

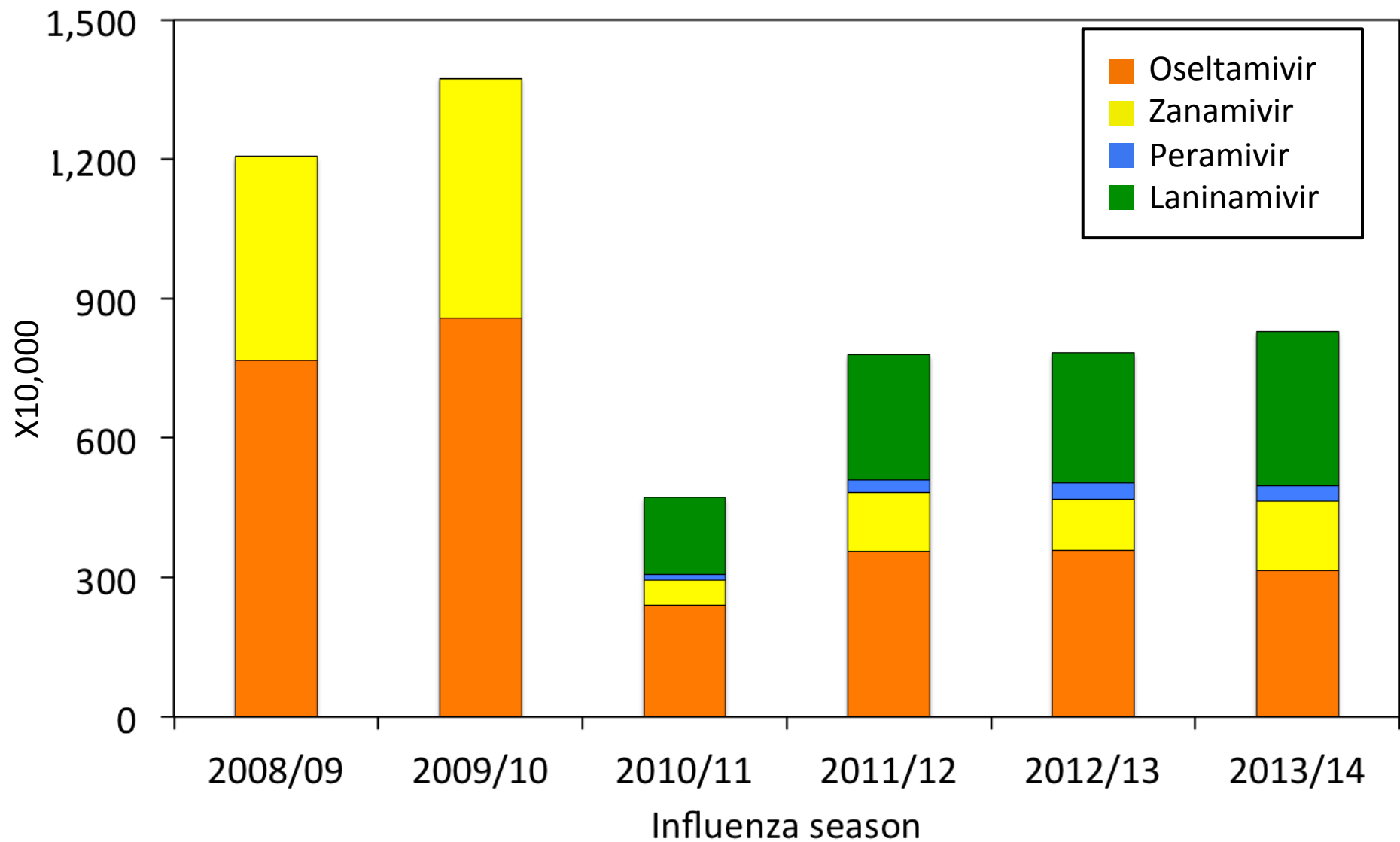
# **Antiviral Drug Resistance**

**Seiichiro Fujisaki**

Laboratory of Influenza Virus Surveillance  
Center for Influenza Virus Research  
National Institute of Infectious Diseases (NIID)  
Tokyo



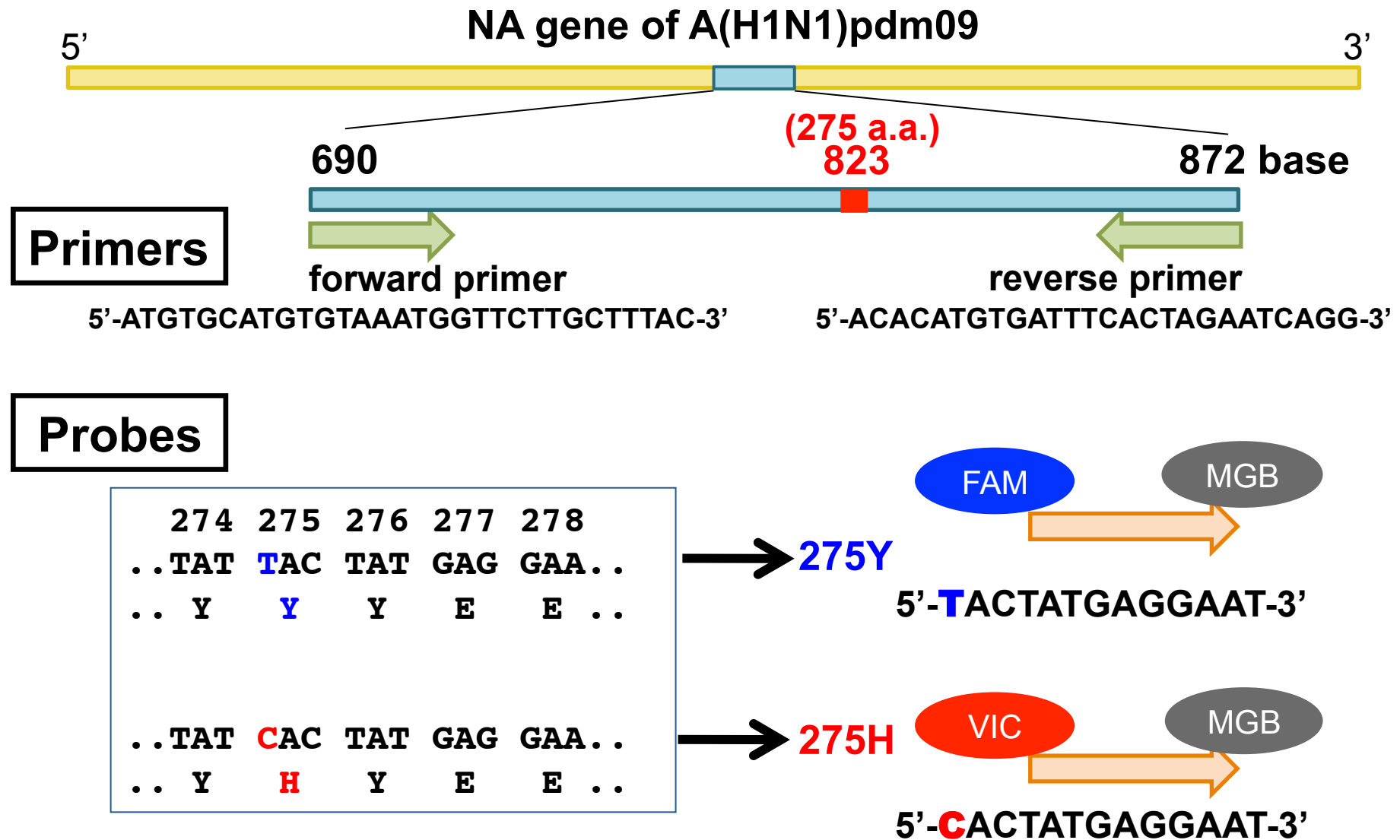
# Neuraminidase inhibitor (NAI) Prescriptions in Japan



## Drug resistant mutations in NA

|              |                                              |
|--------------|----------------------------------------------|
| A(H1N1)pdm09 | H275Y                                        |
| A(H3N2)      | E119I, E119V, R224K, R292K, N294S,...        |
| B            | E117A, E117V, R150K, I221L, R292K, R374K,... |

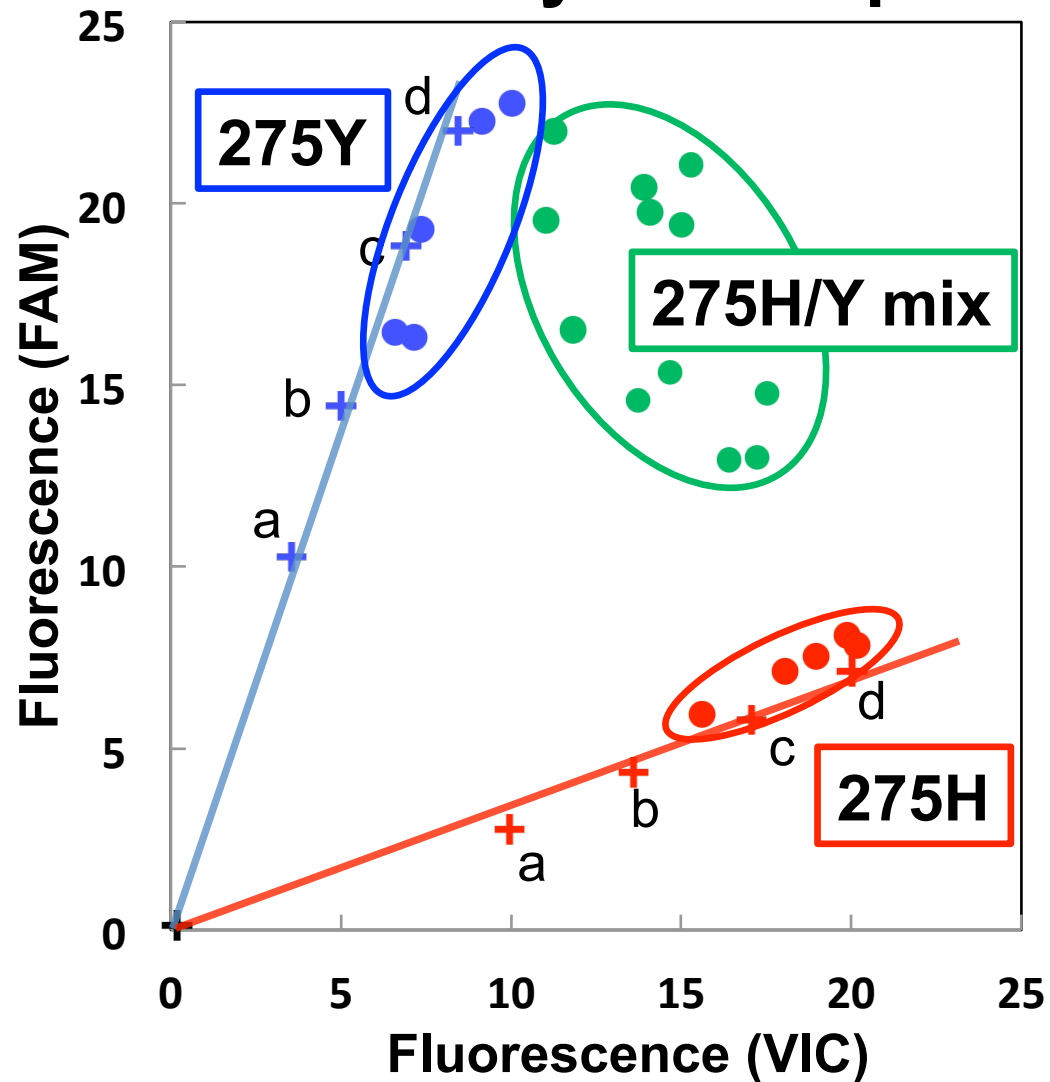
# Allele-specific RT-PCR to detect H275Y



Isolates: without RNA extraction

Clinical specimens: required RNA extraction

# Detection of 275Y and 275H/Y by Allele-specific RT-PCR



- clinical isolates Y275
- clinical isolates H275
- clinical isolates Mix (IC50 >10)
- clinical isolates Mix (IC50 <10)
- + Y275 PC (A/Denmark/528/2009)
- + H275 PC (A/Denmark/524/2009)
- + NC

Positive controls:

- a:  $3.16 \times 10^{-1}$  TCID50/reaction
- b:  $3.16 \times 10^{-0}$  TCID50/reaction
- c:  $3.16 \times 10^{-1}$  TCID50/reaction
- d:  $3.16 \times 10^{-2}$  TCID50/reaction

# Influenza virus surveillance system in Japan

Sentinel hospitals and clinics



Clinical specimens

Local public health institutes

**Virus isolation**

**Allele-specific RT-PCR** or NA gene sequencing  
to detect H275Y substitution for A(H1N1)pdm09



isolates

National Institute of  
Infectious Diseases

NA inhibition assay, NA gene sequencing

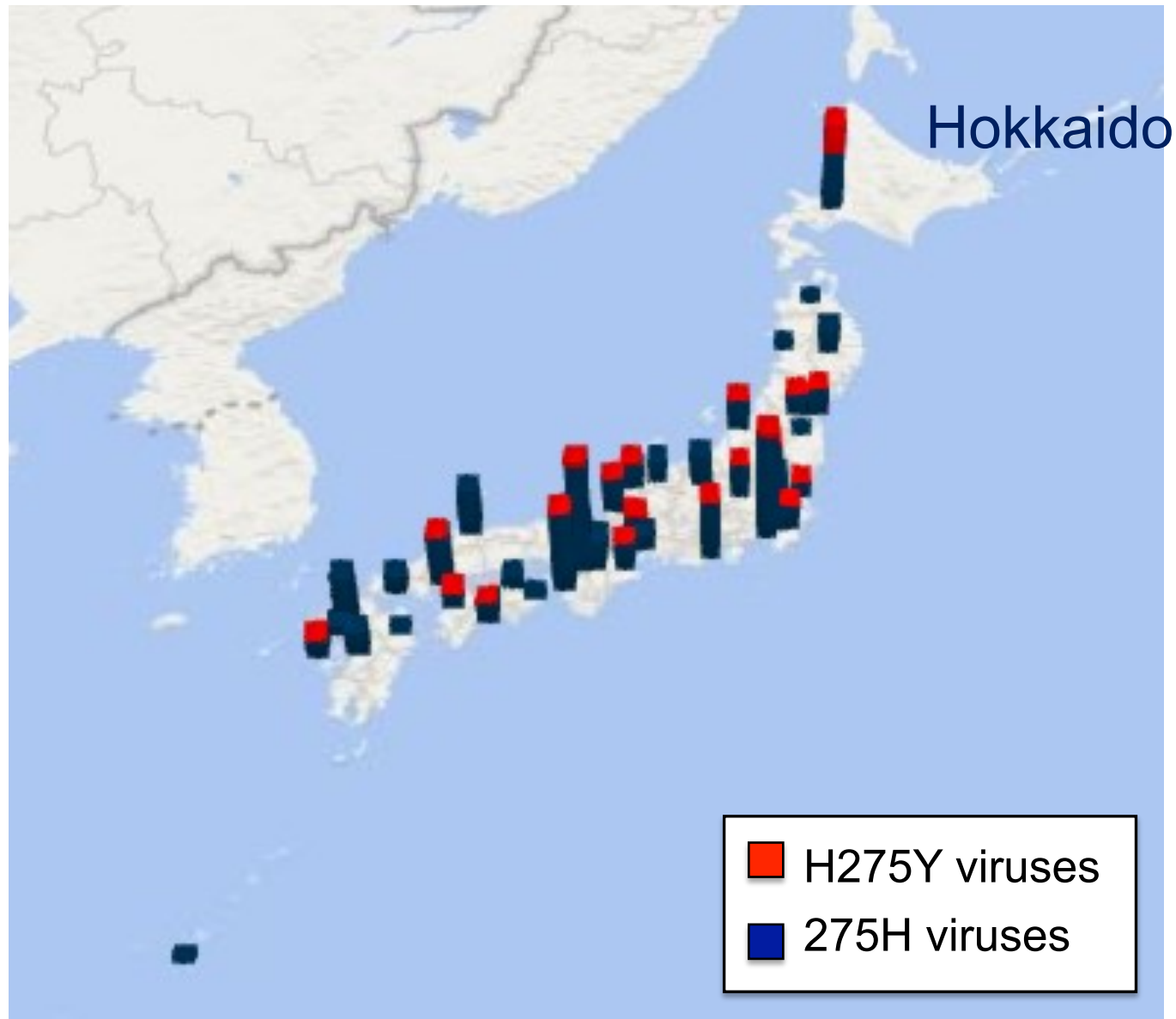
# Detection of NA inhibitor-resistant viruses in Japan

| Influenza season | A(H1N1)pdm09            |                       |                            | A(H3N2)                 |                       |                            | B                       |                       |               |
|------------------|-------------------------|-----------------------|----------------------------|-------------------------|-----------------------|----------------------------|-------------------------|-----------------------|---------------|
|                  | No. of viruses detected | No. of viruses tested | Resistant (%) <sup>a</sup> | No. of viruses detected | No. of viruses tested | Resistant (%) <sup>b</sup> | No. of viruses detected | No. of viruses tested | Resistant (%) |
| 2008/2009        | 9,869                   | 2,168                 | 10<br>(0.5%)               | 2,665                   | 195                   | 0                          | 2,039                   | 141                   | 0             |
| 2009/2010        | 22,142                  | 6,005                 | 69<br>(1.1%)               | 157                     | 49                    | 0                          | 194                     | 113                   | 0             |
| 2010/2011        | 6,262                   | 3,844                 | 78<br>(2.0%)               | 3,865                   | 135                   | 1<br>(0.7%)                | 1,848                   | 147                   | 0             |
| 2011/2012        | 19                      | 11                    | 0                          | 5,148                   | 300                   | 1<br>(0.3%)                | 2,043                   | 265                   | 0             |
| 2012/2013        | 163                     | 111                   | 2<br>(1.8%)                | 5,047                   | 300                   | 0                          | 1,466                   | 337                   | 0             |
| 2013/2014        | 3,493                   | 2,524                 | 105<br>(4.2%)              | 1,720                   | 285                   | 0                          | 2,956                   | 297                   | 0             |

<sup>a</sup> All resistant A(H1N1)pdm09 viruses possessed an H275Y substitution.

<sup>b</sup> All resistant A(H3N2) viruses possessed an R292K substitution.

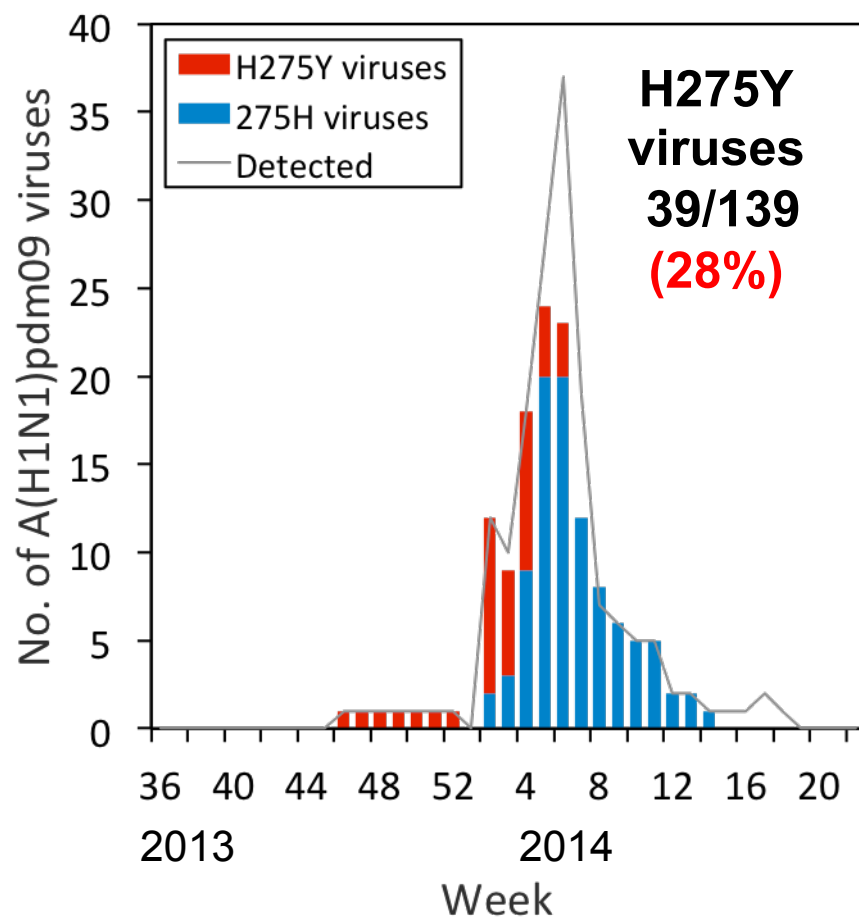
## Distribution of A(H1N1)pdm09 viruses with H275Y substitution in Japan



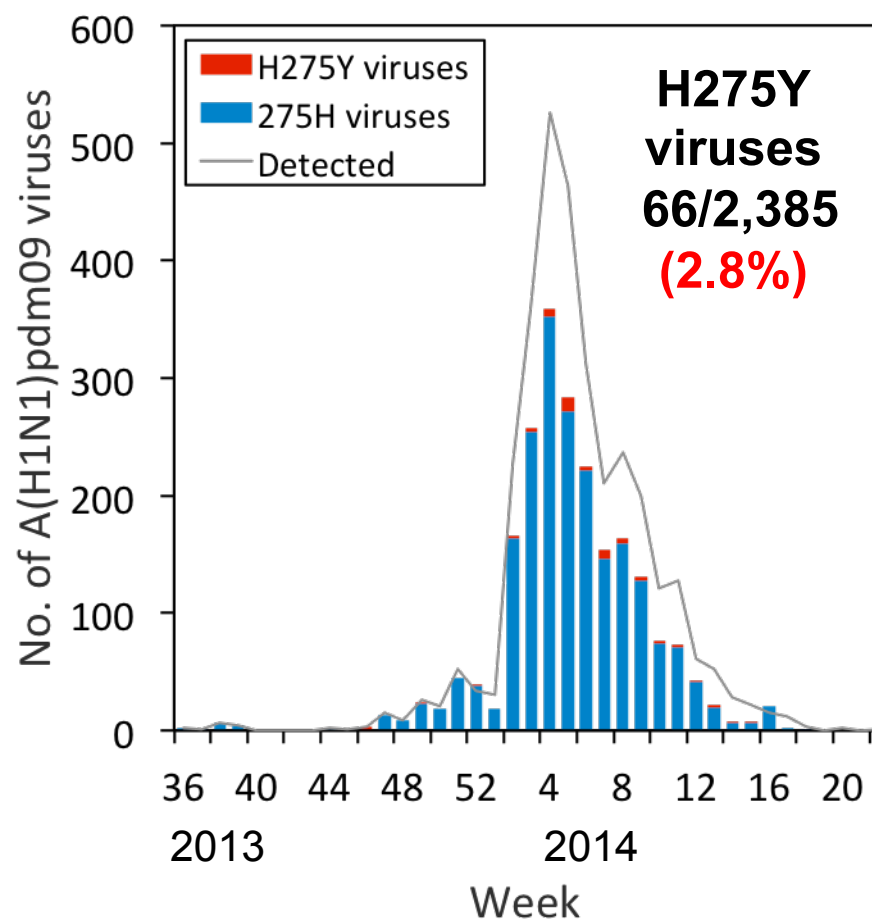


# Detection of A(H1N1)pdm09 viruses with the H275Y substitution in Japan

## Hokkaido

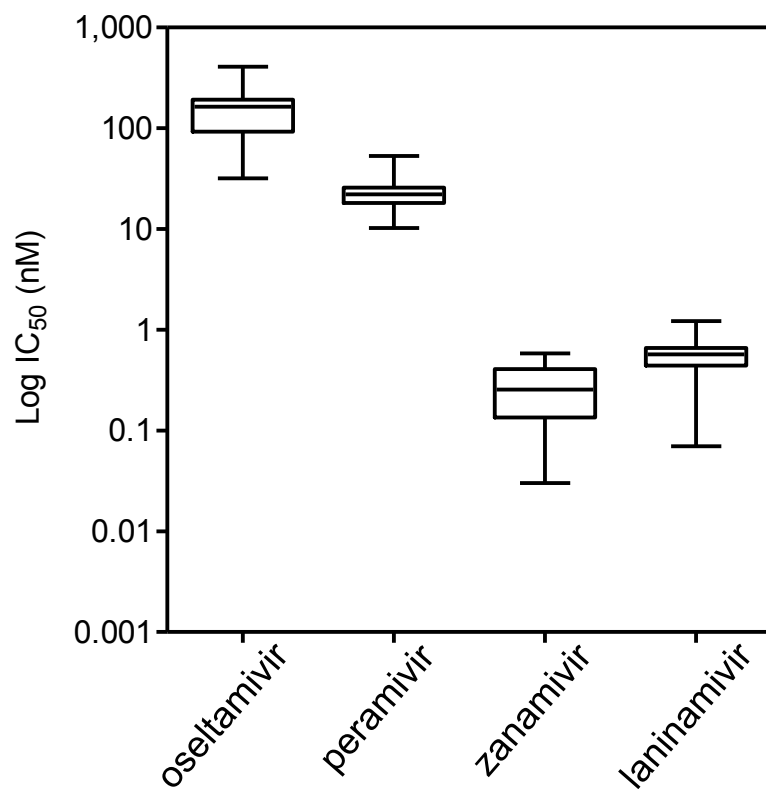


## Outside Hokkaido

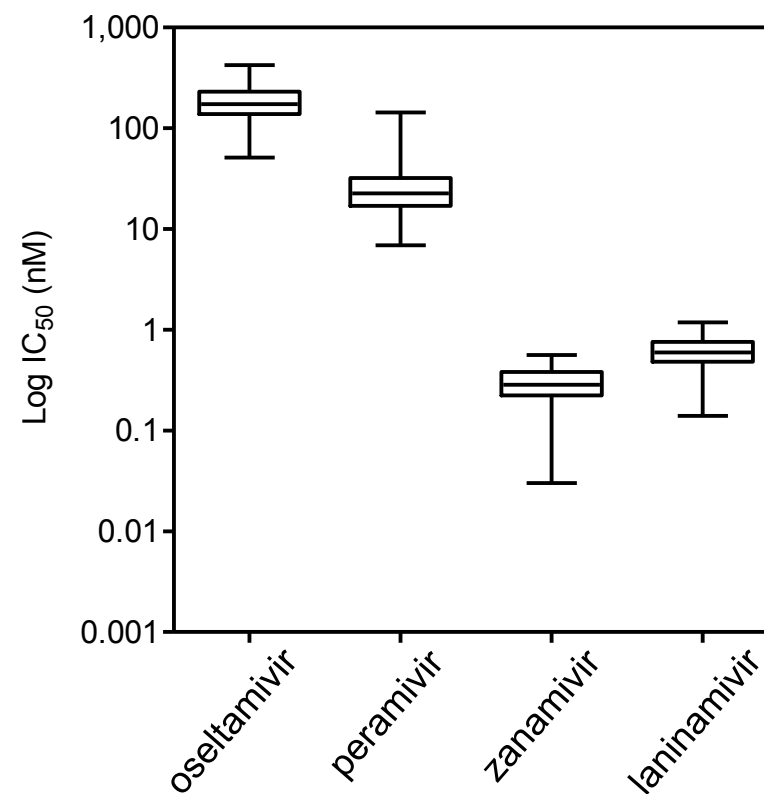


# Susceptibility of H275Y mutant viruses to NA inhibitors

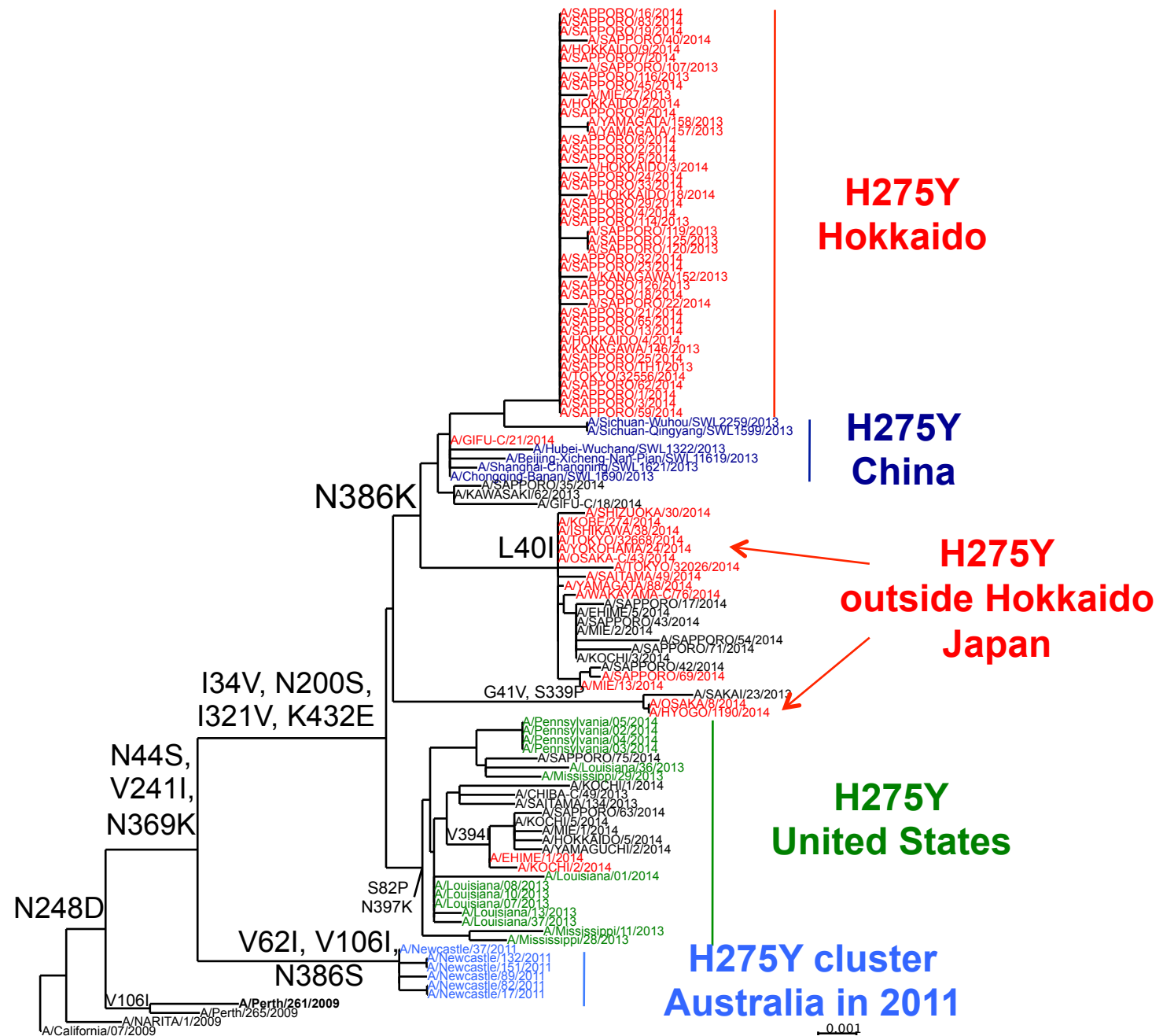
Hokkaido cluster  
(n = 44)



Sporadic cases  
(n = 40)



# Phylogenetic analysis of NA genes



## Characteristic NA amino acids of H275Y mutant viruses

| Viral protein | Amino acid position | Reference<br>California/<br>07/2009 | Newcastle<br>Australia<br>2011 | United<br>States<br>2013-14 | Hokkaido<br>Japan<br>2013-14 |
|---------------|---------------------|-------------------------------------|--------------------------------|-----------------------------|------------------------------|
| NA            | 241                 | V                                   | I                              | I                           | I                            |
|               | 275                 | H                                   | Y                              | Y                           | Y                            |
|               | 369                 | N                                   | K                              | K                           | K                            |
|               | 386                 | N                                   | S                              | N                           | K                            |

# Summary

- A large cluster of influenza A(H1N1)pdm09 virus occurred prior to the main influenza epidemic in Hokkaido, Japan. After wild-type virus invaded Hokkaido, the mutant virus disappeared.
- The structure of the mutant NA molecule was less stable than that of the wild-type virus.
- Given that NA inhibitor-resistant viruses in the community have the potential to be readily transmitted among humans, surveillance of these viruses must continue in order to protect public health and aid in clinical management.