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Swine influenza surveillance in China

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Report including

- General Information
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- Sample collection and virus isolation
- Sequencing and analysis of viruses,2017-2018
- Serological surveillance on HI antibody detection
- Summary
- Acknowledgments

General Information

- China has about half of the world’s swine population;
- China's pig production: from backyard to large-scale;
- Pigs were not routinely vaccinated against swine influenza;
- People and pigs are contact frequently. Sporadic human infection with SIVs have been occasionally reported;
- Driven by commercial profit, long distance transportation of pigs by trunks were common before August, 2018.

The objectives of the surveillance program

- Gain a better understanding of the genetic evolution of swine influenza viruses in China;
- Update diagnostic assays, and vaccine seed stock products;
- To investigate the evolution and biologic properties (virulence, antigenicity, and transmissibility) of swine influenza viruses.

Supported by National Surveillance Plan for Swine Influenza Virus in Pigs

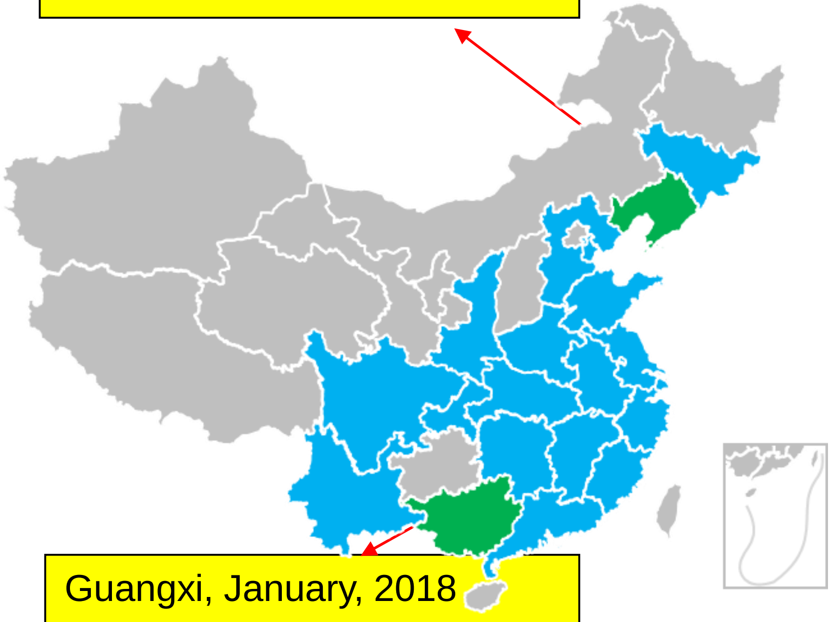
Sample collection

January-April, 2018, sample collection and testing was carried out in the first stage；Over 3,800 nasal swab samples from 2 provinces were analyzed.

November, 2018- January, 2019, sample collection and testing was carried out the second stage;
Over 15,300 nasal and tracheal swab samples from 20 provinces were collected and analyzed.

All samples were collected through abattoir-based surveillance.

Total Nasal and Tracheal swab - 19800
Serum samples - 2000+



Liaoning, January-April, 2018
Nasal swab - 2000

Guangxi, January, 2018
Nasal swab- 1800

🟦
🟩 **Sampling areas**

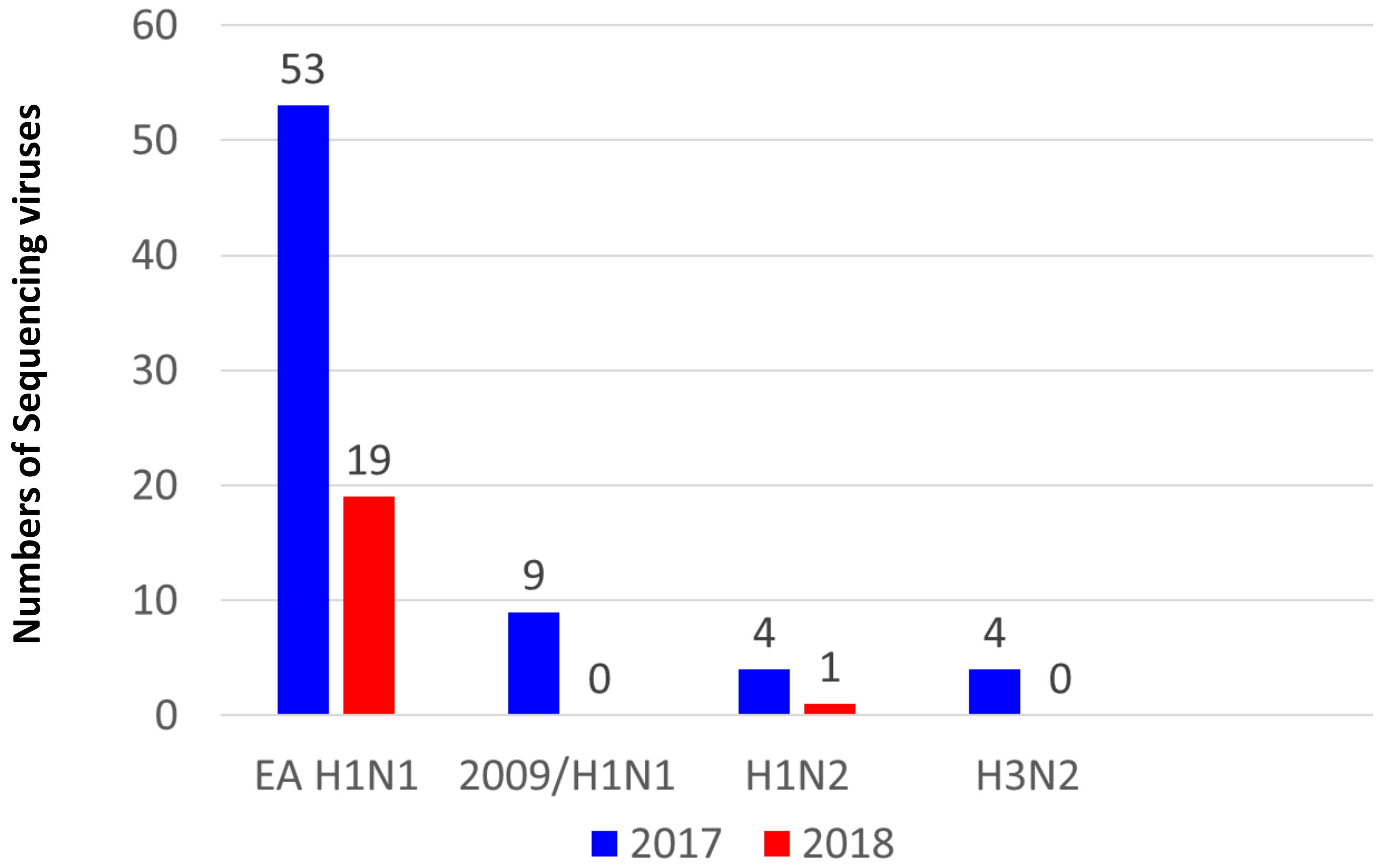
Result of virus isolation

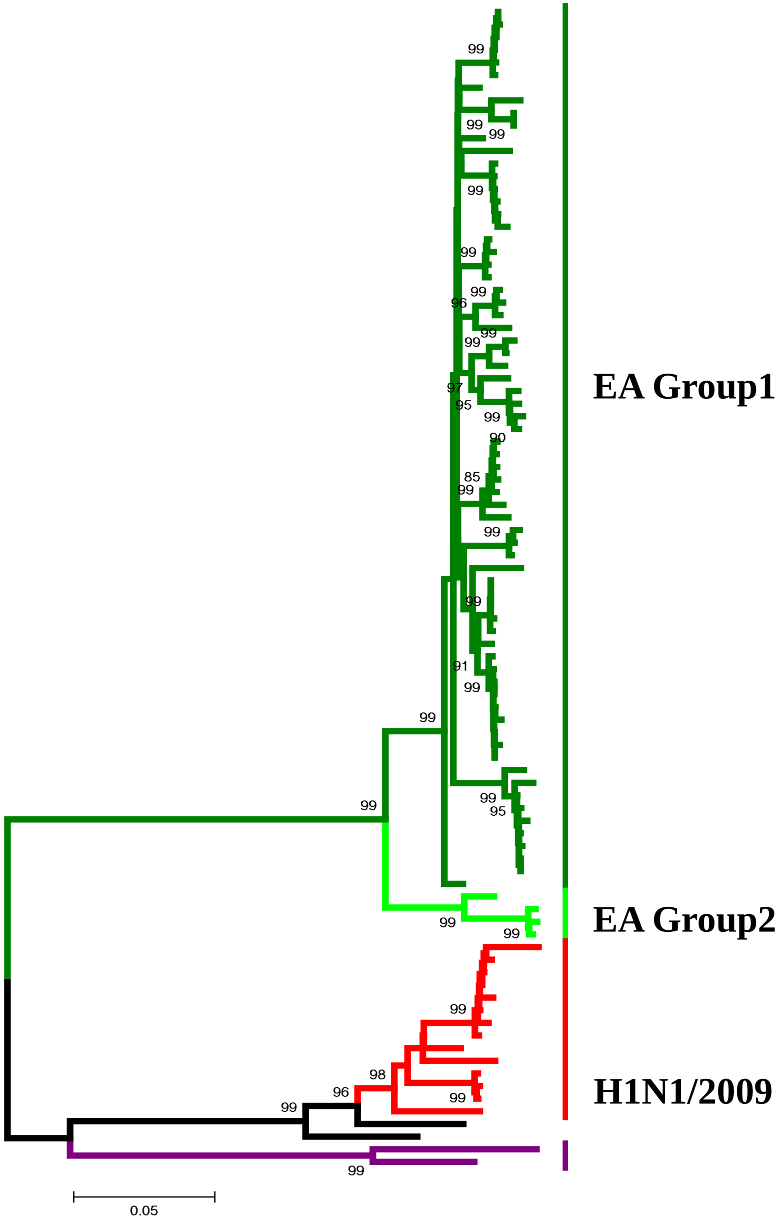
56 strains of SIVs were isolated from samples (56/3800, 1.5%) in 1st stage, including 30 EA H1N1 SIVs isolated from Liaoning province, 25 EA H1N1 and 1 H1N2 SIVs isolated from Guangxi province, respectively.

130 strains of SIVs were isolated from samples collected in 2nd stage; Work is still in progress.


Positive areas of SI, 2017-2018

Sequencing and analysis of viruses isolated from 2017-2018





Phylogenetic tree of H1 subtype swine influenza virus HA genes(2017-2018)

H1 subtype SIVs continue to undergo substantial evolution.
EA Group1 H1N1 swine influenza virus is predominant during 2017 to 2018.

EA Group2 H1N1 swine influenza virus appears in some areas

To better understand the genetic relationship of H1 subtype SIVs from China, the gene segments of HA were sequenced.

Prevalence, genetics, and transmissibility in ferrets of Eurasian avian-like H1N1 swine influenza viruses

Huanliang Yang[a,1], Yan Chen[a,1], Chuanling Qiao[a,1], Xijun He[a], Hong Zhou[b], Yu Sun[b], Hang Yin[a], Shasha Meng[a], Liping Liu[a], Qianyi Zhang[a], Huihui Kong[a], Chunyang Gu[a], Chengjun Li[a], Zhigao Bu[a], Yoshihiro Kawaoka[c,2], and Hualan Chen[a,2]

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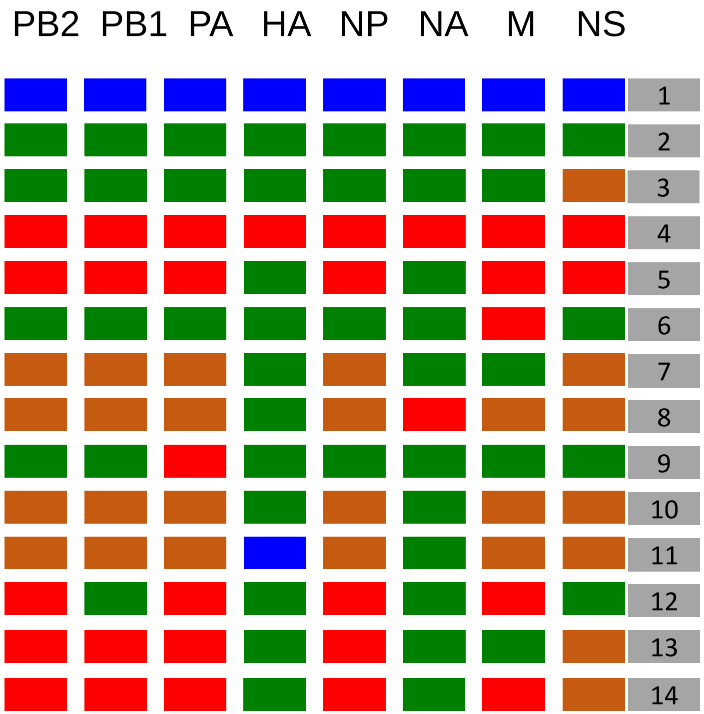
Table 1. Antigenic analysis of the EAH1N1 SIVs

		Ferret antisera		
Virus	HA group	SC/1/09	SW/GX/18/11	SW/GD/104/13
SC/1/09	2009/H1N1	**1280**	320	10
SW/GX/18/11	1	320	**1280**	20
SW/GD/104/13	2	10	40	**1280**
Test viruses				
SW/HuN/26/10	1	160	640	40
SW/TJ/47/11	1	320	320	20
SW/HeN/232/11	1	320	640	40
SW/HLJ/27/12	1	320	1280	40
SW/JS/49/12	1	160	640	40
SW/HuN/30/13	1	160	1280	20
SW/GD/30/13	1	320	640	20
SW/GD/306/13	2	20	10	640

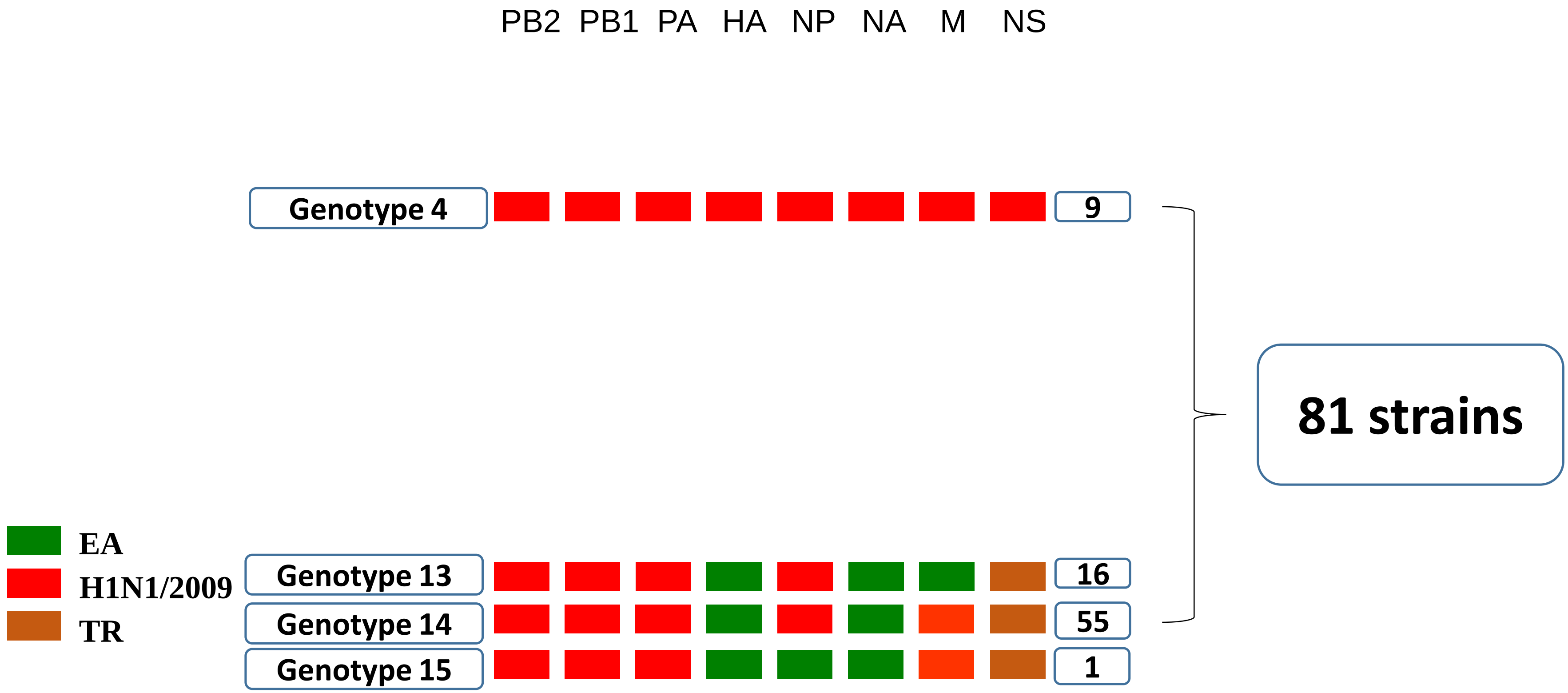
Genotype of H1N1 SIVs in China, 2009-2016



PB2	PB1	PA	HA	NP	NA	M	NS	
🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	1
🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	2
🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟫	3
🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	4
🟥	🟥	🟥	🟩	🟥	🟩	🟥	🟥	5
🟩	🟩	🟩	🟩	🟩	🟩	🟥	🟩	6
🟫	🟫	🟫	🟩	🟫	🟩	🟩	🟫	7
🟫	🟫	🟫	🟩	🟫	🟥	🟫	🟫	8
🟩	🟩	🟥	🟩	🟩	🟩	🟩	🟩	9
🟫	🟫	🟫	🟩	🟫	🟩	🟫	🟫	10
🟫	🟫	🟫	🟦	🟫	🟩	🟫	🟫	11
🟥	🟩	🟥	🟩	🟥	🟩	🟥	🟩	12
🟥	🟥	🟥	🟩	🟥	🟩	🟩	🟫	13
🟥	🟥	🟥	🟩	🟥	🟩	🟥	🟫	14

🟦 **CS**
🟩 **EA**
🟥 **H1N1/2009**
🟫 **TR**

Genotype of H1N1 SIVs in China, 2017-2018

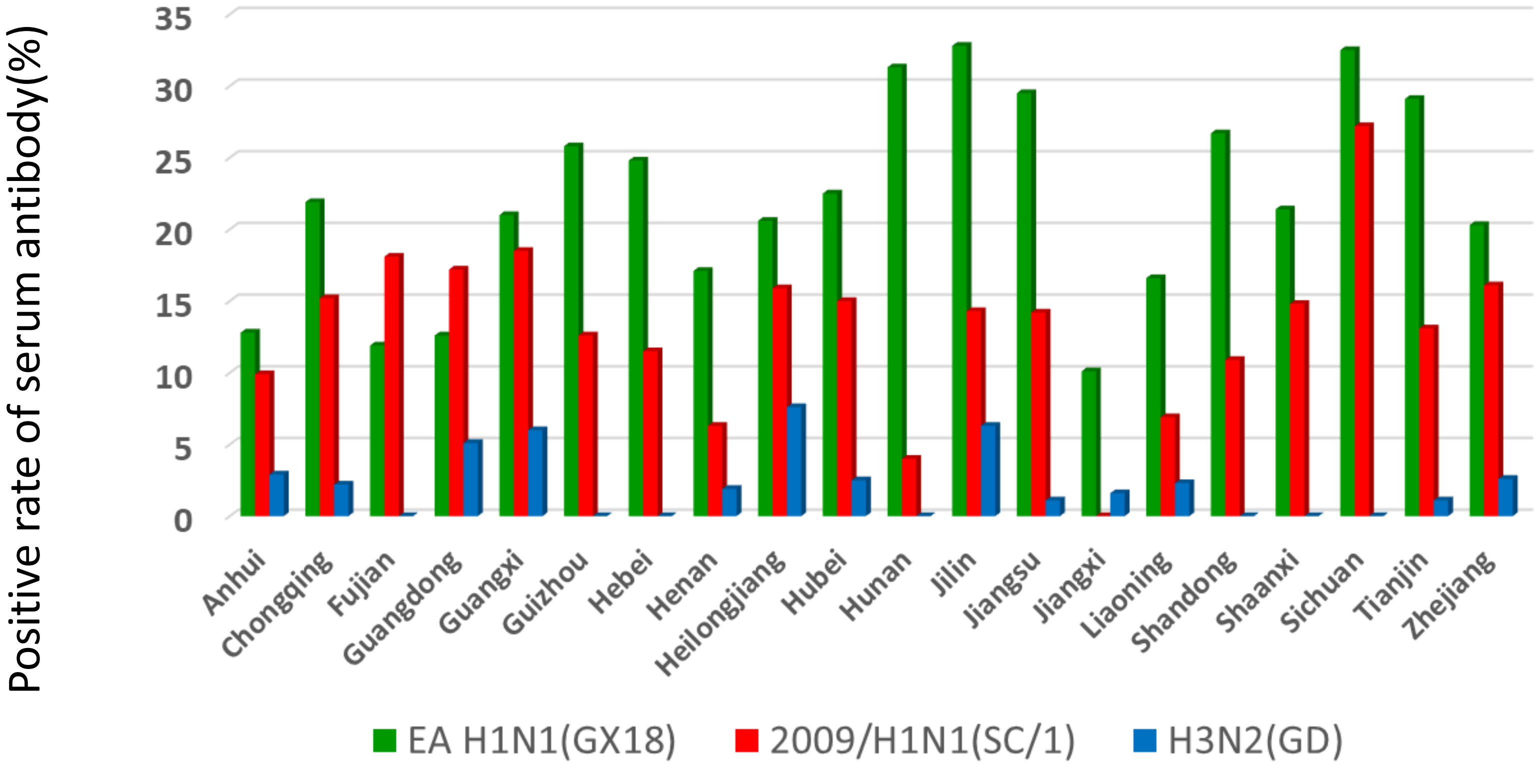


	PB2	PB1	PA	HA	NP	NA	M	NS	
Genotype 4	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	9
Genotype 13	🟥	🟥	🟥	🟩	🟥	🟩	🟩	🟫	16
Genotype 14	🟥	🟥	🟥	🟩	🟥	🟩	🟧	🟫	55
Genotype 15	🟥	🟥	🟥	🟩	🟩	🟩	🟧	🟫	1

81 strains

🟩 **EA**
🟥 **H1N1/2009**
🟫 **TR**

HI antibodies of 3561 serum samples, 2017



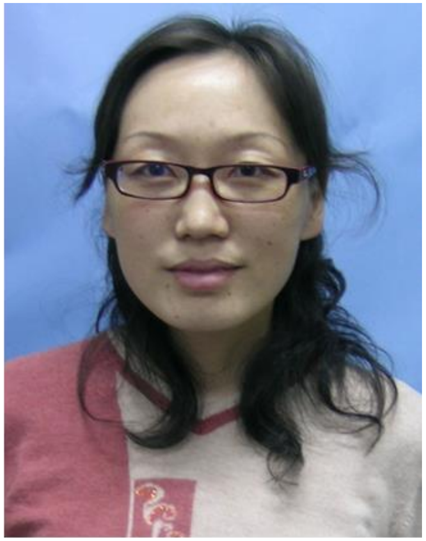
Results of HI test showed that the positive rates of EA H1N1, pH1N1/2009, and H3N2 were 21.1%, 13.2%, and 2.2%, respectively.

Summary

- Multiple subtypes of influenza viruses co-circulated in pigs in China during 2017 to 2018;
- EA Group2 H1N1 swine influenza viruses continue to exist in pigs;
- Triple-reassortant EA H1N1 SIVs— containing the four RNP genes (encoding PB1, PB2, PA, and NP) from 2009/H1N1 became predominant among pigs in China.

Acknowledgments

Dr. Hualan Chen



Dr. Yan Chen