been introduced into such a unit, to prevent pathogens being spread among animal groups within a farm or of being released from the farm ('biocontainment').

The paper stresses that, while larger facilities are often assumed to implement more advanced biosecurity measures, "the intensity of their operations ... poses higher risks for infection and pathogen propagation". It adds that "the design and operational requirements of large scale poultry and swine houses also result in compromises of biosecurity".

It point outs that:

- The ventilation systems that are an essential part of industrial units compromise biosecurity by pumping contaminated air out into the external environment.
- Insects are another means for pathogen entry to and exit from pig houses.
- Influenza and other disease outbreaks have occurred in several countries in large scale industrial pig units with supposedly high biosecurity standards.
- Animals confined in industrial units produce large amounts of waste. In some countries much of this waste, which may contain large quantities of pathogens, is disposed of on land, posing an infection risk for wild mammals and birds.

In conclusion, the balance of scientific evidence suggests that the role of industrial intensive farming should be fully considered when assessing the origin of the current Mexico outbreak. The global consequences of a human influenza epidemic for human health and global trade are of such significance that it is essential that the outbreak's emergence is fully understood, thus minimising the potential for future pandemics.

Yours sincerely

DR LESLEY LAMBERT
Director of Research and Food Policy