

## **SURVEILLANCE OF SWINE INFLUENZA ACROSS THE PIG VALUE CHAIN IN VIETNAM**

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### **Introduction**

Swine is considered as a potential reassortment vessel for the generation of novel influenza viruses that can spread in humans (1). While swine influenza research has increased since the occurrence of the H1N1 2009 pandemic, the surveillance of the viruses in the pig population still remains limited in many parts of the world. Monitoring of swine influenza is needed in places like Vietnam with high human, pig and poultry populations in close contact with each other. Based on a comprehensive study of the pig value chain in Northern Vietnam, different surveillance protocols for the detection of influenza viruses in swine were developed and compared. One year surveillance results and the efficiency of the protocols are described in this paper.

### **Materials and methods**

The study was performed in Northern Vietnam (Hung Yen province and Hanoi). A first study on farm typology and pig movements in the area allowed the description of the different sectors of the pig value chain and of their interconnection. The design of swine influenza surveillance protocols was based on these findings. Monthly sampling was carried out in pigs from May 2013 for 14 months in the familial farming sector in Hung Yen including three local slaughterhouses, a live pig market, and a total of 17 sentinel farms, and in a collective slaughterhouse in Hanoi to target the commercial sector. Nasal swabs and sera were collected from the pigs for virological and serological analyses respectively. Virus isolation on MDCK was performed, followed by sequencing of the influenza isolates. IDExx Influenza A Ab ELISA tests were used to detect influenza antibodies in sera, and the positive were selected for haemagglutination inhibition (HI) tests. Surveillance data were analyzed using R3.1.1, and phylogenetic analyses performed with Mega 6.

### **Results**

A total of 78 viruses were isolated at the collective slaughterhouse. No virus was isolated from the other protocols. A total of 14 H1N1, 27 H3N2, and 35 H1N2 were identified (two isolates need re-sequencing). Based on haemagglutinin and neuraminidase sequencing, twelve H1N1 viruses were related to A(H1N1)pdm09 lineage. For H3N2, 26 viruses were related to a Korean triple reassortant virus (2), and one related to viruses isolated in 2010 in Southern Vietnam (3). All the H1N2

had similar HA and NA originating from different viral strains, and the remaining H1N1 appeared to be reassortants between these H1N2 and A(H1N1)pdm09. Further sequencing of internal genes will be performed. Serological results in the slaughterhouses showed high influenza prevalence with a peak in spring and a drop in summer. On the contrary, the seroprevalence in the live pig market was low to null. Six sentinel farms seroconverted during the study period. Influenza-like illness was observed by the farmers only in three of these sentinel pig groups. On the other hand, these symptoms were observed in seven of the 11 groups that did not seroconvert.

### **Discussion**

In Vietnam, no influenza isolation has ever been successful in the familial swine production sector, as for our study, although influenza circulation was shown by high seroprevalences in local slaughterhouses and confirmed by seroconversion of sentinel farms. This is probably due to the short window of infection in small pig herds. Our results in sentinel farms confirmed the challenges of implementing surveillance based on symptom observation in the Vietnamese context, with multiple respiratory diseases in circulation. Epidemiological data may help to target sampling in order to increase the probability of virus isolation. Surveillance in the commercial sector, especially at the slaughterhouse, was more efficient than the other protocols in terms of virus isolation and characterization. This surveillance protocol has been sustained and is still ongoing. However, information on strains circulating in all sectors is needed, and additional HI tests using a representative strain from each viral subtype isolated will be performed and may provide some elements of link between viruses circulating in the commercial sector and in the familial farms.

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