The influenza A viruses of swine in Japan, Thailand, and Vietnam

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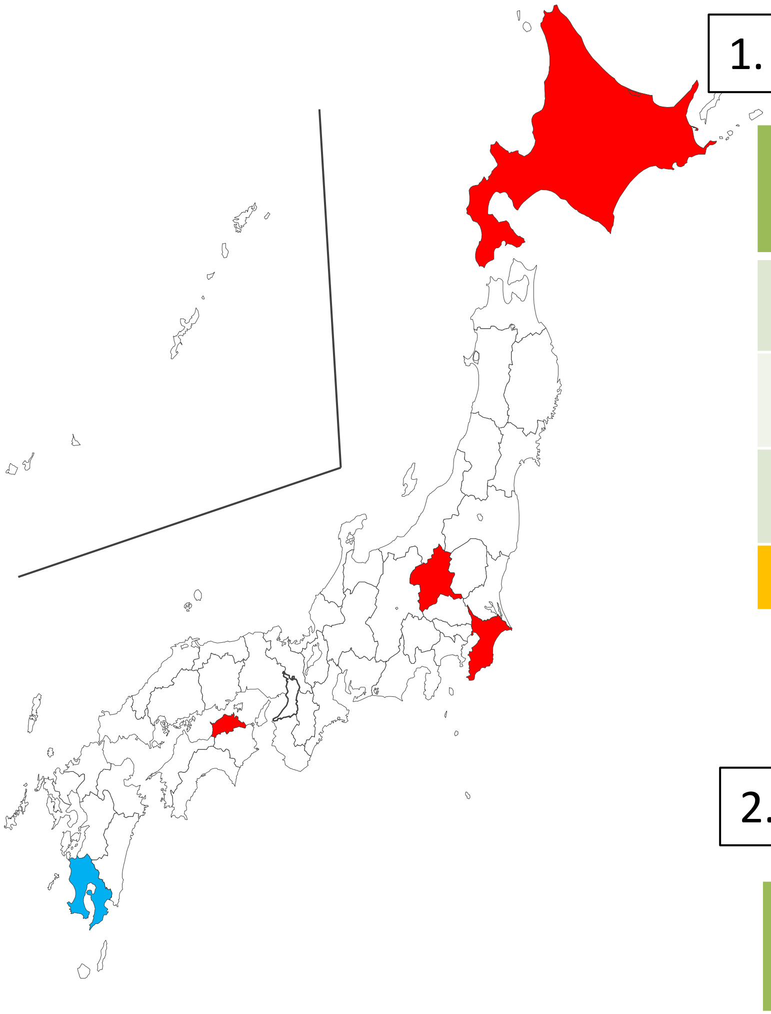
IAV-S surveillance in Japan in 2015



🟥 Provinces under survey in 2015

🟦 IAV-S occurrence in 2015

1. Active surveillance has just been started in Sep. 2015.

Province	Number of farm	Number of nasal swab	Virus isolation	Sampling date
Hokkaido	4	214	1	23rd ~ 29th Oct.
Gunma	7	210	6	10th ~ 30th Nov.
Chiba	1	80	2	29th Sep ~ 24th Nov.
Total	12	504	9	

*Virus isolation and sequencing analysis are in progress.

2. Passive surveillance

Province	Number of sample submitted	Month	Subtype
Kagoshima	1	May	H1N1(pdm09v)

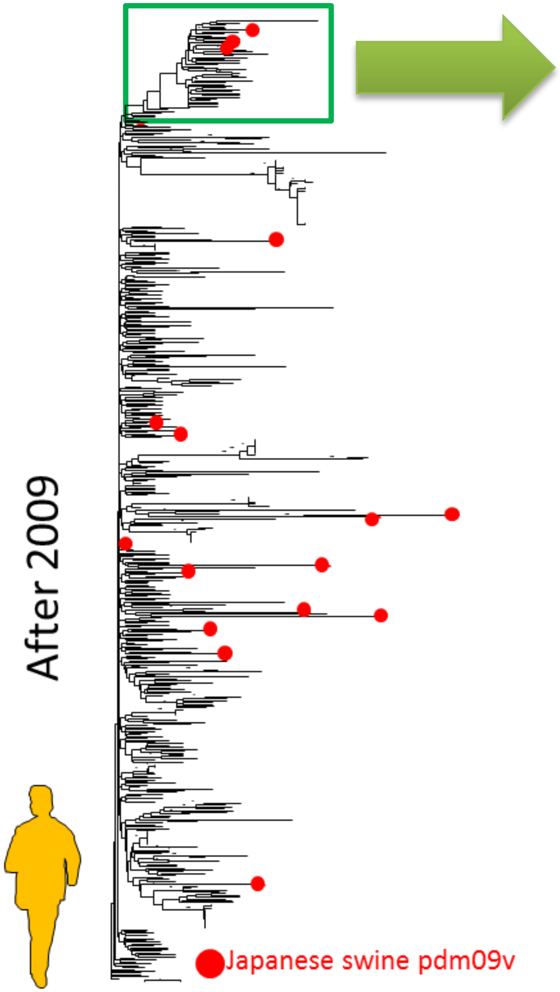
⇨ Genetic analysis

Genetic characterization of the IAV-S in Kagoshima prefecture in Japan in 2015

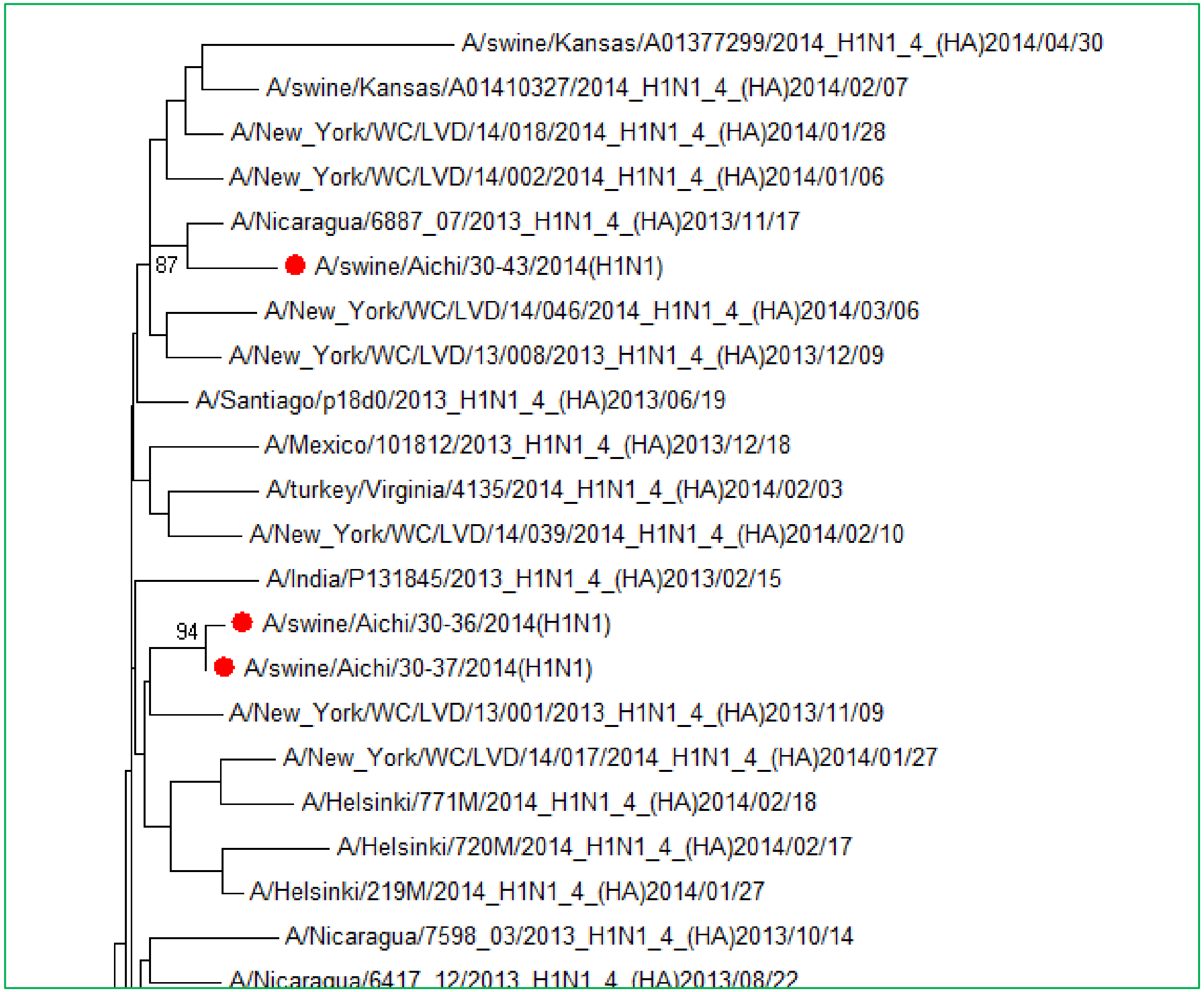
Gene segment	Highest identity with	Identities	Lineage
HA	A/swine/Japan/KU-YG5/2013(H1N1)	1663/1701(98%)	pdm09
NA	A/swine/Japan/KU-YG5/2013(H1N1)	1390/1410(99%)	pdm09
PB2	A/Mexico/24024/2009(H1N1)	2234/2280(98%)	pdm09
PB1	A/Maryland/NHRC0001/2009(H1N1)	2230/2272(98%)	pdm09
PA	A/Singapore/DMS29/2009(H1N1)	2110/2151(98%)	pdm09
NP	A/swine/Thailand/UD402/2009(H1N1)	1490/1515(98%)	pdm09
MP	A/Mexico/24015/2009(H1N1)	972/982(99%)	pdm09
NS	A/Singapore/GP3021/2009(H1N1)	831/844(98%)	pdm09

Genetic characterization of the swine pdm09 viruses in Japan

Phylogenetic trees of H1 pandemic genes (532 taxa selected by CD-Hit)



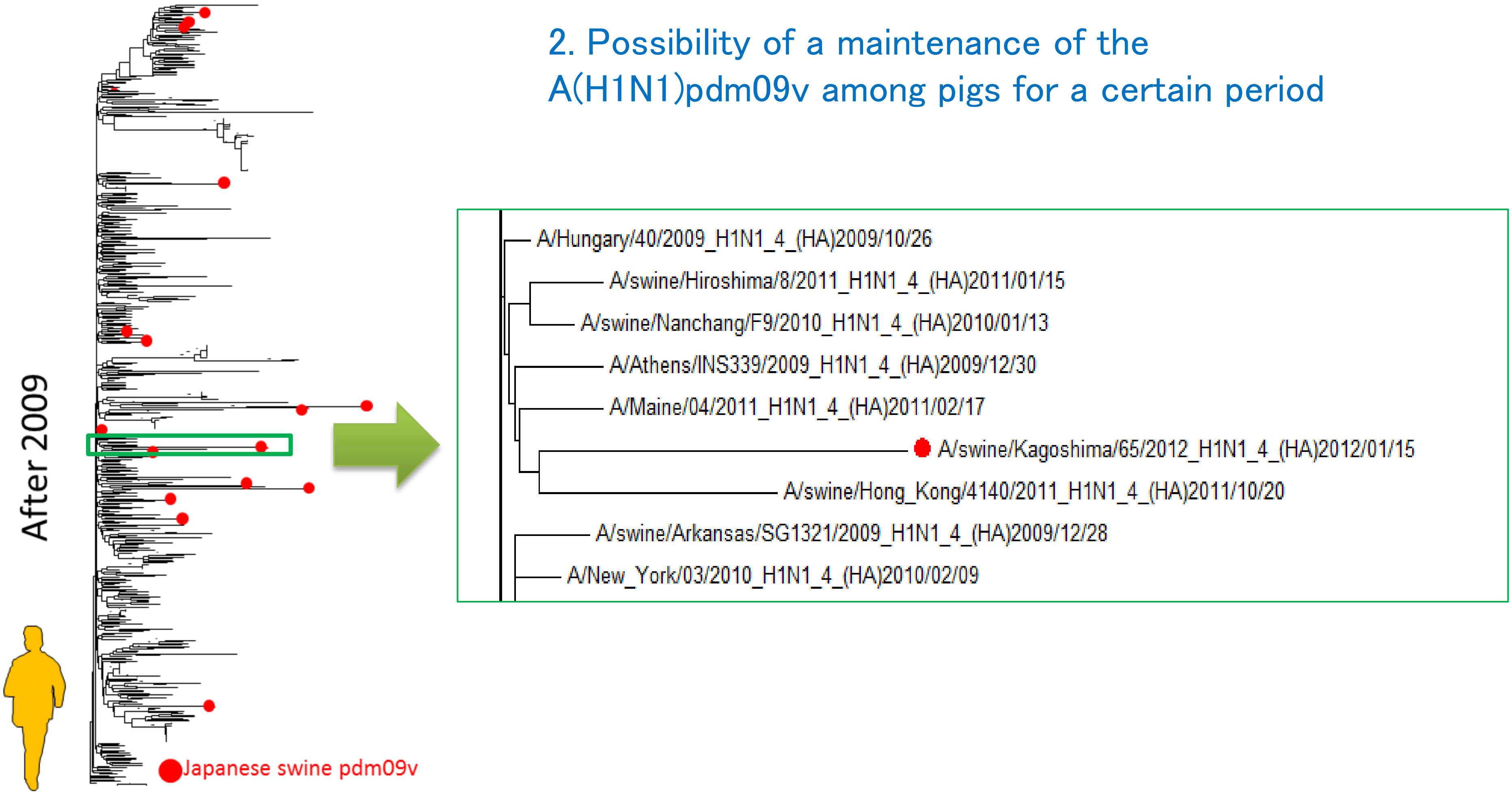
1. Human-to-pig direct transmission of pdm09



Genetic characterization of the swine pdm09 viruses in Japan

Phylogenetic trees of H1 pandemic genes (532 taxa selected by CD-Hit)

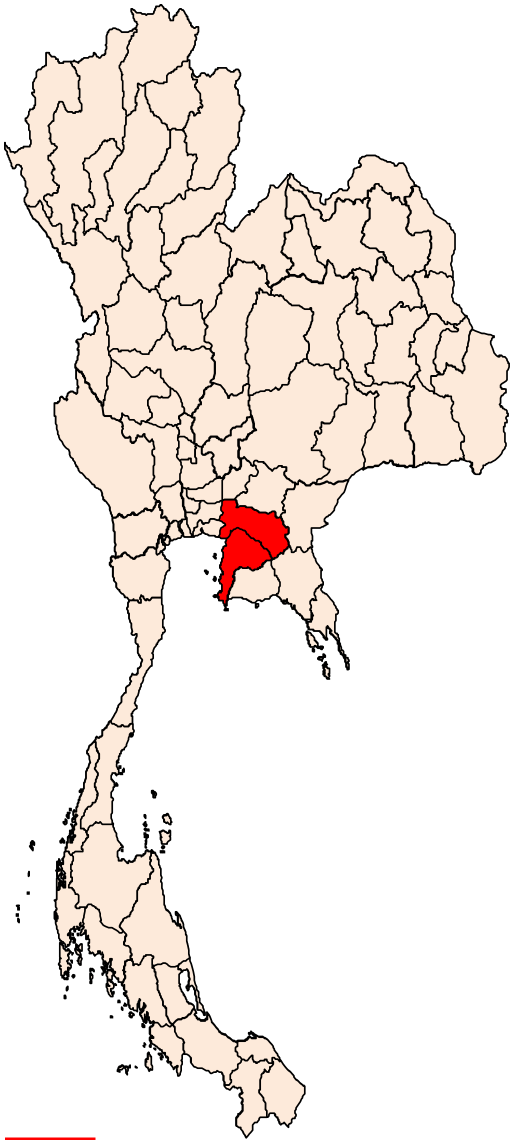
2. Possibility of a maintenance of the A(H1N1)pdm09v among pigs for a certain period



Summary of Japanese IAV-S in 2015

- Active surveillance of the IAV-S in Japan has been started since September 2015.
- Sporadic introductions of A(H1N1)pdm09 viruses from human to pig have occurred since 2009.
- A(H1N1)pdm09 viruses could be maintained among pig populations for a certain.

IAV-S surveillance in Thailand



🟥 Provinces under survey

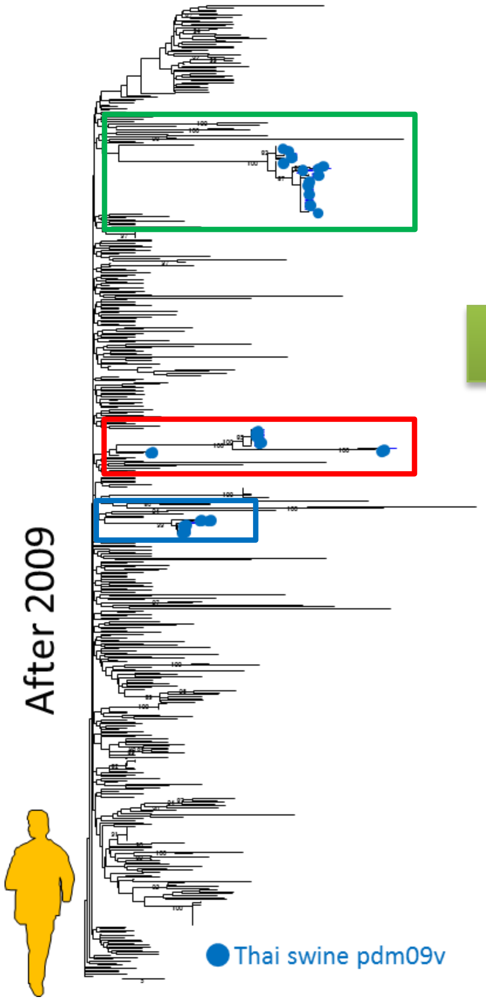
Active surveillance in 2015

Province	Number of farm	Number of nasal swab	Virus isolation	Subtype	Sampling date
Chonburi	2	202	17	H3N2 (15 strains), A(H1N1)pdm09 (2 strains)	1st July
Chachoengsao	2	202	1	H3N2	2nd July
Total	4	404	18		

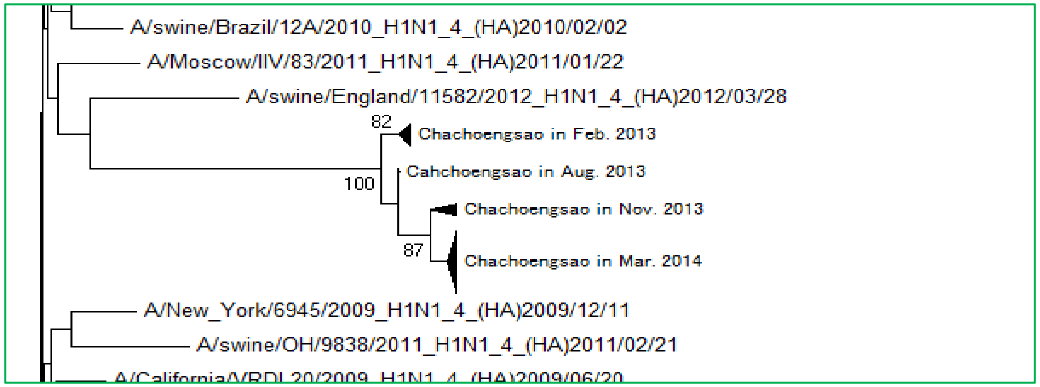
*Sequencing analysis is in progress.

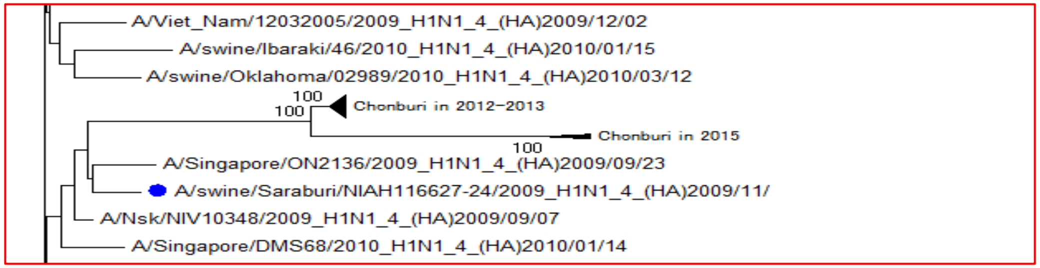
Genetic characterization of the IAV-S in Thailand

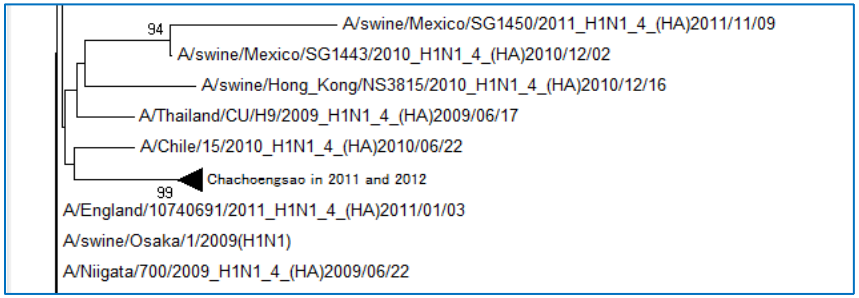
Phylogenetic trees of H1 pandemic genes (532 taxa selected by CD-Hit)



1. Establishment of three lineages of Thai swine pdm09 viruses

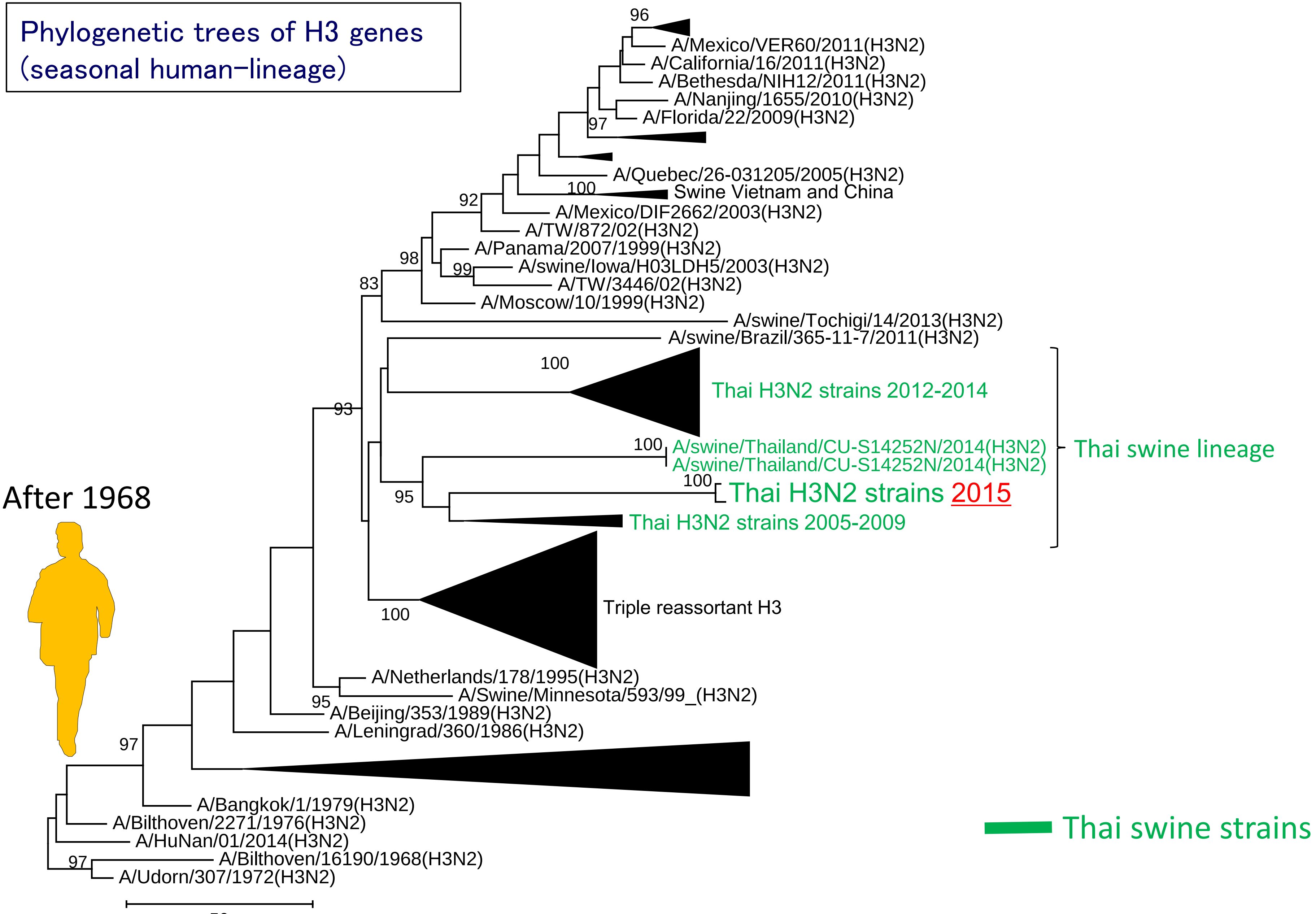






Genetic characterization of the IAV-S in Thailand

Phylogenetic trees of H3 genes
(seasonal human-lineage)

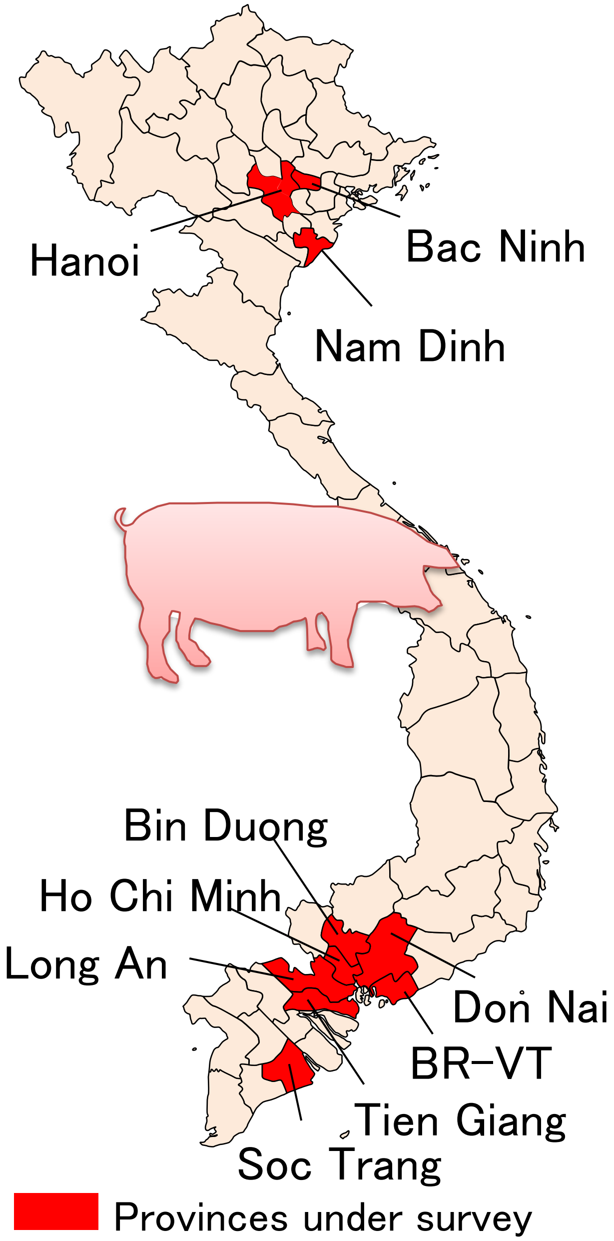


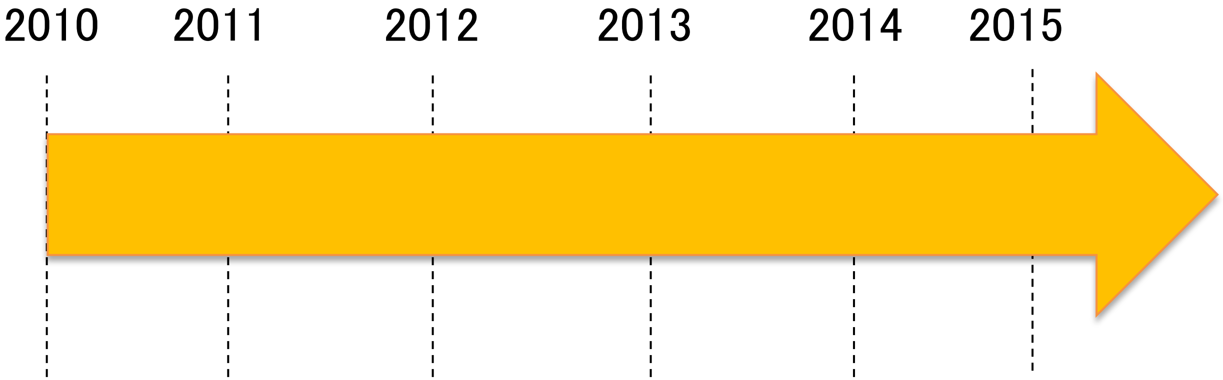
Summary of Japanese and Thai IAV-S in 2015

- At least three lineages of A(H1N1)pdm09 viruses have been circulating in Thai pig population.
- Thai H3N2 lineage possessing seasonal human-like surface antigens has been circulating in Thai pig population since 2005.

Genetic and antigenic analysis of Vietnamese IAV-S

IAV-S surveillance in Vietnam





9584 nasal swabs were collected from **clinically healthy pigs** in **257 pig farms**

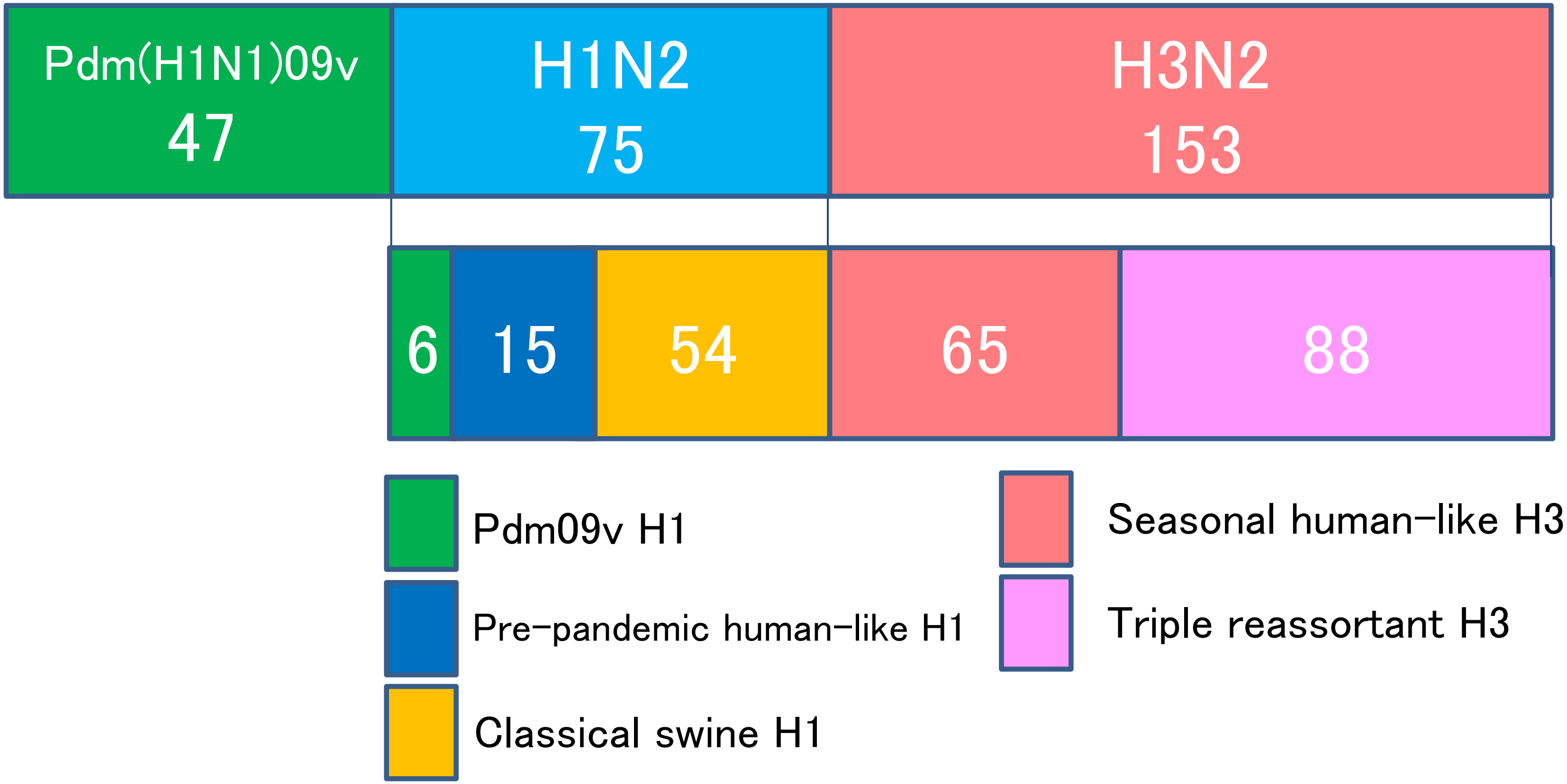
Virus isolation using the floating MDCK cells and/or primary cultures of porcine alveolar epithelial cells

Genetic analysis: To determine the genetic origins of the HA genes.

Antigenic analysis (HI test): To examine the cross-reactivity between the Vietnamese IAV-S and human strains.

HA genes were genetically divided into 5 groups

Subtype:



Pdm(H1N1)09v
47

H1N2
75

H3N2
153

6 | 15 | 54 | 65 | 88

🟩 Pdm09v H1

🟦 Pre-pandemic human-like H1

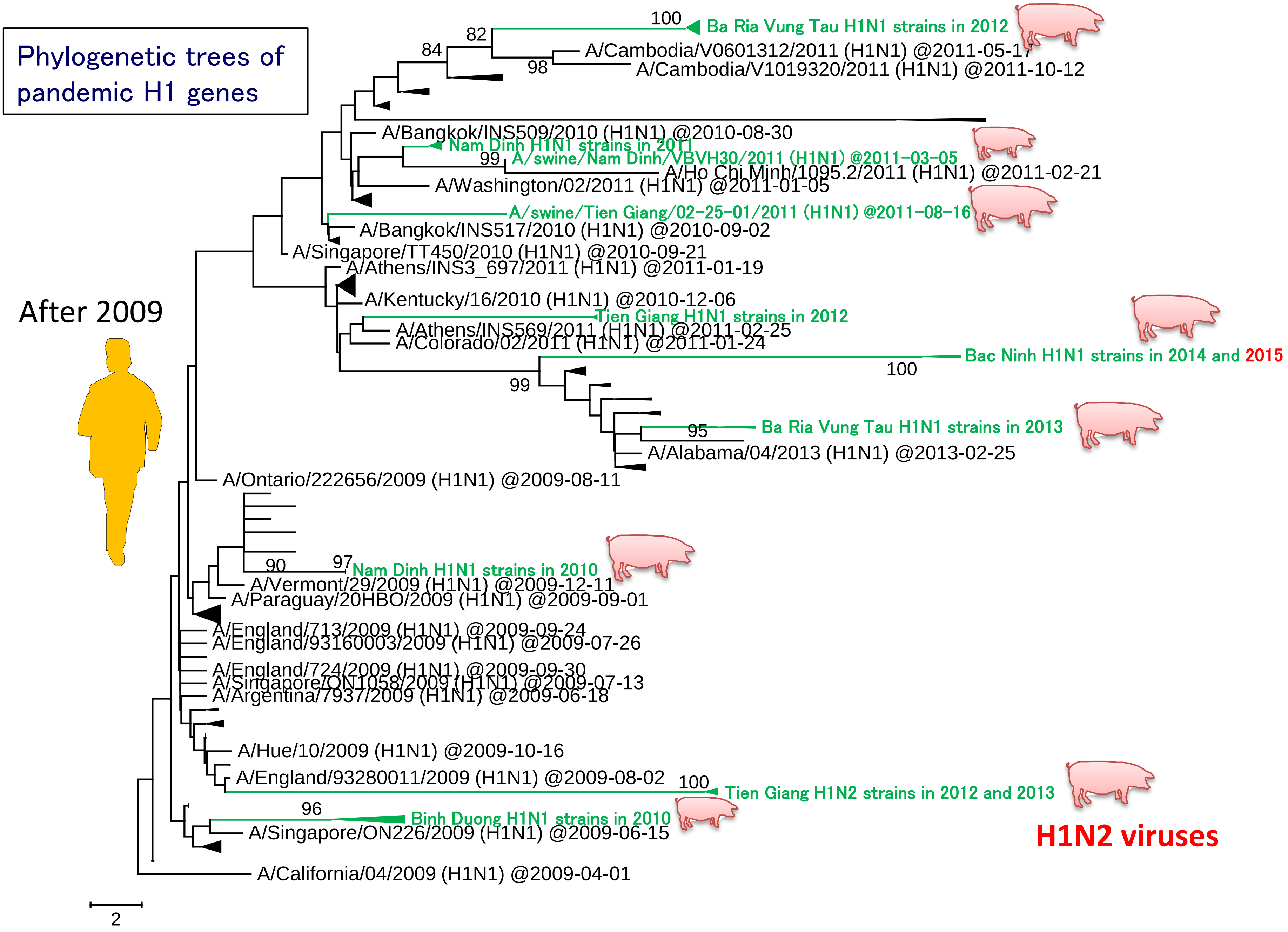
🟨 Classical swine H1

🟥 Seasonal human-like H3

🟪 Triple reassortant H3

Genetic characterization of the IAV-S in Vietnam

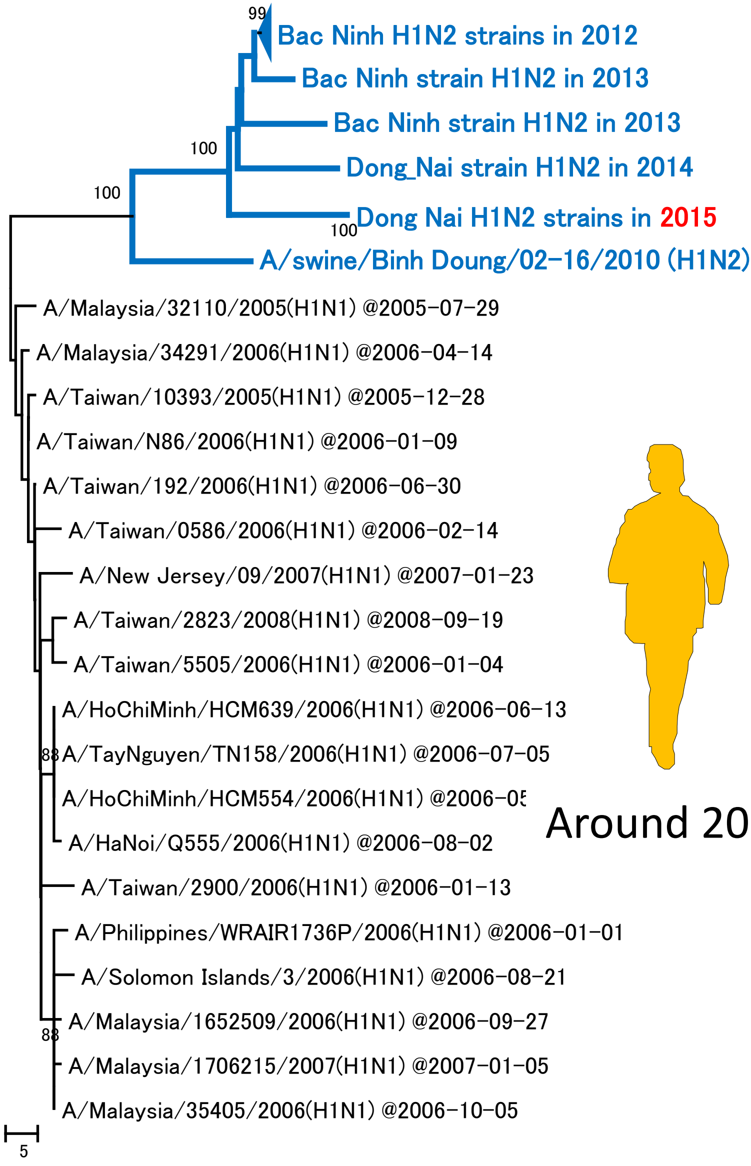
Phylogenetic trees of pandemic H1 genes



Genetic characterization of the IAV-S in Vietnam

Phylogenetic trees of H1 genes

Pre-pandemic human H1



Around 2006

Classical swine H1 (H1 *α*)

Antigenic analysis of Vietnamese H1 IAV-S

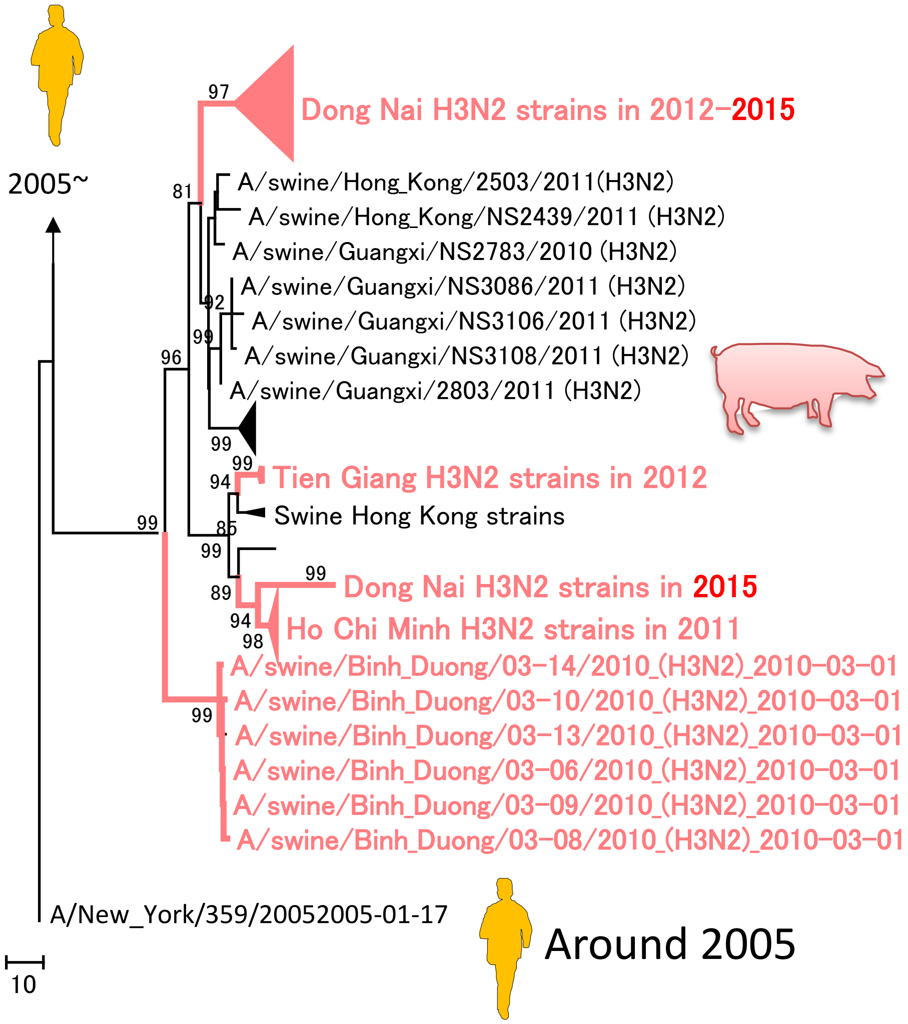
Virus	HI titers of sera from pigs and chikens infected with†				
	A(H1N1)pdm09 virus	Pre-pandemic human-lineage virus			
	Cal04	VN strain	'01~'07	'07~'08	'09~'10
A(H1N1)pdm09 virus					
'09~ vaccine strain	**2560**	<10	20	20	20
VN swine pdm09 virus (2010)	2560	<10	<10	<10	<10
Pre-pandemic human-lineage virus					
VN H1N2 (2010)	<10	**1280**	160	40	20
VN H1N2 (2012)	<10	320	<10	20	10
'01~'07 vaccine strain	<10	160	**80**	20	80
'07~'08 vaccine strain	<10	320	40	**320**	160
'09~'10 vaccine strain	<10	80	<10	40	**160**
Classical H1 IAV-S					
VN H1N2 (2011)	640	10	<10	<10	<10
VN H1N2 (2011)	640	20	20	20	20
VN H1N2 (2012)	640	<10	<10	10	<10

† Homologous HI titers are indicated in bold and underlined.

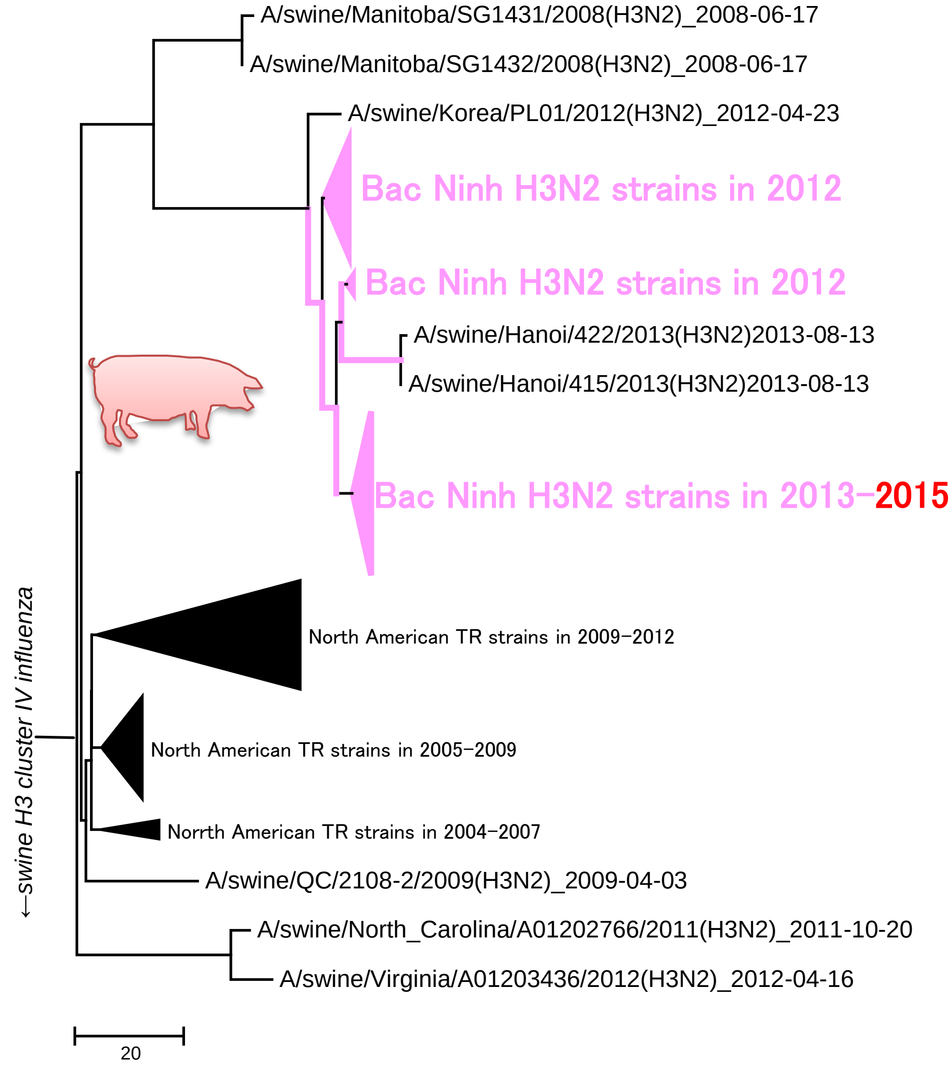
Genetic characterization of the IAV-S in Vietnam

Phylogenetic trees of H3 genes

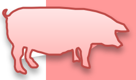
Seasonal human-like H3

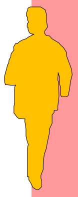


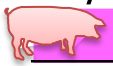
Triple reassortant H3 (Cluster IV)



Antigenic analysis of Vietnamese H3 IAV-S





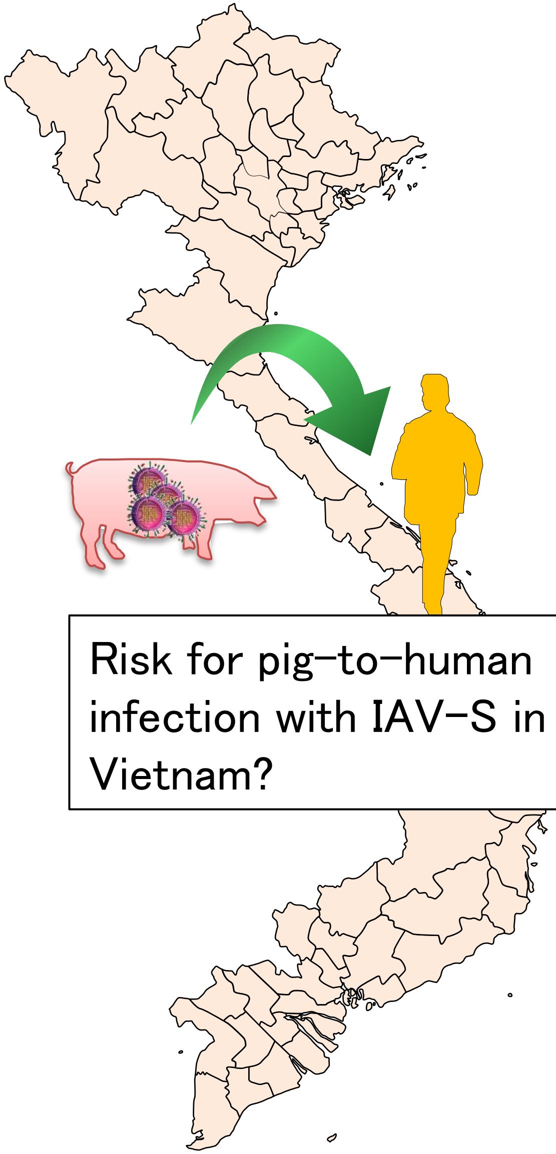


Virus	HI titers of sera from chikens and ferrets infected with[†]							
	Seasonal human-lineage virus							Triple reassortant
	VN strain	'96~'98	'98~'00	'00~'04	'06~'08	'10~'12	'11~'14	VN strain
Seasonal human-lineage virus								
VN H3N2 (2010)	**2560**	20	<10	40	320	320	320	640
VN H3N2 (2011)	160	<10	<10	<10	40	80	160	NT
VN H3N2 (2012)	160	<10	<10	<10	20	40	40	NT
'96~'98 vaccine strain	<10	**320**	160	20	<10	<10	<10	NT
'98~'00 vaccine strain	<10	320	**2560**	1280	160	160	80	NT
'00~'04 vaccine strain	<10	10	160	**1280**	80	10	<10	NT
'06~'08 vaccine strain	<10	40	80	80	**1280**	320	640	NT
'10~'12 vaccine strain	<10	<10	<10	<10	160	**1280**	1280	NT
'11~'14 vaccine strain	10	<10	<10	10	40	320	**640**	NT
Triple reassortant IAV-S								
VN H3N2 (2012)	<10	<10	<10	<10	<10	<10	<10	**5120**

† Homologous HI titers are indicated in bold and underlined.

Sero-surveillance of IAV-S in Vietnam

Sero–surveillance in Vietnamese people using HI test



Risk for pig–to–human infection with IAV–S in Vietnam?

Serum

- 943 sera (Hanoi)
- 2–91 years old (Ave. 33)
- 2011 and 2012

Antigens

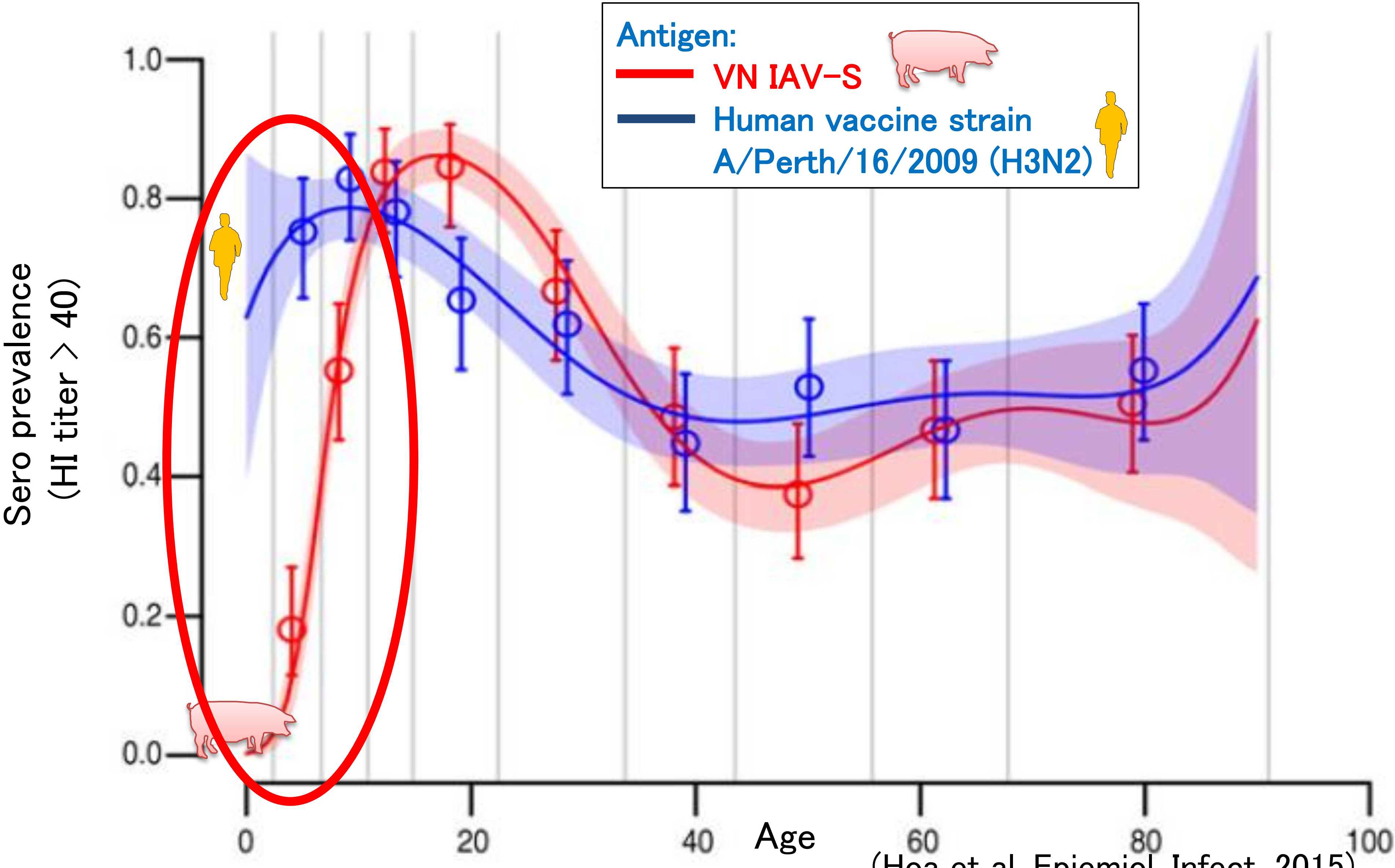
① A novel reassortant H3N2 IAV–S in Vietnam
A/swine/Bing Duong/03—9/2010 (H3N2)

- HA and NA genes from a human H3N2 virus circulating around 2005.
- Internal genes from ‘Triple reassortant’ IAV–S circulating mainly in North America.

② Human seasonal vaccine strain
A/Perth/16/2009 (H3N2)

(Collaboration with Dr. Juliet Bryant from Oxford Univ.)

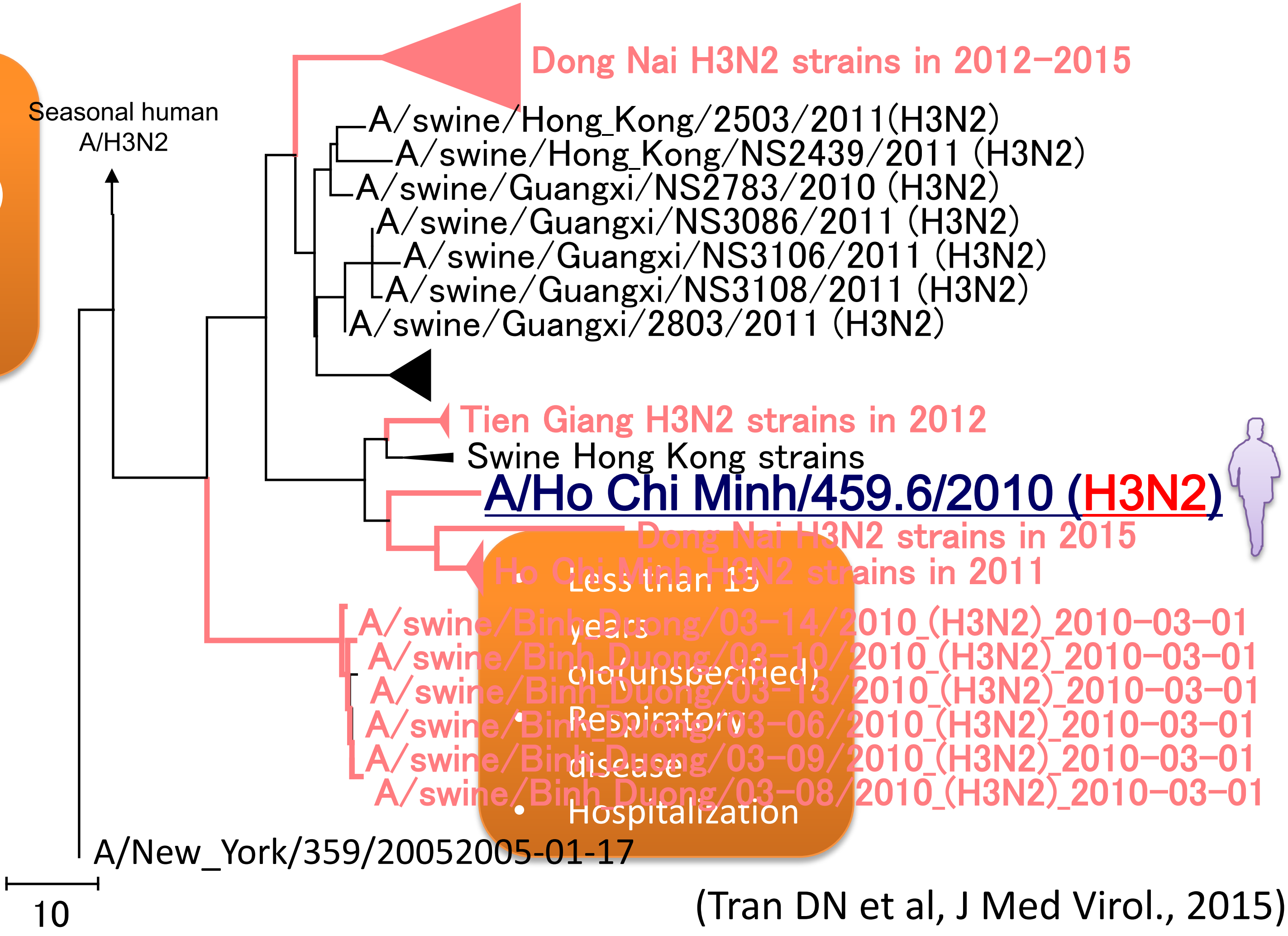
Children may have a higher risk of being infected with Vietnamese IAV-S



(Hoa et al. Epiemiol. Infect. 2015)

Report: **Human infection** with IAV-S in Vietnam

- Less than 15 years old(unspecified)
- Respiratory disease
- Hospitalization



- Less than 15 years old(unspecified)
- Respiratory disease
- Hospitalization

(Tran DN et al, J Med Virol., 2015)

Summary of Vietnamese IAV-S

- Five distinct lineages of IAV-S have been co-circulating in Vietnamese pig population.
- Antigenicity of H1 HA proteins of pre-pandemic human-like and classical lineages differs from the contemporary human seasonal strains.
- Antigenicity of H3 HA proteins of seasonal human and triple reassortant lineages differs from the contemporary human seasonal strains.
- Pig to human infection with IAV-S was evident in Vietnam.

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