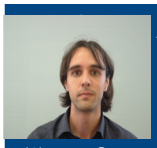

A quantitative assessment of the risk of pig-human transmission of pandemic (H1N1) 2009 swine influenza from exposure on pig holdings in Great Britain

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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.

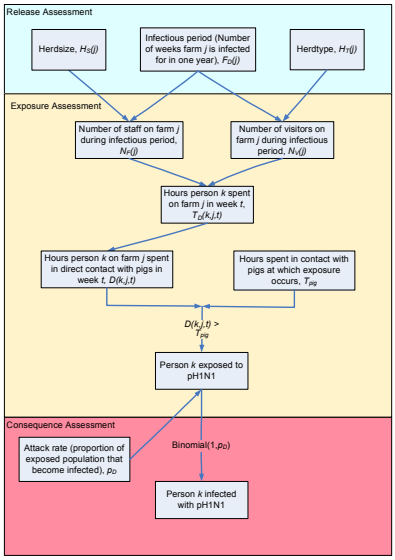

Figure 1: Risk assessment framework

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).

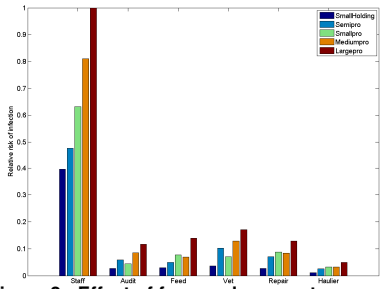

Figure 2: Effect of farm and person type on relative risk of human infection

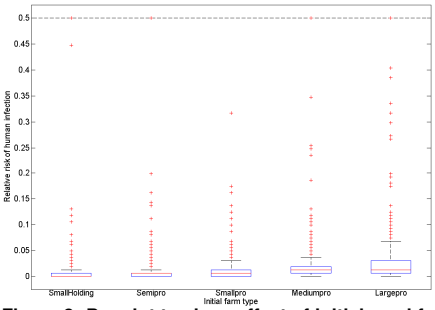

Figure 3: Boxplot to show effect of initial seed farm type on distribution of relative risk of human infection

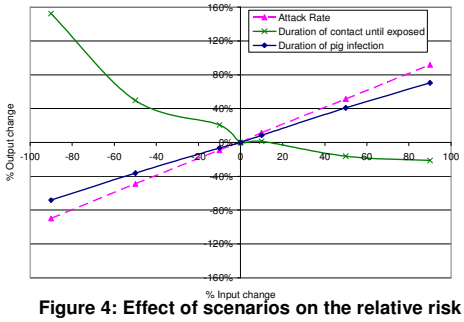

Figure 4: Effect of scenarios on the relative risk of human infection of pH1N1.

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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