Investigating between herd transmission of pandemic (H1N1) 2009 swine Influenza in Great Britain and the implications for pig farm workers

Smith R.P.[1] Sanchez-Vazquez M.[2] Tearne, O.[1] Simons R.[1] Marques D.[2] Arnold M.[1] Gunn G.[2] Breed A.[1]
Cook A.[1] COSI consortium[3]

(1) Centre for Epidemiology and Risk Analysis, Veterinary Laboratories Agency - Weybridge (VLA), Addlestone, Surrey, KT15 3NB, England
(2) Scottish Agricultural College (SAC), West Mains Road, Edinburgh, EH9 3JG, Scotland
(3) Combating Swine Influenza Initiative (COSI) consortium, c/o VLA Weybridge

Aim: The study described here was designed to address key population-level questions relating to spread and persistence of swine influenza in pigs and its detection. This poster describes the current and future actions of this research. The main aims of the modelling are: -

- To determine the likelihood that H1N1v will become endemic in the British pig population;
- To determine how surveillance should be optimised to detect incursion of H1N1v into pigs;
- To investigate how another novel re-assortment influenza virus might spread in the British pig population and pose a threat to human health.

Data collection and validation

To inform the transmission model, official records on pig movements were provided by the Animal Movement Licensing Scheme (AMLS) and Scottish Animal Movement Unit (SAMU). These records include movements to or from over 28,157 locations, including professional, semi-professional, hobby farms and abattoirs and markets/ports.

Official records were validated against information provided from three large pig producer groups, quality assurance programmes and abattoirs.

Overall agreement between officially kept records and the records kept by the producers was good. For example, a comparison of the AMLS data and movement data provided by a pig company (Figure 1) showed a Pearson's correlation coefficient of 0.97. This cross-validation represented 1.2 % of the overall number of movement records kept by AMLS for a single year, and 1.4% of the animals moved. 88% of the records kept by the company were officially registered by AMLS.

Appropriate data from previous British pig studies will also be utilised along with other current research into H1N1v by the full project consortium.

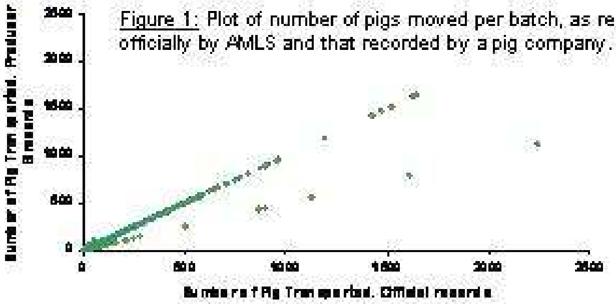


Figure 1: Plot of number of pigs moved per batch, as registered officially by AMLS and that recorded by a pig company.

Farm Transmission Network Model

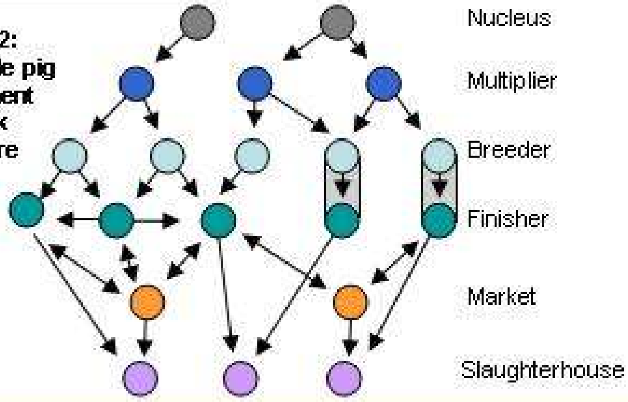
The aim of the between-farm transmission model is to simulate the spread of H1N1v through the network of pig holdings and in particular, the propensity for the virus to become endemic or to die out; determine key factors for optimising surveillance; and investigate hypothetical intervention strategies.

Daily pig movement records will be used to build a model where potentially infected pigs are transported between premises of different types (Figure 2). Different premises types may have different characteristics, e.g. farm link factors and intermixing of batches. Infection may also be spread by other factors, such as vehicle and personnel movements.

Inputs
Pig movements (AMLS)
Farm link factors e.g. Vehicle movements
Virus characteristics

Outputs
Farm-level prevalence
Accuracy of surveillance
Effectiveness of intervention

Figure 2: Example pig movement network structure



Human Infection Risk Model

For this section of the project we aim to develop a quantitative, stochastic, Monte-Carlo simulation model to address the risk question

"What is the risk of human infection with H1N1v (2009), due to exposure to pigs on farms?"

- This will not include the risk from exposure at the abattoir or transient areas such as markets
- Infection via humans or other animals will not be considered

The model will follow a standard risk assessment framework as outlined in the figure below

Release
Prevalence of H1N1v (2009) in pigs on farm

Exposure
Humans on farm: farm workers, visitors, family, public

Consequence
Risk of human infection

- Estimates for the release section will be obtained from the output of the farm transmission network model.
- For the exposure section, we will utilise data collected as part of previous studies that include
  - The number of staff on pig farms,
  - The number of visitors on a pig farm,
  - The reason for the visit (e.g. vet, haulier, repairs),
  - Duration of farm contact during a typical week,
  - Proportion of that time spent in contact with pigs.
- We are currently seeking sources of data to inform the consequence component of the risk model.

For both models, mutations and/or reassortments of current strains within livestock populations will be investigated to examine the effects of hypothetical changes which affect particular characteristics, e.g. increased pathogenicity.

For further information contact: r.smith@vla.defra.gsi.gov.uk

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Centre for Epidemiology and Risk Analysis
Veterinary Laboratories Agency-Weybridge,
Addlestone, Surrey KT15 3NB, UK.
Tel. 01932 34111 www.defra.gov.uk/corporate/vla

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