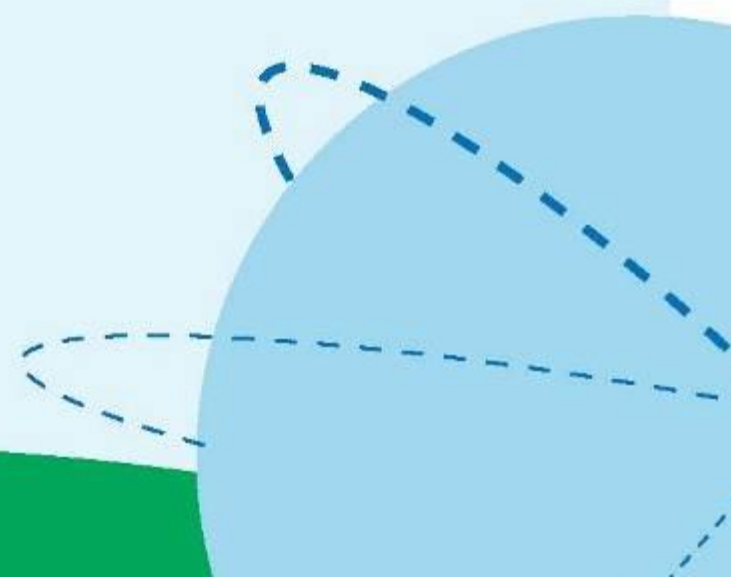




*OFFLU Swine Influenza Virus technical meeting
27 – 28 February 2019
OIE Headquarters, Paris, France*

Takehiko Saito
National Institute of Animal
Health, NARO, Japan



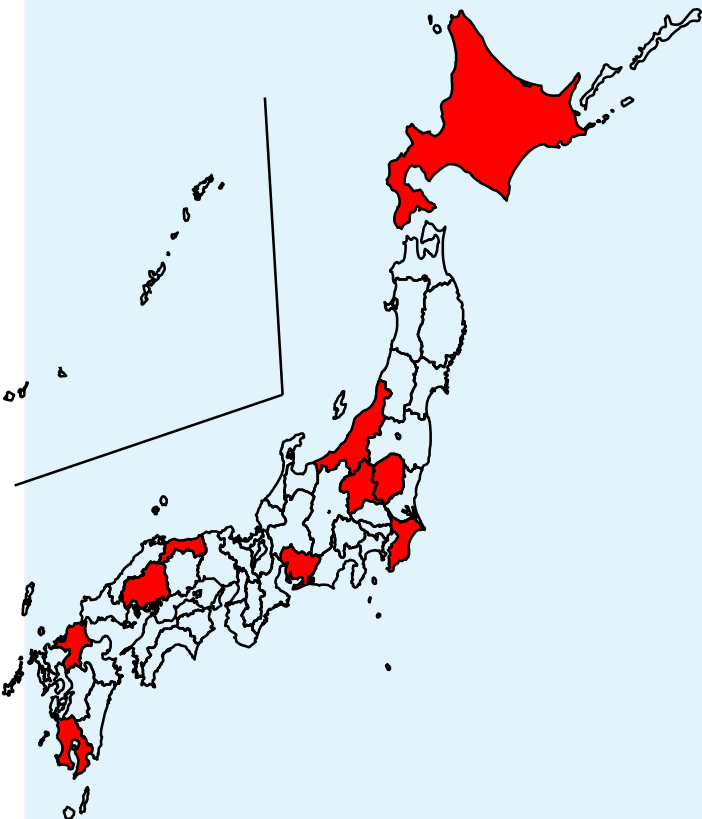
IAV-S surveillance in Japan in 2018


Active surveillance

| Prefecture | Number of farm | Number of nasal swab/lung |
|--------------|----------------|---------------------------|
| Hokkaido | 4 | 216 |
| Chiba | 1 | 60 |
| Gunma | 8 | 450 |
| Tochigi | 2 | 16 |
| Tottori | 1 | 31 |
| Hiroshima | 1 | 32 |
| Kagoshima | 2 | 79 |
| Fukuoka | 1 | 30 |
| Total | 20 | 914 |

Passive surveillance

| Prefecture | Number of farm | Number of virus |
|--------------|----------------|-----------------|
| Tochigi | 1 | 3 |
| Aichi | 1 | 1 |
| Niigata | 1 | 2 |
| Total | 3 | 6 |



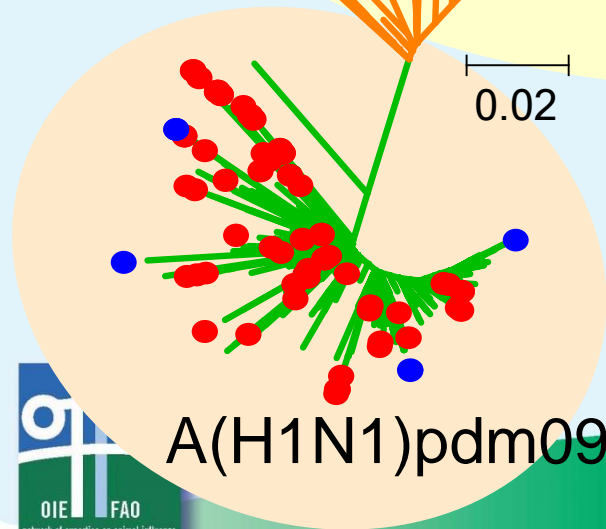
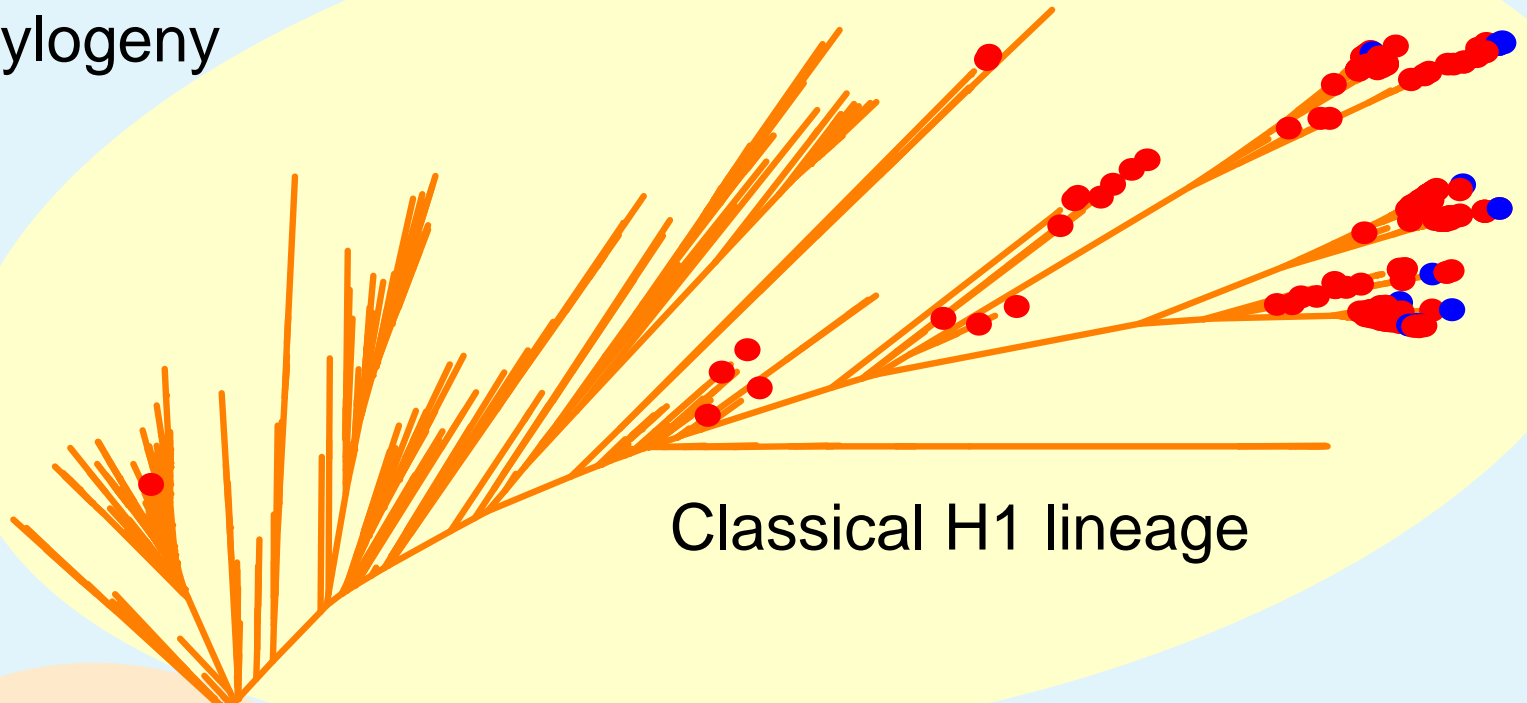
 Provinces under survey in 2018

Japanese IAV-S isolated in 2018

| Subtype | Origins of the genes | | | Number of viruses | Number of farms |
|---------|----------------------|----------------------|---|-------------------|-----------------|
| | HA | NA | Internal genes | | |
| H1N1 | A(H1N1)pdm09 | A(H1N1)pdm09 | A(H1N1)pdm09 | 8 | 5 |
| | Classical swine | A(H1N1)pdm09 | NP: Classical swine Others: A(H1N1)pdm09 | 3 | 1 |
| H1N2 | Classical Swine | Human-like(seasonal) | A(H1N1)pdm09 | 24 | 8 |
| | Classical Swine | Human-like(seasonal) | NP: Classical swine Others: A(H1N1)pdm09 | 5 | 1 |
| | A(H1N1)pdm09 | Human-like(seasonal) | A(H1N1)pdm09 | 2 | 1 |
| H3N2 | Human-like(seasonal) | Human-like(seasonal) | A(H1N1)pdm09 | 1 | 1 |
| Total | | | | 43 | 15 |

Japanese H1 IAV-S isolated in 2018

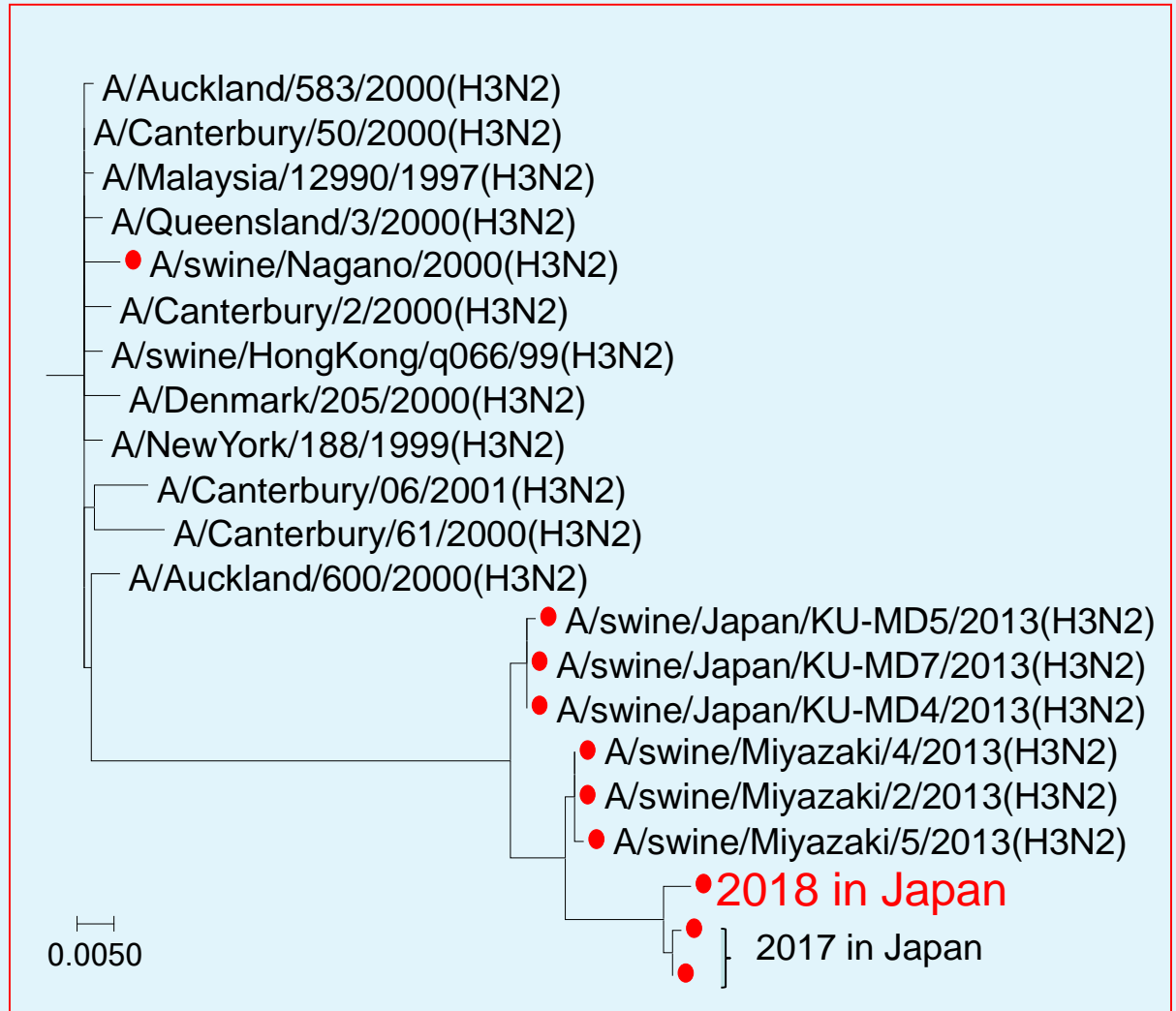
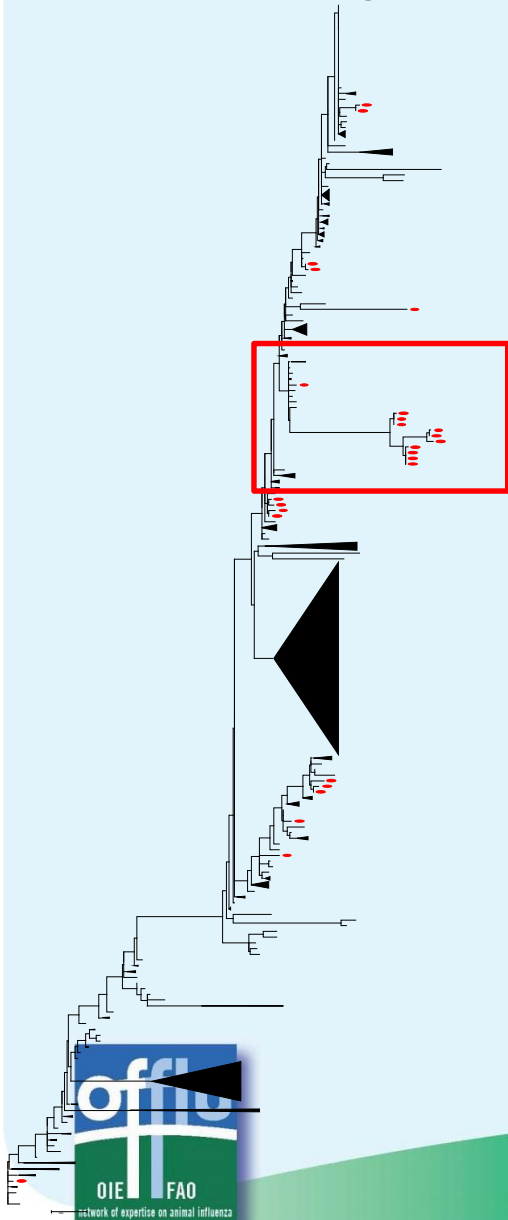
H1 phylogeny



- Japanese IAV-S (before 2017)
- Japanese IAV-S in 2018

Japanese H3 IAV-S isolated in 2018

H3 phylogeny



IAV-S surveillance in Vietnam in 2018



| Prefecture | Number of farm | Number of nasal swabs collected |
|--------------|----------------|---------------------------------|
| Bac Nihn | 15 | 840 |
| Tien Giang | 4 | 240 |
| Ho Chi Minh | 3 | 180 |
| BR-VT | 3 | 180 |
| Dong Nai | 6 | 240 |
| Total | 31 | 1680 |

■ Provinces under survey in 2018

Vietnamese IAV-S isolated in 2018

| Subtype | Origins of the genes | | | Number of viruses | Number of farms |
|---------|------------------------------------|-----------------------|--|-------------------|-----------------|
| | HA | NA | Internal genes | | |
| H1N1 | A(H1N1)pdm09 | A(H1N1)pdm09 | A(H1N1)pdm09 | 29 | 5 |
| H1N2 | Pre-2009 human-like ($\delta 1$) | Triple reassortant | MP: A(H1N1)pdm09 Others: Triple reassortant | 16 | 2 |
| | Pre-2009 human-like (Seasonal) | Triple reassortant | MP: A(H1N1)pdm09 Others: Triple reassortant | 17 | 3 |
| H3N2 | Human-like (seasonal) | Human-like (seasonal) | A(H1N1)pdm09 | 21 | 1 |
| Total | | | | 83 | 10 |

Vietnamese H1 IAV-S isolated in 2018

H1 phylogeny of Vietnamese IAV-S isolated from 2010 to 2018

● 2018 strains in Vietnam

Pre-2009 human-like lineage

Avian-like IAV-S originated from Europe

Classical H1 originated from North America

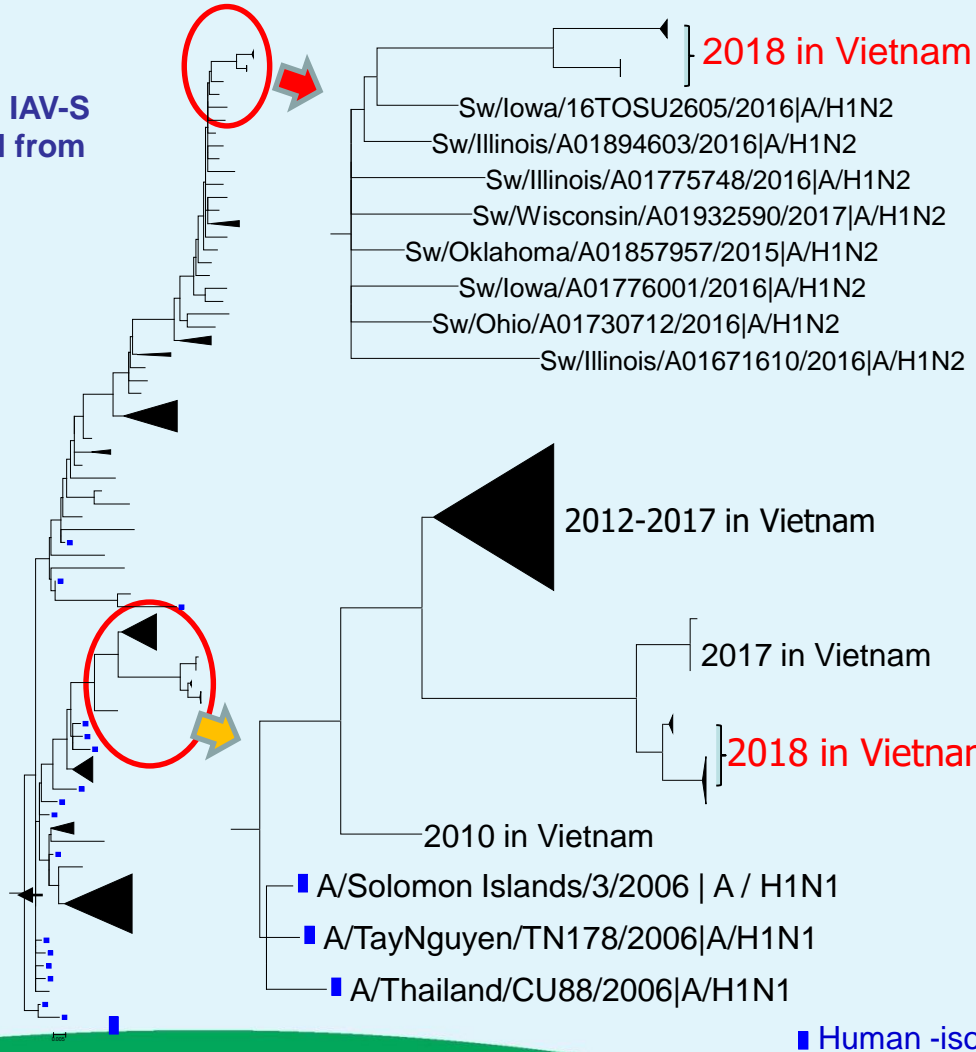
dm09 lineage

0.05



Pre-2009 human H1 phylogeny

Pre-2009 human-like viruses



2018 in Vietnam

1B.2.2.1

(δ 1 lineage)

2012-2017 in Vietnam

2017 in Vietnam

2018 in Vietnam

2010 in Vietnam

1A.3.3.2

(Vietnamese)

■ Human -isolates

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