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Mr Robert Murfin
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6th December 2011

Dear Mr Murfin,

I am writing with four further pieces of scientific and policy evidence that are relevant to the application by Midland Pig Producers (MPP) for a 25,000 pig unit at Foston, Derbyshire, planning application CW9/0311/174.

I apologise for writing so close to the time when your Council will be considering the application, but some of this new research has only just been published (in October and November this year), and some is the result of extensive searches we have undertaken in the scientific literature. We would emphasise that much of the research in this area is new, the science is evolving, and uncertainties remain.

However, we are conscious that in response to our original evidence about health risks of large scale pig units, the Health Protection Agency has advised the Council that:

"Recent research has found that those living up to 150m downwind of an intensive swine farming installation could be at risk of adverse human health effects associated with exposure to multi- drug resistant organisms."

Regarding the proposal for Foston, the HPA said they believe that:

"The application does not provide detailed analysis and risk assessment of potential point source and fugitive emissions to air, of odour; particulate matter; ammonia; bioaerosols; or emissions from the proposed CHP plant."

We know that the applicants, MPP, have responded by suggesting that these are technical matters to be dealt with by the Environment Agency once they have been given planning permission. We disagree.

The risks to human health associated with large pig units, risks to the workers inside the unit, as well as to their friends and families, in addition to local residents, are serious public health rather than environmental issues, and we submit should be considered by the Council. These are not simply questions of air quality and smell, but rather risks increasingly recognised as being inherent in any large-scale pig unit. The Dutch certainly control smells from their pig industry, but that has not stopped MRSA spreading rapidly through their intensive pig farms. We report below a very recent recommendation about large pig farms from the Dutch Government, the Dutch health authorities, and the Dutch association of local authorities.

New scientific research that has been published since we submitted our original evidence, and since the Health Protection Agency gave their advice, clearly add weight to the concerns we raised about the risks to public health posed by the proposed development at Foston.

The four points we wish to draw to your attention are as follows (detailed references are included at the end of this letter).

1. The Dutch Government proposes a 900 sow limit on new pig farms for public health, socio-economic and ethical reasons

The Dutch Government announced last month, November 2011, new proposed size limits for future livestock farm developments in the Netherlands. The Dutch Agriculture Deputy Minister Henk Bleker announced (1) that he is working on legislation to limit the size of farms in specific locations, for public health and ethical reasons and because of social-economic effects. For pigs, the proposed size limit is 900 sows or 6,000 finisher pigs (compared to the proposed 2,500 sows and 25,000 total numbers at Foston).

2. Dutch local authorities association and municipal health services recommend no large-scale pig farms within 250 metres of residential property

In October 2011, the Dutch municipal health services and the association representing Dutch local authorities recommended that no new, large-scale pig unit should be permitted within 250 metres of any residential building. As you know from MPP’s application, the women’s prison is around 150 metres from the nearest pig house, and the proposed new workers’ houses are about 75 metres from the nearest pig house. The Dutch Association of Municipalities (VNG), supported by the GGD (the umbrella organisation which advises and informs over 400 Municipal Health Services in Holland) have recommended, based on current research (2), a limit of 250 metres. Their reason is that ‘within this distance higher concentrations of particulate matter, endotoxin, and livestock-associated MRSA’ have been measured, ‘with possible adverse health effects’. While MRSA has thankfully not yet been found in British pigs we cannot assume this will remain the case throughout the life of a new pig unit, and there is in any event additional scientific evidence to demonstrate that other pathogenic bacteria can also be disseminated in this way.

3. Higher levels of swine flu in large British pig farms, and their staff more likely to be infected - published late 2011

Two scientific posters (summaries of recent research) published in 2011 found a higher prevalence of swine flu on British farms than expected, and a model to estimate transmission of disease found that staff from large commercial holdings are by far the most likely to be infected. The first study (3) found a higher prevalence of swine flu on British farms than expected. The most common strain was H1N2, and the second most common was H1N1 which can cause infections in humans. Risk factors include practices associated with larger units. The second study (4) found that ‘infection in pigs in larger holdings is more likely to result in pig-human infection', and that ‘there is a clear positive correlation between the size of the initial farm and the risk of human infections'.

4. Anaerobic digesters do not kill all of the pathogens - this answers a point made by MPP

There are several key bugs in pig slurry to be concerned about: salmonella, campylobacter, Clostriuim difficile and certain types of E.coli. It is of particular note that since we first set out our concerns about the proposed development at Foston, monophasic salmonella DT 193 has become the second most common strain of salmonella in British pigs. Numerous UK residents have been infected with this strain and both the Health Protection Agency and the Animal Health and Veterinary Laboratories Agency have acknowledged that it is spreading through the food chain.

One argument that Midland Pig Producers make is that they will be using an anaerobic digester which will kill off many of the pathogens. We have already provided evidence to show that the digester is unlikely to kill C. difficile spores. While other pathogens may be killed, their antibiotic-resistance genes can survive the digestion unharmed.

Three studies (5, 6, 7) we have identified found slightly differing results, but together they show that antibiotic-resistance genes can survive both aerobic and anaerobic digesters. One study found that ‘mesophilic digestion and lagoon storage did not appreciably reduce any of these antibiotic-resistance genes’ and that ‘antibiotic resistance arising from swine-feeding operations can survive typical swine waste treatment processes and thus treatments that are more effective in destructing AR on farms are required’. Resistance genes which survive digestion can then be picked up by bacteria in the environment which then become antibiotic-resistant. This, then, can pose a threat to the local population.

It seems clear from this research that the temperature at which digesters operate is important for eliminating antibiotic resistance genes. Mesophilic digesters usually operate at 37 degrees whereas thermophilic digesters operate at higher temperatures. In MPP’s response to the Soil Association’s initial evidence, they claimed that their digester would be operating at 46 degrees, however, on p17 of their planning statement the temperature 37 degrees is mentioned, and as far as we are aware, nowhere in the application do they refer to 46 degrees. Also, they say that their digester will be a '“plug flow” digestion system' made by the company GHD. GHD's plug flow digestion system for cattle is mesophilic (http://www.ghdinc.net/gordondale_report_final.pdf), therefore one operating at a lower temperature, and MPP have not said that their AD unit will be a different, thermophilic, version.

We have commissioned one further piece of research, on the climate change and environmental impacts of AD units linked to large livestock units, such as the one proposed by MPP at Foston, and we plan to send you that before the end of the year. I would be grateful if you could acknowledge receipt of this letter, and confirm the contents will be considered as part of the evidence submitted in respect of this application.

Yours sincerely,

Peter Melchett
Policy Director
Soil Association

Cc: Members of the Planning Committee

References

1. Dutch restrict maximum pig house building size

28 Nov 2011
Future livestock farm projects in the Netherlands will most probably have to be built within size limits, the Dutch government announced.
In his plans, Dutch agriculture deputy minister Henk Bleker announced last week he is working on legislation to limit the size of farms in specific locations. These limits will depend on ethical reasons, reasons of public health or social-economic effects.

He emphasised that the limits will only apply to extreme cases. Family farms will continue to be able to develop until the size of 300-400 cattle; 900 sows; 6,000 finisher pigs; 200,000 broilers or 100,000 layers, he said. Local authorities will decide on whether farms will fit into their surroundings.

Sustainability
Creating a more sustainable livestock industry is another requirement for the future. The Dutch government wishes to see that the 2020 livestock industry is safe, healthy, top quality and socially accepted, with special attention for animal welfare and care for animals. Risks for public health ought to be minimised – and mineral consumption should be fully controlled.

The Dutch government has indicated that the sustainability is all up to the industry to build. Referring to an earlier report, Bleker said only sustainably produced meat should be found in supermarkets by 2020. "National authorities will only facilitate this process," Bleker said, leaving room for a level playing field in the European market.

A mixed bag of reactions could be heard from the political scene. Worries have been voiced about a lack of attention for livestock producers, as well as a lack of ambition in the plans. Animal welfarists and environmentalists repeated their demand that large livestock houses ought to be banned rightaway.

2. O'Connor AM, Auvermann B, Bickett-Weddle D, Kirkhorn S, Sargeant JM, Ramirez A, Von Essen; SG. (2010), The association between proximity to animal feeding operations and community health: a systematic review. PLoS One. 2010 Mar 10;5(3):e9530.

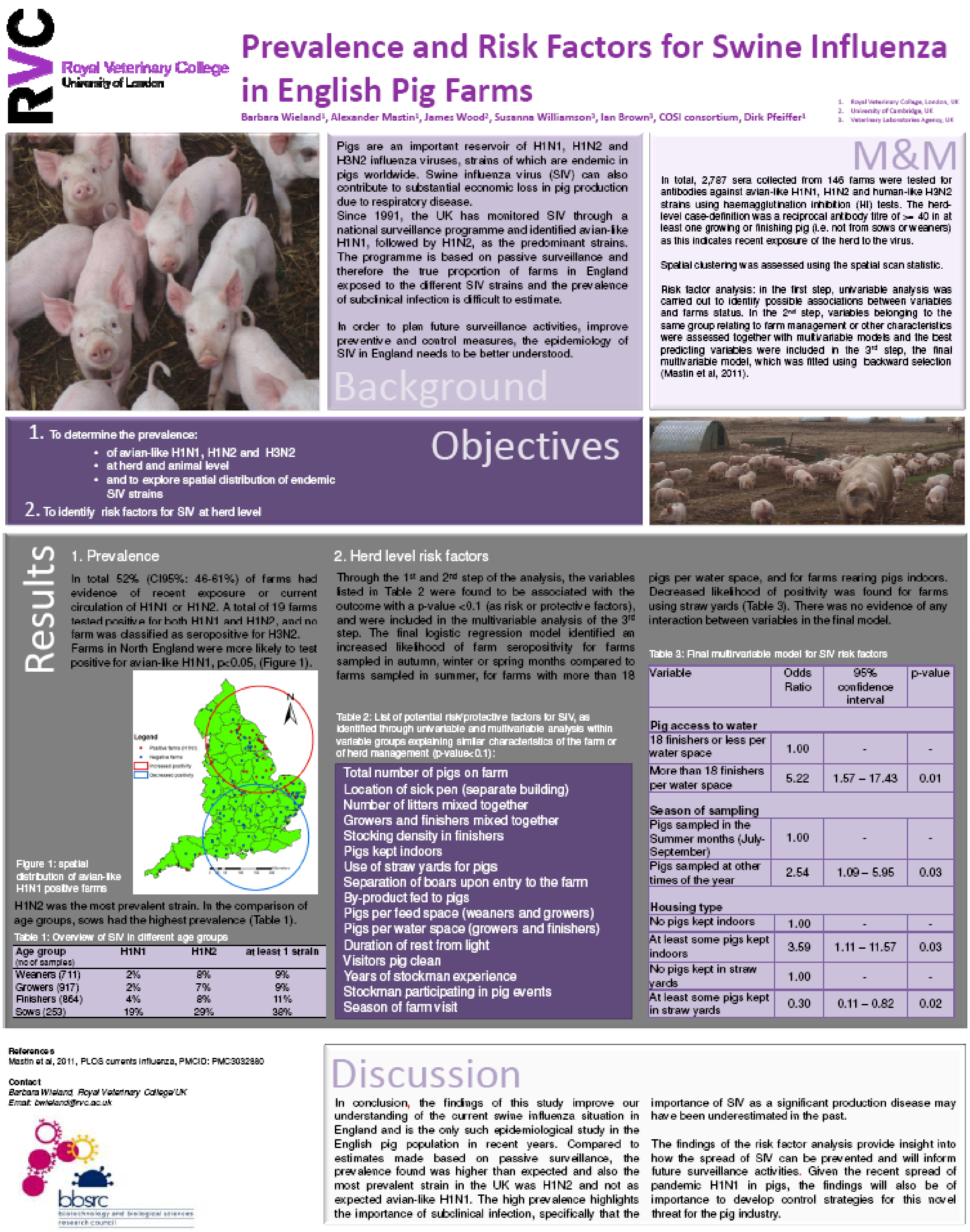
Cambra-López M, Aarnink AJ, Zhao Y, Calvet S, Torres AG. Airborne particulate matter from livestock production systems: a review of an air pollution problem. Environ Pollut. 2010 Jan;158(1):1-17. Epub 2009 Aug 4.

Radon K, Schulze A, Ehrenstein V, van Strien RT, Praml G, Nowak. Environmental exposure to confined animal feeding operations and respiratory health of neighboring residents. Epidemiology. 2007; May;18(3):300-8.

The University of Utrecht: the latest scientific research has just been published (2011) in the Netherlands by a research group at the University of Utrecht. The found elevated concentrations of particulate matter (20-25% more than the background level), and elevated concentrations of endotoxins (till 90 EU/m3) in the vicinity of intensive lifestock. Near chicken farming were found higher concentrations than in the vicinity of pig farming.

Regarding the health effects they found more pneumonia and eczema in residents near intensive lifestock. This was from the registration of general practitioners over the last three years. Interestingly there was no increase in astma, rather a reduction. Also the people with astma have more exacerbations of respiratory symptoms and respiratory infections.

3. The first poster (Prevalence and risks factors of swine flu on British pig farms, Wieland et al. 2011) finds a higher prevalence of swine flu on British farms than expected. The most common strain was H1N2, and the second most common was H1N1 which can cause infections in humans. The poster does not give herd prevalences by swine variant, but 52% of farms had one of these two strains. In total, 19% of sows had H1N1. The risk factors they found include at least some pigs kept indoors, and incidence was reduced if at least some pigs kept in straw yards.



Royal Veterinary College
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Prevalence and Risk Factors for Swine Influenza in English Pig Farms

Barbara Wieland[1], Alexander Mastin[1], James Wood[2], Susanna Williamson[3], Ian Brown[3], COSI consortium, Dirk Pfeiffer[1]

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2. University of Cambridge, UK
3. Veterinary Laboratories Agency, UK

Background

Pigs are an important reservoir of H1N1, H1N2 and H3N2 influenza viruses, strains of which are endemic in pigs worldwide. Swine influenza virus (SIV) can also contribute to substantial economic loss in pig production due to respiratory disease.
Since 1991, the UK has monitored SIV through a national surveillance programme and identified avian-like H1N1, followed by H1N2, as the predominant strains. The programme is based on passive surveillance and therefore the true proportion of farms in England exposed to the different SIV strains and the prevalence of subclinical infection is difficult to estimate.

In order to plan future surveillance activities, improve preventive and control measures, the epidemiology of SIV in England needs to be better understood.

M&M

In total, 2,787 sera collected from 146 farms were tested for antibodies against avian-like H1N1, H1N2 and human-like H3N2 strains using haemagglutination inhibition (HI) tests. The herd-level case-definition was a reciprocal antibody titre of >= 40 in at least one growing or finishing pig (i.e. not from sows or weaners) as this indicates recent exposure of the herd to the virus.

Spatial clustering was assessed using the spatial scan statistic.

Risk factor analysis: in the first step, univariable analysis was carried out to identify possible associations between variables and farms status. In the 2nd step, variables belonging to the same group relating to farm management or other characteristics were assessed together with multivariable models and the best predicting variables were included in the 3rd step, the final multivariable model, which was fitted using backward selection (Mastin et al, 2011).

Objectives

1. To determine the prevalence:
   - of avian-like H1N1, H1N2 and H3N2
   - at herd and animal level
   - and to explore spatial distribution of endemic SIV strains
2. To identify risk factors for SIV at herd level

Results

1. Prevalence

In total 52% (CI95%: 46-61%) of farms had evidence of recent exposure or current circulation of H1N1 or H1N2. A total of 19 farms tested positive for both H1N1 and H1N2, and no farm was classified as seropositive for H3N2.
Farms in North England were more likely to test positive for avian-like H1N1, p<0.05, (Figure 1).

Figure 1: spatial distribution of avian-like H1N1 positive farms

H1N2 was the most prevalent strain. In the comparison of age groups, sows had the highest prevalence (Table 1).

Table 1: Overview of SIV in different age groups

Age group (no of samples)	H1N1	H1N2	at least 1 strain
Weaners (711)	2%	8%	9%
Growers (917)	2%	7%	9%
Finishers (864)	4%	8%	11%
Sows (253)	19%	29%	38%

2. Herd level risk factors

Through the 1st and 2nd step of the analysis, the variables listed in Table 2 were found to be associated with the outcome with a p-value <0.1 (as risk or protective factors), and were included in the multivariable analysis of the 3rd step. The final logistic regression model identified an increased likelihood of farm seropositivity for farms sampled in autumn, winter or spring months compared to farms sampled in summer, for farms with more than 18 pigs per water space, and for farms rearing pigs indoors. Decreased likelihood of positivity was found for farms using straw yards (Table 3). There was no evidence of any interaction between variables in the final model.

Table 2: List of potential risk/protective factors for SIV, as identified through univariable and multivariable analysis within variable groups explaining similar characteristics of the farm or of herd management (p-value<0.1):

Total number of pigs on farm
Location of sick pen (separate building)
Number of litters mixed together
Growers and finishers mixed together
Stocking density in finishers
Pigs kept indoors
Use of straw yards for pigs
Separation of boars upon entry to the farm
By-product fed to pigs
Pigs per feed space (weaners and growers)
Pigs per water space (growers and finishers)
Duration of rest from light
Visitors pig clean
Years of stockman experience
Stockman participating in pig events
Season of farm visit

Table 3: Final multivariable model for SIV risk factors

Variable	Odds Ratio	95% confidence interval	p-value
Pig access to water			
18 finishers or less per water space	1.00	-	-
More than 18 finishers per water space	5.22	1.57 – 17.43	0.01
Season of sampling			
Pigs sampled in the Summer months (July-September)	1.00	-	-
Pigs sampled at other times of the year	2.54	1.09 – 5.95	0.03
Housing type			
No pigs kept indoors	1.00	-	-
At least some pigs kept indoors	3.59	1.11 – 11.57	0.03
No pigs kept in straw yards	1.00	-	-
At least some pigs kept in straw yards	0.30	0.11 – 0.82	0.02

References

Mastin et al, 2011, PLOS currents influenza, PMCID: PMC3032880

Contact

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bbsrc
biotechnology and biological sciences research council

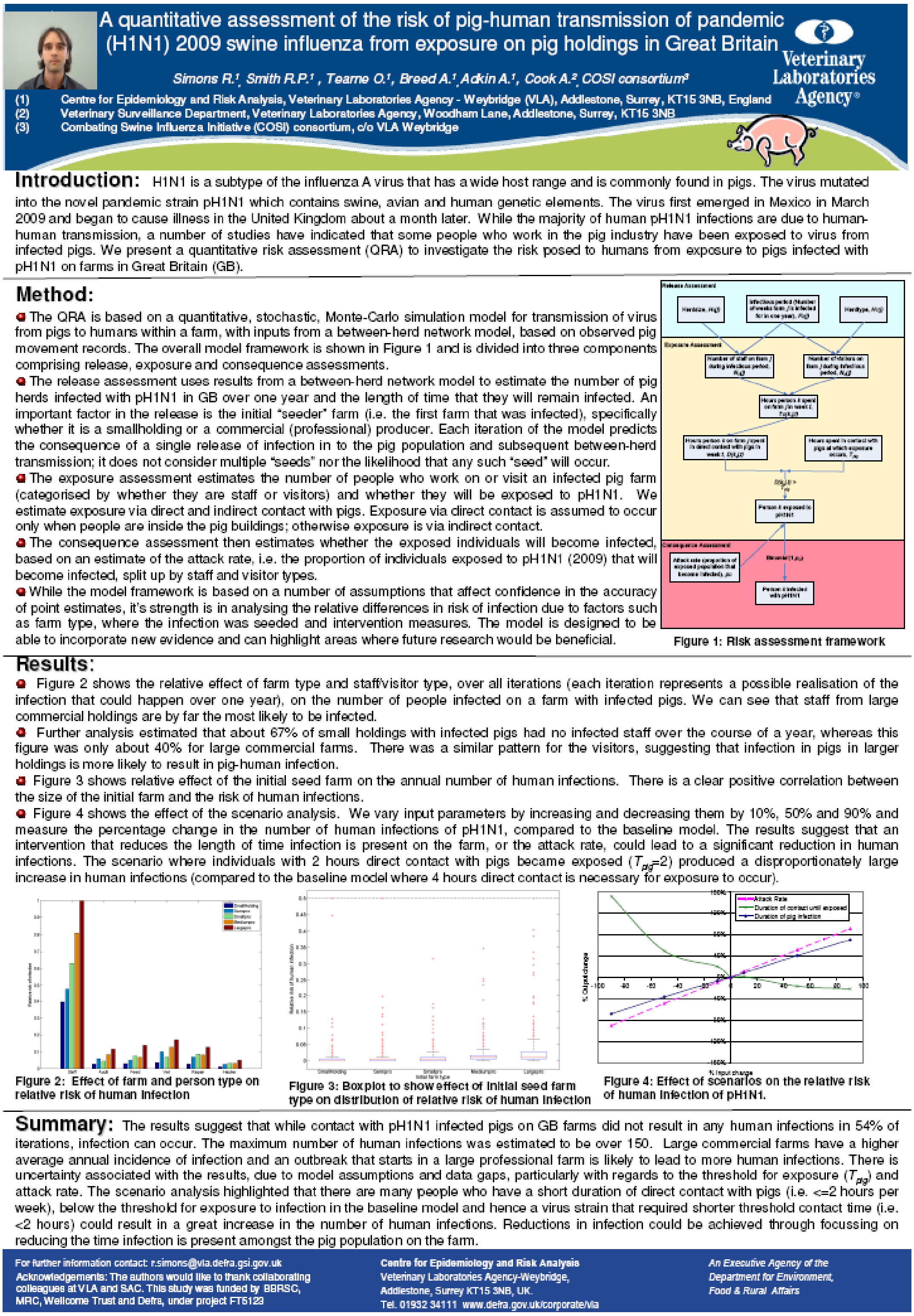
Discussion

In conclusion, the findings of this study improve our understanding of the current swine influenza situation in England and is the only such epidemiological study in the English pig population in recent years. Compared to estimates made based on passive surveillance, the prevalence found was higher than expected and also the most prevalent strain in the UK was H1N2 and not as expected avian-like H1N1. The high prevalence highlights the importance of subclinical infection, specifically that the importance of SIV as a significant production disease may have been underestimated in the past.

The findings of the risk factor analysis provide insight into how the spread of SIV can be prevented and will inform future surveillance activities. Given the recent spread of pandemic H1N1 in pigs, the findings will also be of importance to develop control strategies for this novel threat for the pig industry.

4. The second poster (Risk of transmission of swine flu to humans on UK farms, Simons et al. 2011) uses a model to estimate the risk of transmission of swine flu strain pH1N1, the epidemic strain which caused the huge outbreak in humans. The model found that:
-'staff from large commercial holdings are by far the most likely to be infected'.
- 'Further analysis estimated that about 67% of small holdings with infected pigs had no infected staff over the course of a year, whereas this figure was only about 40% for large commercial farms. There was a similar pattern for the visitors, suggesting that infection in pigs in larger holdings is more likely to result in pig-human infection.'

-' There is a clear positive correlation between the size of the initial farm and the risk of human infections'



A quantitative assessment of the risk of pig-human transmission of pandemic (H1N1) 2009 swine influenza from exposure on pig holdings in Great Britain

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(3) Combating Swine Influenza Initiative (COSI) consortium, c/o VLA Weybridge

Veterinary Laboratories Agency

Introduction: H1N1 is a subtype of the influenza A virus that has a wide host range and is commonly found in pigs. The virus mutated into the novel pandemic strain pH1N1 which contains swine, avian and human genetic elements. The virus first emerged in Mexico in March 2009 and began to cause illness in the United Kingdom about a month later. While the majority of human pH1N1 infections are due to human-human transmission, a number of studies have indicated that some people who work in the pig industry have been exposed to virus from infected pigs. We present a quantitative risk assessment (QRA) to investigate the risk posed to humans from exposure to pigs infected with pH1N1 on farms in Great Britain (GB).

Method:

- The QRA is based on a quantitative, stochastic, Monte-Carlo simulation model for transmission of virus from pigs to humans within a farm, with inputs from a between-herd network model, based on observed pig movement records. The overall model framework is shown in Figure 1 and is divided into three components comprising release, exposure and consequence assessments.
- The release assessment uses results from a between-herd network model to estimate the number of pig herds infected with pH1N1 in GB over one year and the length of time that they will remain infected. An important factor in the release is the initial "seeder" farm (i.e. the first farm that was infected), specifically whether it is a smallholding or a commercial (professional) producer. Each iteration of the model predicts the consequence of a single release of infection in to the pig population and subsequent between-herd transmission; it does not consider multiple "seeds" nor the likelihood that any such "seed" will occur.
- The exposure assessment estimates the number of people who work on or visit an infected pig farm (categorised by whether they are staff or visitors) and whether they will be exposed to pH1N1. We estimate exposure via direct and indirect contact with pigs. Exposure via direct contact is assumed to occur only when people are inside the pig buildings; otherwise exposure is via indirect contact.
- The consequence assessment then estimates whether the exposed individuals will become infected, based on an estimate of the attack rate, i.e. the proportion of individuals exposed to pH1N1 (2009) that will become infected, split up by staff and visitor types.
- While the model framework is based on a number of assumptions that affect confidence in the accuracy of point estimates, it's strength is in analysing the relative differences in risk of infection due to factors such as farm type, where the infection was seeded and intervention measures. The model is designed to be able to incorporate new evidence and can highlight areas where future research would be beneficial.

Figure 1: Risk assessment framework

Results:

- Figure 2 shows the relative effect of farm type and staff/visitor type, over all iterations (each iteration represents a possible realisation of the infection that could happen over one year), on the number of people infected on a farm with infected pigs. We can see that staff from large commercial holdings are by far the most likely to be infected.
- Further analysis estimated that about 67% of small holdings with infected pigs had no infected staff over the course of a year, whereas this figure was only about 40% for large commercial farms. There was a similar pattern for the visitors, suggesting that infection in pigs in larger holdings is more likely to result in pig-human infection.
- Figure 3 shows relative effect of the initial seed farm on the annual number of human infections. There is a clear positive correlation between the size of the initial farm and the risk of human infections.
- Figure 4 shows the effect of the scenario analysis. We vary input parameters by increasing and decreasing them by 10%, 50% and 90% and measure the percentage change in the number of human infections of pH1N1, compared to the baseline model. The results suggest that an intervention that reduces the length of time infection is present on the farm, or the attack rate, could lead to a significant reduction in human infections. The scenario where individuals with 2 hours direct contact with pigs became exposed (T_{pig}=2) produced a disproportionately large increase in human infections (compared to the baseline model where 4 hours direct contact is necessary for exposure to occur).

Figure 2: Effect of farm and person type on relative risk of human infection

Figure 3: Boxplot to show effect of initial seed farm type on distribution of relative risk of human infection

Figure 4: Effect of scenarios on the relative risk of human infection of pH1N1.

Summary: The results suggest that while contact with pH1N1 infected pigs on GB farms did not result in any human infections in 54% of iterations, infection can occur. The maximum number of human infections was estimated to be over 150. Large commercial farms have a higher average annual incidence of infection and an outbreak that starts in a large professional farm is likely to lead to more human infections. There is uncertainty associated with the results, due to model assumptions and data gaps, particularly with regards to the threshold for exposure (T_{pig}) and attack rate. The scenario analysis highlighted that there are many people who have a short duration of direct contact with pigs (i.e. <=2 hours per week), below the threshold for exposure to infection in the baseline model and hence a virus strain that required shorter threshold contact time (i.e. <2 hours) could result in a great increase in the number of human infections. Reductions in infection could be achieved through focussing on reducing the time infection is present amongst the pig population on the farm.

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An Executive Agency of the Department for Environment, Food & Rural Affairs

5. Environ Sci Technol. 2010 Dec 1;44(23):9128-33. Epub 2010 Nov 9.
Effect of temperature on the fate of genes encoding tetracycline resistance and the

integrase of class 1 integrons within anaerobic and aerobic digesters treating municipal wastewater solids.
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Abstract

The objective of this research was to investigate the ability of anaerobic and aerobic digesters to reduce the quantity of antibiotic resistant bacteria in wastewater solids. Lab-scale digesters were operated at different temperatures (22 °C, 37 °C, 46 °C, and 55 °C) under both anaerobic and aerobic conditions and fed wastewater solids collected from a full-scale treatment facility. Quantitative PCR was used to track five genes encoding tetracycline resistance (tet(A), tet(L), tet(O), tet(W), and tet(X)) and the gene encoding the integrase (intI1) of class 1 integrons. **Statistically significant reductions in the quantities of these genes occurred in the anaerobic reactors at 37 °C, 46 °C, and 55 °C, with the removal rates and removal efficiencies increasing as a function of temperature. The aerobic digesters, in contrast, were generally incapable of significantly decreasing gene quantities**, although these digesters were operated at much shorter mean hydraulic residence times. This research suggests that high temperature anaerobic digestion of wastewater solids would be a suitable technology for eliminating various antibiotic resistance genes, an emerging pollutant of concern.

6. Microb Ecol. 2010 Oct;60(3):479-86. Epub 2010 Feb 6.
Occurrence and persistence of erythromycin resistance genes (erm) and tetracycline resistance genes (tet) in waste treatment systems on swine farms.
Chen J, Michel FC Jr, Sreevatsan S, Morrison M, Yu Z.
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Abstract

Animal manure from modern animal agriculture constitutes the single largest source of antibiotic resistance (AR) owing to the use of large quantities of antibiotics. After animal manure enters the environment, the AR disseminates into the environment and can pose a potentially serious threat to the health and well-being of both humans and animals. In this study, we evaluated the efficiency of three different on-farm waste treatment systems in reducing AR. Three classes of erythromycin resistance genes (erm) genes (B, F, and X) conferring resistances to macrolide-lincosamides-streptogramin B (MLS(B)) and one class of tetracycline resistance genes (tet) gene (G) conferring resistance to tetracyclines were used as models. Real-time polymerase chain reaction assays were used to determine the reservoir sizes of these AR genes present in the entire microbiome. These classes of AR genes varied considerably in abundance, with erm(B) being more predominant than erm(F), erm(X), and tet(G). These AR genes also varied in persistence in different waste treatment systems. **Aerobic biofiltration reduced erm(X) more effectively than other AR genes, while mesophilic anaerobic digestion and lagoon storage did not appreciably reduce any of these AR genes**. Unlike chemical pollutants, some AR genes could increase after reduction in a preceding stage of the treatment processes. Season might also affect the persistence of AR. These results indicate that AR arising from swine-feeding operations can survive typical swine waste treatment processes and thus treatments that are more effective in destructing AR on farms are required.

7. Environ Sci Technol. 2011 Sep 15;45(18):7855-61. Epub 2011 Aug 19.

Effect of various sludge digestion conditions on sulfonamide, macrolide, and tetracycline resistance genes and class I integrons.

Ma Y, Wilson CA, Novak JT, Riffat R, Aynur S, Murthy S, Pruden A.
Via Department of Civil and Environmental Engineering, 418 Durham Hall, Virginia Tech, Blacksburg, Virginia 24061, USA.

Wastewater treatment processes are of growing interest as a potential means to limit the dissemination of antibiotic resistance. This study examines the response of nine representative antibiotic resistance genes (ARGs) encoding resistance to sulfonamide (sulI, sulII), erythromycin (erm(B), erm(F)), and tetracycline (tet(O), tet(W), tet(C), tet(G), tet(X)) to various laboratory-scale sludge digestion processes. The class I integron gene (intI1) was also monitored as an indicator of horizontal gene transfer potential and multiple antibiotic resistance. Mesophilic anaerobic digestion at both 10 and 20 day solids retention times (SRTs) significantly reduced sulI, suII, tet(C), tet(G), and tet(X) with longer SRT exhibiting a greater extent of removal; however, tet(W), erm(B) and erm(F) genes increased relative to the feed. **Thermophilic anaerobic digesters operating at 47 °C, 52 °C, and 59 °C performed similarly to each other and provided more effective reduction of erm(B), erm(F), tet(O), and tet(W) compared to mesophilic digestion. However, thermophilic digestion resulted in similar or poorer removal of all other ARGs and intI1.** Thermal hydrolysis pretreatment drastically reduced all ARGs, but they generally rebounded during subsequent anaerobic and aerobic digestion treatments. To gain insight into potential mechanisms driving ARG behavior in the digesters, the dominant bacterial communities were compared by denaturing gradient gel electrophoresis. The overall results suggest that bacterial community composition of the sludge digestion process, as controlled by the physical operating characteristics, drives the distribution of ARGs present in the produced biosolids, more so than the influent ARG composition.

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