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Different herd level factors associated with H1N1 or H1N2 influenza virus infections in fattening pigs

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ABSTRACT

Herd-level factors associated with European H1N1 or H1N2 swine influenza virus (SIV) infections were assessed by mean of a cross-sectional study carried out in 125 herds in France. Serum samples from 15 fattening pigs in each herd were tested by haemagglutination inhibition. Data related to herd characteristics, biosecurity, management and housing conditions were collected by questionnaire during the farm visit. Climatic conditions in the post-weaning and fattening rooms, where the sampled pigs were housed, were measured over 20 h. Factors associated with H1N1 or H1N2 sero-positive status of the herd were identified by logistic regressions for binary outcome. For both subtypes, the odds for a herd to be SIV sero-positive increased if there were more than two pig herds in the vicinity (OR = 3.2, 95% confidence interval (95% CI): 1.4–7.6, $p < 0.01$ and OR = 3.5, 95% CI: 1.5–8.1 $p < 0.01$ for H1N1 and H1N2 respectively). Different factors were specifically associated with either H1N1 or H1N2 SIV infections. The odds for a herd to be H1N1 sero-positive were significantly increased by having a large number of pigs per pen in the post-weaning room (OR = 3.2, 95% CI: 1.2–8.6, $p = 0.02$), temperature setpoints below 25 °C (OR = 2.6, 95% CI: 1.1–6.4, $p = 0.03$) and below 24 °C (OR = 2.6, 95% CI: 1.1–6.1, $p = 0.03$) for the heating device in the farrowing room and the ventilation controller, respectively, and moving the pigs to the fattening facility *via* a room housing older pigs (OR = 3.3, 95% CI: 1.1–9.6, $p = 0.03$). A H1N2 sero-positive status was associated with a brief down period in the farrowing room (OR = 2.6, 95% CI: 1.1–6.3, $p = 0.03$), small floor area per pig in the post-weaning pen (OR = 2.9, 95% CI: 1.2–7.0, $p = 0.02$), large-sized fattening room (OR = 2.5, 95% CI: 1.1–5.9, $p = 0.03$), lack of all-in all-out management in the fattening room (OR = 2.4, 95% CI: 1.0–5.8, $p = 0.04$) and a temperature range of less than 5 °C controlling ventilation in the fattening facilities (OR = 3.2, 95% CI: 1.4–7.4, $p < 0.01$). Factors related to external and internal biosecurity and to the control of inside climatic conditions should be considered together when implementing programmes to better control SIV infections.

1. Introduction

Swine influenza viruses (SIVs) are widespread in pig populations throughout a large part of the world (Maldonado et al., 2006; Poljak et al., 2008; Suriya et al., 2008; Torremorell et al., 2012). Three SIV subtypes, H1N1, H3N2 and H1N2, are in current circulation among pigs worldwide, but lineages within each subtype may vary

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according to the geographical location (North America, Europe and Asia) due to various mechanisms of emergence (Olsen et al., 2006; Kuntz-Simon and Madec, 2009). In Europe, viruses from the avian-like swine H1N1, the human-like reassortant swine H3N2 and the human-like reassortant swine H1N2 lineages have co-circulated for many years within the swine population, with individual occurrences that may vary in time and differ from one country to another (Kuntz-Simon and Madec, 2009; Kyriakis et al., 2011, 2013). Thus, only H1N1 and H1N2 viruses have been found in United-Kingdom and Northwestern France since the 2000s, whereas all three subtypes have been detected in Belgium, Italy and Spain (http://www.esnip3.com; Simon et al., 2013).

The clinical course of influenza infection in pigs is similar to that in humans. The infection is characterized by fever, lethargy, anorexia, coughing, dyspnoea and weight loss (Olsen et al., 2006). In its typical epizootic form in pig herds, influenza virus infection is recognized clinically as an acute febrile respiratory tract infection usually characterized by a low mortality rate (less than 1%) but a high morbidity (almost 100%) (Olsen et al., 2006). In recent years, influenza outbreaks in densely populated pig areas where pigs are raised indoors, have led to the establishment of enzootic infections in herds. Indeed, under certain circumstances thought to be related to population dynamics and husbandry practices, SIV can constantly circulate within the population, sometimes without producing obvious clinical signs (Madec et al., 1985; Elbers et al., 1992; Brown, 2000; Simon-Grife et al., 2012; Kyriakis et al., 2013). Swine influenza viruses have also been reported as viral pathogens contributing to the porcine respiratory disease complex (PRDC) in fattening pigs, enhancing the severity of lung lesions (Deblanc et al., 2012; Fablet et al., 2012b). Diseases associated with SIV infection have been recognized as an important cause of economic losses for pig farmers due to medication costs and the decreased growth rate (Bennett and Ljpelaar, 2005; Brons et al., 2011).

Apart from their impact on pig health, SIV infections also raise public health concerns owing to (i) the zoonotic potential of SIVs and (ii) the potential for pigs to serve as intermediate hosts in interspecies transmission and creation of novel reassortant viruses with possible pandemic potential (Olsen et al., 2006).

Hence, interest in the epidemiology of influenza in pigs was aroused by the emergence in 2009 of a pandemic influenza A/H1N1 virus with genes originating from several enzootic SIVs (Smith et al., 2009).

Despite concerns regarding the huge impact of influenza infection in pigs and the possible transmission of SIVs to humans, few studies have investigated the risk factors for such virus infection in pigs. However, knowledge of the main factors influencing SIV infections would be useful to (i) implement adequate control strategies to reduce their occurrence in pigs and prioritize the corrective measures to be taken and (ii) provide accurate information for modeling studies, i.e. parameterization and validation of epidemiological models on the spread and maintenance of infectious diseases in pig units.

We therefore used data from a cross-sectional study for respiratory diseases carried out from 2006 to 2008 in 125 herds located in western France to assess herd-level factors associated with SIV infections. This paper reports the relationships between factors related to farm characteristics, management practices, housing and indoor climate and H1N1 or H1N2 sero-positivity measured in slaughter-aged pigs raised in these farrow-to-finish herds.

2. Materials and methods

2.1. Study design

Data and sera from 125 herds involved in a cross-sectional study of respiratory diseases in pigs were used. Details of the sampling scheme were presented elsewhere (Fablet et al., 2012a,b). Briefly, the study was carried out from November 2006 to February 2008 in western France where approximately 73% of French pigs are produced (Agreste, 2010). Eighteen farmer organizations (representing approximately 94% of the pigs produced in the area) provided a sampling base of 494 farrow-to-finish herds for which the respiratory health status for the previous year was known (herds with moderate or severe or without respiratory problems). The 125 herds were then selected using stratified random sampling with two selection factors: farm organization and respiratory status group (35% of herds selected in the group presumed to be lowly affected by respiratory diseases, 30% in the moderately-presumed affected group, 35% in the severely-presumed affected group). The farm organization stratum was considered to obtain a balanced sample according to affiliation and the presumed respiratory status group assignment was used to ensure the relevant spectrum of herd level disease to be present in the sample. Thus, herds with or without SIV infections would be expected in the final sample. Sample size calculation was based on logistic and economic constraints.

2.2. Herd data collection

Each herd was visited once to collect blood samples and the information on potential risk factors. The visit consisted of a face-to-face interview with the farmer by one investigator while three other investigators examined the herd and took blood samples from fattening pigs.

2.2.1. Blood sampling

Blood samples were taken from a random sample of 15 fattening pigs (selected using a randomization procedure, SAS, 2001) in a batch almost ready for shipment to the slaughterhouse ($\geq$22 weeks of age). The number of pigs to be sampled was chosen to detect viral infections with a minimum within-herd prevalence of 25% ($\alpha = 0.05$). Samples were collected by jugular vein puncture, using evacuated tubes (Vacuette, Dutscher SAS, Brumath, France) without additive. Sera were obtained by centrifugation for 10 min at $3500 \times g$ and stored at $-20\,^{\circ}$C until subsequent analysis.

2.2.2. Herd, management and climatic conditions

Data related to neighbourhood description, biosecurity and hygiene practices, management practices and housing