Surveillance along the pig value chain for the detection of swine influenza in Northern Vietnam

SCHOOL OF PUBLIC HEALTH
THE UNIVERSITY OF HONG KONG
香 港 大 學 公 共 衞 生 學 院

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Eugénie Baudon[1,2], Dao Duy Tung[3], Leo L.M. Poon[1], Pham Thi Nga[3], Benjamin J. Cowling[1], Marisa Peyre[2], Nguyen Viet Khong[3], Malik Peiris[1]

[1]The University of Hong Kong, Hong Kong Special Administrative Region, China; [2]French Agricultural Research Center for International Development (CIRAD), Montpellier, France; [3]National Institute of Veterinary Research, Hanoi, Vietnam.

Background

The emergence of the H1N1 2009 pandemic influenza emphasized the importance of swine in the epidemiology of influenza viruses. However, in most developing countries with a high pig population like Vietnam, there is no surveillance of swine influenza performed on a regular basis. Surveillance strategies suitable to the socio-economic context of these countries are needed.

Objectives

The objective of this study was to develop and evaluate surveillance protocols for the detection of swine influenza taking into account the specific organization of the pig value chain in Vietnam.

Methods

One-year surveillance protocols were started in May 2013 in Hung Yen and Hanoi, two provinces of the Red River Delta in the North. Sampling was performed monthly in an industrial slaughterhouse in Hanoi, three local slaughterhouses, a live pig market, and eight sentinel farms in Hung Yen province (Images 1&2). Blood samples were collected and the sera analyzed by ELISA; nasal swabs samples were taken, then inoculated on MDCK for virus isolation, and the isolated viruses were sequenced. The data analysis was performed with R3.0.2, and the phylogenetic trees were constructed using Bioedit and Mega 5.

Results

A total of 78 viruses were isolated in the industrial slaughterhouse from May 2013 to June 2014 (Table2), while no virus was isolated within the other protocols. To date, the samples from May to October 2013 were analyzed (Table 3). From August to October 2013, nine H3N2 and eight H1N1 viruses were isolated and sequenced, while there was no virus isolated in the previous months. High seroprevalences in the industrial slaughterhouse were observed from May to July, while seroprevalences in the local slaughterhouses varied and did not show specific trends. In the live pig market, the seroprevalence was low to null (Figure 1). Finally, in five sentinel farms, a seroconversion was observed at different ages and months (Figure 2).

Table 1: General description of the surveillance protocols

Locations	Age of pigs	Faming systems represented			Number of samples per month	
		Industrial farms or companies	Large familial farms	Small familial farms	Blood	Swabs
Industrial slaughterhouse (n=1)	4-6 months	+++	++	-	70	150
Local slaughterhouses (n=3)	4-6 months	+	+++	++	up to 75	up to 75
Live pig market (n=1)	2 months	-	+	+++	50	60
Sentinel farms (n=8)	From 1 to 6 months	-	++	+++	50	50
Syndromic surveillance (n=39 participants)	All	-	++	+++	na	na

Table 2. Number of viruses isolated in the collective slaughterhouse by subtype per month

Sampling month	May-Jul	Aug	Sep	Oct	Nov	Dec	Jan	Feb	Mar	Apr	May	June
Number of viruses by subtype	0	4 H1N1 9 H3N2	2 H1N1	2 H1N1	2	2	4	10	12	4	27	0
					Confirmed by BD Directigen™ Flu A+B Test Kit only							

Image 1. Industrial slaughterhouse, Hanoi

Image 2. Sampling at a local farm

Table 3. Lineages of the viruses isolated in August and September identified through phylogenetic analyses

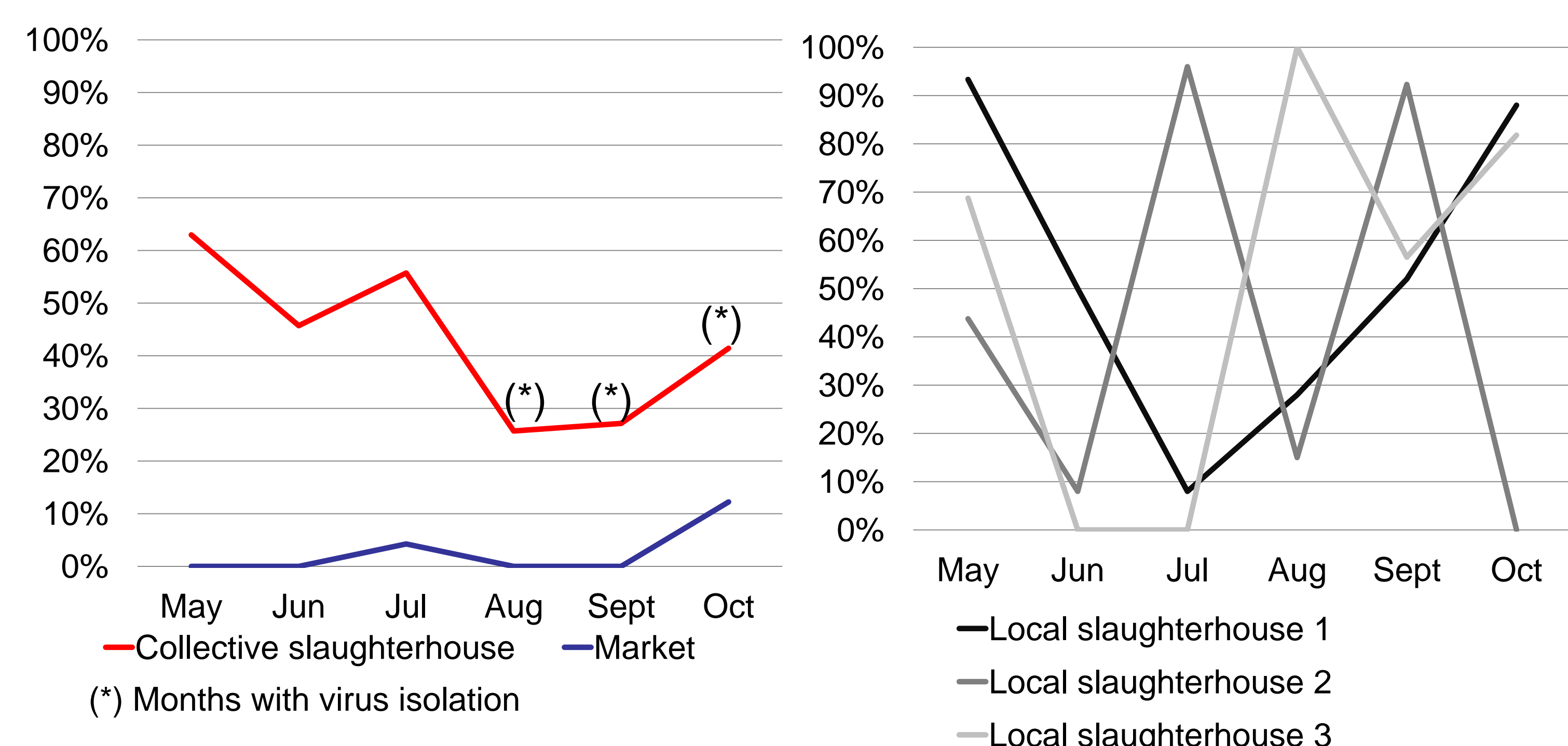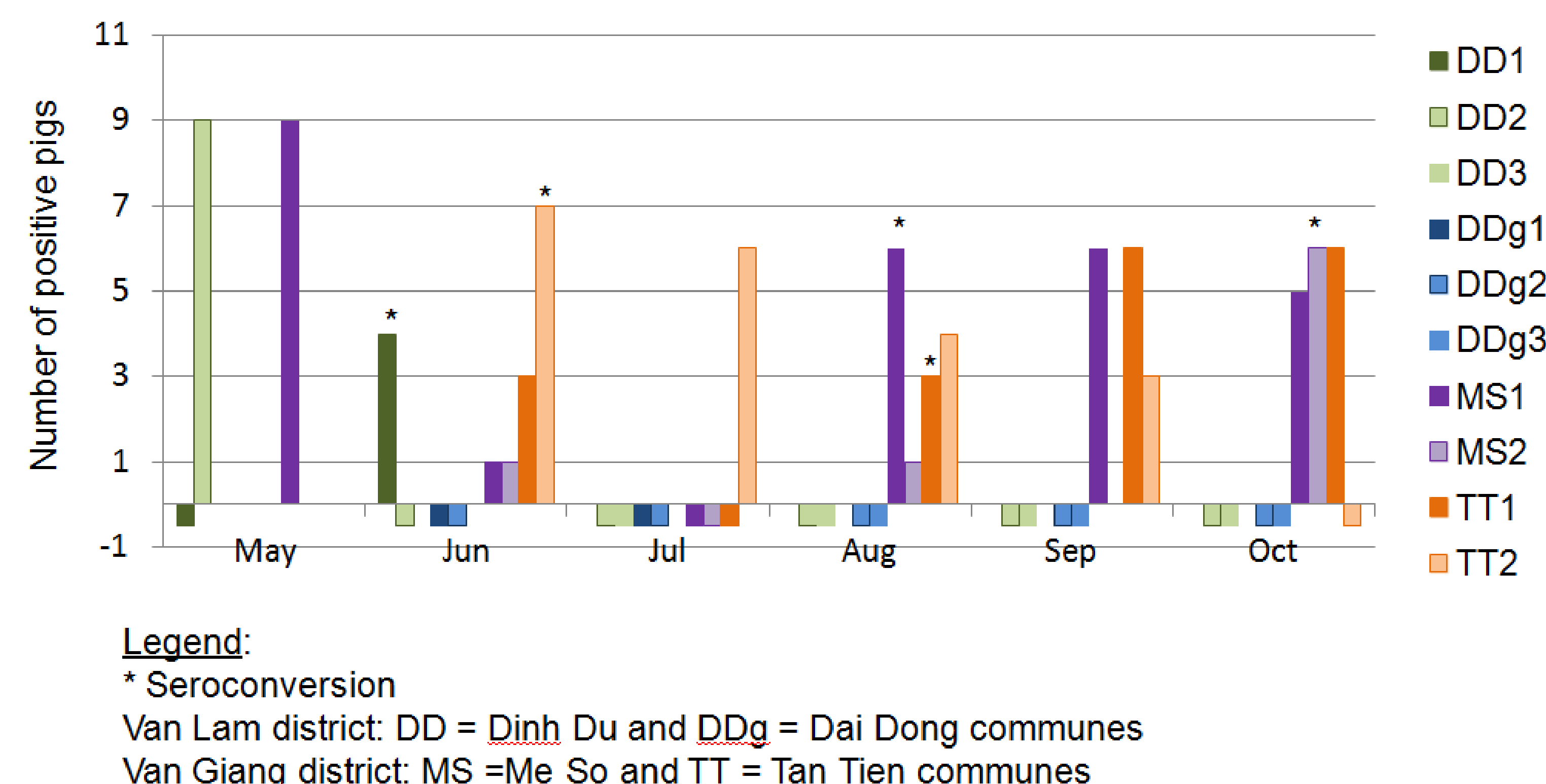| Viruses	HA	NA	PB2	PB1	NS	PA	NP	M
H1N1	A(H1N1)pdm09 *HA and NA related to human viruses from 2010*							
H3N2	Triple reassortant *A/swine/Korea /PL01/2012*		Triple reassortant *American lineages*			A(H1N1)pdm09		

Figure 1. Seroprevalences in different locations, May to October 2013

—Collective slaughterhouse —Market

(*) Months with virus isolation

—Local slaughterhouse 1 —Local slaughterhouse 2 —Local slaughterhouse 3

Figure 2. Serological results for individual farms showing seroconversion over time

DD1 DD2 DD3 DDg1 DDg2 DDg3 MS1 MS2 TT1 TT2

Legend:
* Seroconversion
Van Lam district: DD = Dinh Du and DDg = Dai Dong communes
Van Giang district: MS =Me So and TT = Tan Tien communes

Conclusion

The preliminary results showed a high circulation of swine influenza in the region in the familial and industrial sectors, and a potential seasonal trend suggested by the number of virus isolation per month. Virus isolation was not possible in the familial sector although serology showed evidence of influenza circulation. Further analyses of the results will support the design of targeted surveillance protocols to optimize the cost-effectiveness of swine influenza surveillance.

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