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Swine Surveillance for Public Health Planning

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Key Points

- Only swine influenza A subtypes H1N1, H3N2 and H1N2 are endemic in pigs worldwide. However, because pigs are susceptible to both avian and human influenza strains, they can be host to reassortment events and interspecies transmission.
- Case reports of interspecies influenza transmission from pigs to humans and from humans to pigs have been documented.
- Compared to person with no exposure to pigs, persons working closely with pigs – e.g. farmers, veterinarians, meat processors – are at increased risk of exposure to and infection with swine influenza.
- Influenza in swine is generally not notifiable, thus rendering the true number of influenza outbreaks in swine difficult to ascertain.
- In risk-based surveillance, public health and economic and trade consequences of diseases play an important role in the selection of diseases to include for surveillance purposes and certain strata of the population are preferentially sampled. Particular emphasis should be placed on regions where there is a high likelihood of human-animal contact and high levels of influenza activity in animal hosts. Indeed, integrated surveillance of pigs and swine workers was recommended as a method to better understand and detect cross-species transmission and diversity of influenza viruses.
- The U.S. and a number of European countries have implemented surveillance programs to gain a better understanding of the epidemiology of endemic and emerging swine influenza in pigs.
- In Canada, the Canadian Food Inspection Agency and the Canadian Public Health Laboratory Network (CPHLN) have established the Canadian Animal Health Surveillance Network (CAHSN) in collaboration with federal, provincial and university laboratories to improve the capacity to detect emerging diseases in real-time, particularly potentially zoonotic diseases.

Background

During April 2009, a novel pandemic influenza A (H1N1) virus (pH1N1) was causing illness in California and Mexico (1). Within weeks through human-to-human contact pH1N1 had spread to 30 countries worldwide (2). The major influenza pandemics of the last century occurred in 1968 and 1957 as a result of reassortment between human and animal influenza A viruses (3). The pH1N1 virus is unrelated to the seasonal human influenza A (H1N1) virus but genetically related to swine influenza viruses (SIV) (1). Most influenza researchers agree that the pH1N1 virus arose from a reassortment of two swine influenza viruses: a North American H1N2 virus and a Eurasian H1N1 virus, each of which themselves arose from prior reassortment events (4). The nearest common ancestor in pigs may have been circulating for at least a decade (5, 6). However, there is a gap in the knowledge of gene sequences of isolates that bridge the time and phylogenetic steps between pH1N1 and its closest ancestors (7, 8).

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knowledge that's contagious!

Des saviors qui se transmettent!

Type A influenza virus is a negative-sense single-stranded RNA virus of the family Orthomyxoviridae characterized by subtypes based on combinations of its surface antigens hemagglutinin (HA) and neuraminidase (NA) (9). These two viral surface proteins are targets for humoral immunity. Influenza A has immense capacity for mutating its genetics sequences, including those encoding antigenic regions of HA targeted by antibodies. The process of evolution of a single HA serotype, referred to as antigenic drift, can render antibody immunity gained in one influenza season ineffective in the next (9). A more serious problem arises from the segmented nature of the influenza virus genome (9). The 8 distinct strands of influenza A genomic RNA replicate separately (10). In the unlikely event of a double infection of two different strains in a single host, reassortment of gene segments, known as antigenic shift, can occur (9). The resulting series of novel combinations in the progeny viruses may be the source of new pandemic influenza viruses (9). The 2009 outbreak of pH1N1 virus underscores the potential for a swine-origin influenza virus to spread through human-to-human contact – a scenario not previously conclusively documented (11).

This Evidence Review summarizes and highlights the current state of knowledge and the key issues of swine influenza virus surveillance to inform public health policies, programs and practices. Specific objectives include:

- a critical assessment and consolidation of swine pH1N1 research findings
- a review of pH1N1 findings for the Canadian context
- a comparison of response efforts and policies implemented in Canada and other countries.

Influenza A virus in swine

In its epidemic form, SIV can cause acute clinical febrile respiratory disease characterized by high morbidity and low mortality (12). Endemic swine influenza may spread more slowly and be clinically unapparent (12). An outbreak of pH1N1 in swine in Alberta from June 12 through July 4, 2009, revealed that 94% of the swine that were positive for viral isolates from nasal swabs had few or no symptoms (13).

There are 16 serotypes of HA (H1-H16) and 9 serotypes of NA (N1-N9) (9). Only influenza A subtypes H1N1, H3N2 and H1N2 are endemic in pigs worldwide (11). These swine subtypes differ in origin, and in genetic and antigenic characteristics in different regions of the world (14). Pigs are critical hosts. Since they are susceptible to both avian and human influenza strains, they can be host to reassortment events and interspecies transmission (15).

Only influenza A subtypes H1N1, H3N2 and H1N2 are endemic in pigs worldwide.

Though some wholly avian or human influenza subtypes are capable of causing illness in pigs they are not known to transmit from pig to pig. Gene sequencing of influenza A virus from swine surveillance samples in China from 2005 to 2007 detected avian Y280-like[1] influenza H9N2 viruses in ill pigs in 10 southern Chinese provinces (16). The H9N2 subtype virus is known to infect not only chickens, ducks and pigs, but also humans (16). In China, the H9N2 virus was first isolated from a chicken in Guangdong province in 1992 and now is the most prevalent subtype of influenza virus in poultry in China (16). In Ontario, an outbreak of pneumonia on a swine farm implicated a wholly avian H4N6 virus (17). In Alberta from June 12 to July 4, 2009, an outbreak of pH1N1 in swine on a research farm was epidemiologically linked to humans known to be infected with pH1N1 (13). This study provides evidence that influenza infection in humans could potentially be a threat to the health of a swine herd.

Co-infection of the same host with two viruses of different origin-lineages can lead to progeny reassortant viruses through gene segment swaps and the formation of a hybrid virus (11). Generally these reassortant viruses are evolutionary dead ends, being either biologically unfit, or unable to compete with their better adapted parental strains, and fail to reproduce and thrive. On rare occasions, reassortment can produce a competitive new virus – as we saw with the pH1N1 virus. The success of interspecies transmission of influenza virus depends on the viral gene constellation with the ability to replicate in the new host (18).

[1] Avian influenza A (H9N2) viruses are endemic in the poultry populations across Asia and Middle East. The majority of these viruses belong to one of two lineages – G1 and Y280 – represented by prototype viruses A/quail/Hong Kong/G1/97 and A/duck/Hong Kong/Y280/97, respectively. H9N2 viruses can infect multiple avian species; in addition, infrequent transmission from poultry to humans and pigs has also been reported.

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The epidemiology of SIV has changed dramatically since 1997 (19). In North America, the classic swine H1N1 lineage was most common from 1930 to 1998 (19). Although antigenic drift H1N1 variants have been isolated since 1991, a dramatic shift occurred in 1997-1998 with the emergence of H3N2 viruses with genes derived from humans, swine and avian sources. Since then, these H3N2 viruses have become endemic SIVs in North America (1, 19). Multiple reassortant SIV variants between the classic swine H1N1 and the triple-reassortant H3N2 virus, and other influenza viruses have emerged as new reassortant H1N2 and H1N1 subtypes (20, 21).

The classic swine H1N1 continues to circulate in pigs in Asia, the Americas and, until the 1980s, in Europe (1). The first significant outbreak of SIV in mainland Europe occurred in the late 1970s following the transmission of an H1N1 virus from wild ducks (14). Since 1979, a novel H1N1 virus of avian origin has replaced classic swine H1N1virus in Europe (14). The triple reassortant virus continued to undergo antigenic shift generating triple reassortant H1N1 and H1N2 viruses that become increasingly diverse and distant to classic SIV (1). A novel reassortant swine H1N2 strain with genes derived from the human pH1N1 2009 virus was implicated in a respiratory disease outbreak on a swine farm in Italy in May 2010 (18).

Based on the Ontario Swine Sentinel Project surveillance program, the proportion of H1N1 seropositive Ontario finisher herds (seropositive herds had > 3 reactors) (n=46) in 2004 and 2005 was 19.5% and 30.5% respectively (21). The H1N1 ELISA test used for the study was determined to have a sensitivity and specificity of 98.8% and 91.6%, respectively (21). For the H3N2 subtype the point prevalence of positive herds (>3 reactors) in 2004 and 2005, was 6.5% and 40.8% respectively. The H3N2 ELISA test used for the study was determined to have a sensitivity and specificity sensitivity 96.1% and 89.0%, respectively (21).

In Europe, results of the 2002-2003 European Surveillance Network for Influenza in Pigs 1 (ESNIP 1) survey involving 7 countries (Belgium, Germany, Italy, Spain, Ireland, Poland and Czech Republic) reported variable seropositivity ratios among unvaccinated sows (n=4,190) from 651 herds. No country had test results that were free from H1N1 seropositivity (14). Sows from countries with large populations of pigs – Belgium, Germany, Italy and Spain – had antibodies to two or three subtypes with seroprevalence ratios to each of the three SIV subtypes ranging from 30% to 50%. In Ireland, the Czech Republic and Poland, where swine farming is less intensive, H1N1 was the dominant subtype with H1N1 seroprevalence ranging from 8% to 12% and H1N2 and H3N2 seroprevalence ranging from 0% to 4% (14). All sera were tested in hemagglutination-inhibition (HI) tests against one H1N1, one H3N2 and two H1N2 swine influenza viruses.

In China until 2008 the co-circulating classic H1N1 and H3N2 subtypes were predominant in swine (22). A recent study of isolates from nasal swabs taken from healthy pigs (n=1,344) at abattoirs from 2007 to 2008 revealed that all H1N1 isolates belonged to the avian-origin European H1N1 lineage (22). An abattoir-based study in China from 2006 to 2009 (n=3,546) reported that H1N1, H1N2 and H3N2 co-circulate with the isolation proportion for H1N1 and H3N2 as 0.54% and 0.25% respectively (23).

A random-selection cross-sectional serologic study of finisher herds (n=53) conducted in Korea with serum samples collected between November 1, 2005 and February 28, 2006 reported herd seropositivity to classic swine H1N1, swine H3N2 and both as 83%, 70% and 47% respectively (24). Prospective passive

serosurveillance of pigs with respiratory disease in Korea from 2002 to 2006 (n=8,427) and virus isolation from nasal swabs from 2004 to 2007 (n=687) revealed that the 3 subtypes H1N1, H1N2 and H3N2 co-circulate and are undergoing active evolution by independent reassortment events (25). Serology was conducted using HI tests as outlined by the U.S. Centers for Disease Control and Prevention (U.S. CDC) 1975; however the technique's sensitivity and specificity were not reported.

In Malaysia, a 2005 study of randomly selected farms reported that the H1N1 seroprevalence among pigs (n=727) was 12.2% and among farms (n=41) was 41.4% (26). The H1N1 ELISA test used for the study was determined to have a sensitivity and specificity of 98.8% and 91.6%, respectively (26). According to Poljak *et al.* [2008], ELISA is more specific and sensitive than HI test. However, unlike HI test, ELISA may not identify positive animals at the early stage of infection, particularly when the virus is introduced into a naive swine population (26).

In New Zealand (NZ), a 1996 SIV serosurveillance study among 429 pigs at slaughter from 48 geographically dispersed farms reported seropositivity in 86% of pigs of which 79% were seropositive to H3N2 virus, the typical swine H3N2 that is closely related to a human strain (27). Samples were tested using a type-specific influenza A nucleoprotein blocking-ELISA (NP-B-ELISA) with 25% also being tested by HI to determine subtypes present; however, the test's sensitivity and specificity were not reported.

Swine influenza and zoonotic infections

Among the 18 known animal hosts for influenza A virus, only pigs and birds are reported to transmit influenza virus to humans (9). Seropositivity to swine influenza A strains has been reported in humans since the late 1970s. A voluntary cohort (n=803) of agricultural workers, their spouses, and non-agricultural workers from Iowa, USA enrolled in the 2004 Agricultural Health Study were followed for 2 years to determine their risk of exposure to swine H1N1 (28). Swine-exposed participants and their non-swine exposed spouses had 55 times and 28 times the odds of elevated antibody levels to swine H1N1 respectively compared to non-swine exposed persons (28). In a separate study, among the swine-exposed workers (n=342), the odds of an elevated titre to swine H1N1 was greatest among farmers, followed by veterinarians, then meat processers, compared to non-swine exposed persons (29). A Thai case-control study conducted in late 2008 to early 2009 showed that swine workers from 2 farms were at increased odds to have serological evidence for exposure to swine H1N1 and H1N2 viruses compared to non-swine workers (30).

At least 11 sporadic human cases of triple-reassortant swine influenza A (H1) were confirmed by the U.S. CDC between 2005 and 2009. Nine of the patients had had exposure to pigs, five through direct contact and four through visits to a location where pigs were present but without contact. In another patient, human-to-human transmission was suspected (31).

Recently, Haß *et al.* used a simultaneous Baysean inference technique to examine the phylogeny and ancestral hosts from all human, avian and swine H1 and N1 full length sequences available from the NCBI Flu-database (as of October 31, 2009) to assess the role of swine as "mixing vessel" in interspecies transmission of H1N1 influenza A virus (32). Interspecies transmission was rare, particularly between humans and birds. No human isolates were found in the avian clade and only one avian isolate was found in the human clade and this isolate may have resulted from laboratory contamination (32). The H1N1 host switches involved pigs as either the source or recipient of the interspecies transmission event. Swine isolates showed a more universal spectrum of amino acids at receptor binding sites partly explaining the role of swine as "mixing vessel" for influenza A viruses (32). However, there was some ambiguity about the deeper nodes in this study. The authors warned against over-interpretation of the results and suggest data characterized by relatively few interspecies transmission events and over-represented by human isolates could have led to an unknown bias (32).

No other reports of the probability of reassortment events or transmission and the exact nature of contact for transmission of swine influenza viruses to humans was found at this time. Though serologic surveys and case reports demonstrate that persons working closely with pigs are at increased risk of exposure and infection, subsequent human-to-human transmission of SIV appears to be rare and unconfirmed.

Experimental infection of piglets with the A/Mexico/InDRE4487/2009 and A/swine/Alberta/OTH-33-8/2009 strains of pH1N1 virus failed to result in virus recovery from skeletal muscle, blood or rectal swab samples from viremic, clinically ill pigs that yielded virus from their respiratory tissues (33). There is no evidence that the consumption of pork and pork products from influenza A infected

animals is a threat to human health (33).

Human influenza virus in swine

The true number of pH1N1 outbreaks in swine is difficult to ascertain as it is generally a non-notifiable disease in swine (34). As of May 2010, antibodies to pH1N1 had been reported in pigs and turkeys in 24 countries worldwide, including Canada (35, 36). The chronology of the outbreak of pH1N1 in a closed swine research farm and matching of isolates among infected pigs and humans supports the suspicion that pigs can become infected with pH1N1 through transmission from people and that the pH1N1 virus can spread readily among pigs in a modern confined animal feeding operation (13). According to the Department for Environment, Food and Rural Affairs, UK, other cases of pH1N1 in pigs worldwide were suspected of being the result of infection transmitted from humans but this claim was unsubstantiated (34).

In Japan, during 10 years of SIV serosurveillance among abattoir pigs (n=6,146) from 1978 to 1987, increased incidence of seropositivity to human H1N1 virus strains coincided with 2 periods of human influenza epidemics, in 1984 and 1986/1987 (37).

The case for swine influenza virus surveillance

Until the apparently sudden emergence of pH1N1, animal surveillance of influenza A virus was focused on the avian H5N1 strain in poultry (38). A lack of SIV gene sequence surveillance presents a knowledge gap regarding the precise evolution of pH1N1. It is unknown if the pH1N1 virus, a reassortant virus, circulated in a particular swine population or individual pigs prior to transmission to humans or alternatively, if the final steps in the evolution of pH1N1 virus occurred in humans (39).

Reassortment of influenza viruses can occur not only in swine but also in humans as demonstrated by a recent case of co-infection of pH1N1 and seasonal H3N2 in an infant in Ontario leading to a novel reassortant virus (40).

In risk-based surveillance, public health, and economic and trade consequences of diseases play an important role in the selection of diseases to include for surveillance purposes and certain strata of the population are preferentially sampled (41). Particular emphasis should be placed on regions where there is a high likelihood of human-animal contact and high levels of influenza activity in animal hosts (41).

A lack of SIV gene sequence surveillance presents a knowledge gap regarding the precise evolution of pH1N1.

Academic experts have recommended integrated surveillance of pigs and swine workers as a method to better understand and detect cross-species transmission and diversity of influenza viruses (42, 43). Based on a report of a novel H3N2 virus that closely resembled swine H3N2 virus in a child on a communal farm in Alberta in 2007, Dr. Joan Robinson of the Public Health and Provincial Laboratory in Edmonton recommended routine surveillance for cases among swine workers to enable early detection of a strain with the potential for person-to-person transmission (44). In addition, Haß *et al.* suggests that more comprehensive and detailed analyses of interspecies transmission should also consider other host species and probably need to incorporate not only H1N1 but also other subtypes of the influenza A virus to account for the role of reassortment (32).

Through an evolutionary comparative analysis, Christman *et al.* provides support for the 'unsampled pig herd' theory in which precursors of the pH1N1 went unsampled in swine herds for 9-12 years for the six North American swine influenza viral genes and 12-17 years for the two Eurasian genes (NA and M), thereby refuting a suggested theory posited by Gibbs *et al.* that the pH1N1 virus arose through a reassortment of escaped laboratory strains that are not generally subjected to routine surveillance (4, 7).

The level of risk for another pandemic swine-origin influenza strain to emerge in the human population is unknown. Pandemic influenza viruses in the past have occurred through reassortment events that by their very nature are impossible to predict. Studies and case reports have demonstrated that reassortment can occur in both humans and pigs. Minimization of opportunities for human-swine or swine-human novel reassortant viruses to emerge and early detection of potentially pandemic strains together with an enhanced understanding of the characteristics that contribute to influenza A transmissibility and pathogenicity may help protect the public.

Challenges to swine influenza virus surveillance

Swine influenza, as a non-reportable disease is investigated on a voluntary and anonymous basis in most jurisdictions worldwide (45). Effective surveillance will require a globally agreed-upon framework for process and nomenclature of newly emerging viruses (46, 47). Comprehensive surveillance of emerging and reassortant strains requires more efficient tools and laboratory capacity for viral genetic characterization (48).

Establishing a unified international administrative framework coordinating all animal and human influenza A research, surveillance and commercial work (e.g. vaccine production) and a detailed registry of all influenza isolates held for research and vaccine production will strengthen such surveillance (7, 49).

Monitoring for novel strains requires virus isolation followed by molecular assays, the most sensitive and specific technique for SIV surveillance. In addition, the type of sample, and timing and handling of the sample are important factors in the accurate assessment of the presence and identification of SIV. Samples should be collected from acutely affected untreated pigs in the febrile stage (50). However, as demonstrated by the outbreak of pH1N1 in swine described by Forgie *et al.*, initiation of surveillance practices and biosecurity measures, as a result of detecting clinical symptoms of cases, to respectively detect and prevent interspecies transmission could be circumvented by preclinical and asymptomatic shedding of influenza virus A in swine and humans (13).

Though it is accepted that the pH1N1 virus in pigs does not pose a threat to pigs themselves nor to humans in contact with infected pigs or to consumers of pork products, Gray *et al.* acknowledges the considerable concern that the pH1N1 strain might become enzootic in modern pigs and that progeny strains from reassortment with other swine influenza strains might emerge in pigs and threaten both humans and pigs with even greater morbidity (36). Indeed, reassortment of pH1N1 with endemic SIV strains has already been documented in China, Thailand and Argentina (36, 51).

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Serologic studies and/or surveillance could be used to monitor the evolution of SIV and pH1N1 in swine provided that appropriate local, novel and vaccine strain antibodies can be utilized. Typical of industrialized countries, on intensively reared swine operations in the Netherlands, the optimum time to test seroprevalence of SIV in non-vaccinated pigs on farrow-to-finish operations was 16 weeks of age through to 22 weeks whereas, on finishing operations, antibodies were maximized at the end of the 22 week finishing period (52). Pacific Rim countries such as China, Japan and New Zealand have all conducted swine influenza serosurveys using data collected at abattoirs (22, 27, 37).

Throughout much of the world including North America, swine influenza virus surveillance is largely passive and voluntary and generally requires a sentinel event (e.g. unusual illness in pigs). Gray *et al.* notes that during the initial stages of the 2009 influenza pandemic, the diagnostic requests for influenza virus detections among U.S. pigs markedly declined at least temporarily as a result of swine farmers' concerns that pH1N1 detections in their pigs would prevent their pigs from entering consumer or export markets (36). Similarly, in Canada, the producers' experience of market consequences or perceived government response to positive pH1N1

herds during the early stages of the pandemic led to a reduction of requests for SIV testing to levels below those prior to 2009 (53).

In the U.S., university, state and private laboratories maintain SIV databases including genome sequences (45). However, this has only provided a limited national picture and has been challenged by proprietary restrictions on isolate sharing (45).

Swine influenza virus reassortment events that may generate pandemic influenza viruses are viewed by researchers in the field as a potential public health problem and not by producers as a health threat to swine. Private sector commitment to surveillance and reporting will require a better understanding of the potential health consequences of novel SIVs to swine workers and their families, the risks to market access if an undetected case was exported, and meaningful producer compensation for additional costs or loss of revenue (46).

Surveillance of swine H1N1 in Canada

In Canada on April 19, 2009, discovery of pH1N1 triggered an alert to the Canadian animal health community, whereby owners and veterinarians of swine populations were encouraged by Canadian Food Inspection Agency (CFIA) to report any outbreaks of influenza-like illness (ILI) for full investigation (46). A National Working Group on pH1N1 worked with provincial jurisdictions to develop a framework for farm investigations of pH1N1 in swine and, due to the emerging nature of the disease, to notify the World Organization for Animal Health (OIE) of pH1N1 swine outbreaks (46, 54). Because the role of pigs in the spread of pH1N1 was still uncertain, this resulted in the mass depopulation of one affected herd in Alberta in June 2009 during a pH1N1 outbreak (54).

In Alberta, under the Animal Health Act implemented in January 2009, influenza in pigs became a notifiable disease (55). In Manitoba, since the Animal Reportable Diseases Regulation was passed in 2008, pH1N1 became the first major disease to be reportable (54).

The zoonotic transmission of influenza A among swine and swine workers is being examined in the "Flu Zoonotic Study" using a prospective cohort design on swine-producing Hutterite colonies in Alberta and on Alberta swine farms experiencing SIV outbreaks. The purpose of the study is to assess and characterize influenza virus transmission between swine and humans (56). Active surveillance will include collection of baseline serum samples in the fall among Hutterite colony members and their swine herds (56). ILI among colony members and/or swine workers triggers virological and paired serological sample collection among the affected individuals and among the pigs in the herd (56). ILI among the swine herds triggers virological and paired serological sample collection among all swine workers (56). Alberta swine farms experiencing an outbreak of ILI are invited to participate in the study with test positive swine triggering testing of the swine workers (56).

In Canada, the CFIA and the Canadian Public Health Laboratory Network (CPHLN) have established the Canadian Animal Health Surveillance Network (CAHSN) in collaboration with federal, provincial and university laboratories to improve the capacity to detect emerging diseases in real-time, particularly potentially zoonotic diseases (57). Common protocols and reagents among the laboratories will allow for interoperability and sharing of expertise. Surveillance data received from multiple sources will be combined to allow for simultaneous alerts to human and animal health authorities when potential animal disease threats are identified (57).

Surveillance of swine H1N1 in the United States

In July 2010, the U.S. Department of Agriculture (USDA) Animal and Plant Health Inspection Service (APHIS) announced the revised National Surveillance Plan for Swine Influenza in Pigs, outlining the objectives of better understanding the epidemiology of endemic and emerging SIV, making SIV isolates available for research and establishing an objective database to allow proper isolate selection for development of updated diagnostic tools and vaccines (45). Participation in the surveillance program is recommended but not required (45). Pigs exhibiting ILI on farms or at points of comingling (e.g. auctions, markets, fairs or swine exhibitions) and swine populations epidemiologically linked to a confirmed human case of SIV (including the pH1N1 2009 virus) will be sampled by producers themselves, veterinarians or animal health officials under an anonymous protocol, or a traceable protocol with the owner's permission (38). On-farm swine populations epidemiologically linked to a human SIV case, as determined by public health authorities, should be investigated with the swine owner's consent by the attending veterinarian under the traceable protocol. The industry, through the National Pork Board and other industry stakeholders together with APHIS, will be responsible for the appropriate education/communication materials to produc-

ers, swine veterinarians and industry representatives (45, 58). The USDA will bear the laboratory costs of the program and regular reports will be provided to stakeholders (45).

Surveillance of swine H1N1 in other international jurisdictions

On June 2, 2009 in Brussels during the H1N1 pandemic, the European Commission recommended focusing surveillance activities on pigs exhibiting ILI and those that had possibly been exposed to pH1N1-infected humans to determine if swine were the source of human exposure or if the virus could be detected in swine populations (59). The Food and Agriculture Organization (FAO) guidelines for general surveillance strategies for SIVs in swine suggest that animals showing clinical signs should be sampled, and consideration should be given to targeted or active surveillance of pigs with ILI in slaughterhouses and animal markets with trace-back to the pig farm of origin for further investigation (59). Currently the OIE FAO Animal Influenza Network of international laboratories offers a list of reference laboratories and recommendations for sample collection and shipment (59).

Building on the European Surveillance Network for Influenza in Pigs 2 (ESNIP 2) initiative, the European Commission has launched the ESNIP 3 program which includes governmental, academic and industry partners from 15 countries: the U.K., Belgium, France, Italy, Denmark, Poland, Spain, Germany, Finland, Hungary, The Netherlands, Greece, Israel, China and the U.S. (60). The ESNIP 3 program will expand the knowledge of the epidemiology and evolution of SIV in Europe through extensive virological and serological surveillance of pigs with ILI over a 36-month period (60). In particular, the spread and evolution of pH1N1 will be monitored (60). Diagnostic techniques and surveillance approaches will be harmonized; a European SIV databank will be established and information will be shared with Network partners focusing on human, avian and equine host species (60). By subtyping and genetic sequencing, SIV virus evolution will be tracked (60). The European SIV virus bank and electronic database for the scientific community will be expanded (60). Further details regarding preliminary results, costs of the program and logistics of the partnership arrangements were not available through this review process.

Since 1991, the U.K. National Swine Influenza Surveillance Program operated by the Veterinary Laboratories Agency has offered free-of-charge laboratory testing for the detection of SIV (61).

Conclusions

It remains unclear exactly how the swine-origin pH1N1 virus evolved. Integrated surveillance of influenza A in pigs, humans and avian species may help determine the bidirectional transmission of influenza between human and swine, and the emergence of novel strains particularly at the human-swine interface, where potential for reassortment events is maximized and early detection of zoonotic strains would be most likely. Canada could benefit from joining international partners to enhance the understanding and early detection of the emergence of novel swine influenza strains.

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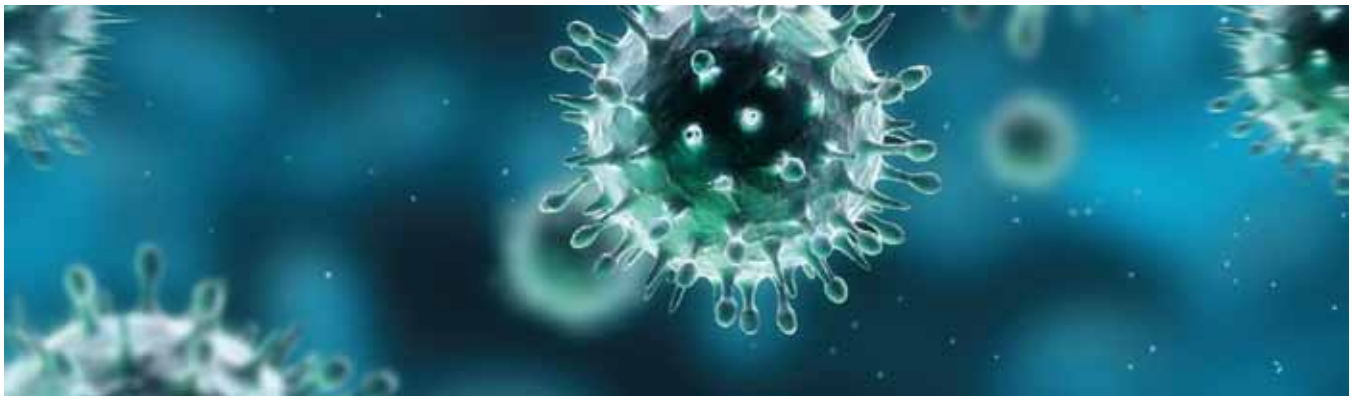

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