

Surveillance activity in Japan

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Background information of the condition in Japan



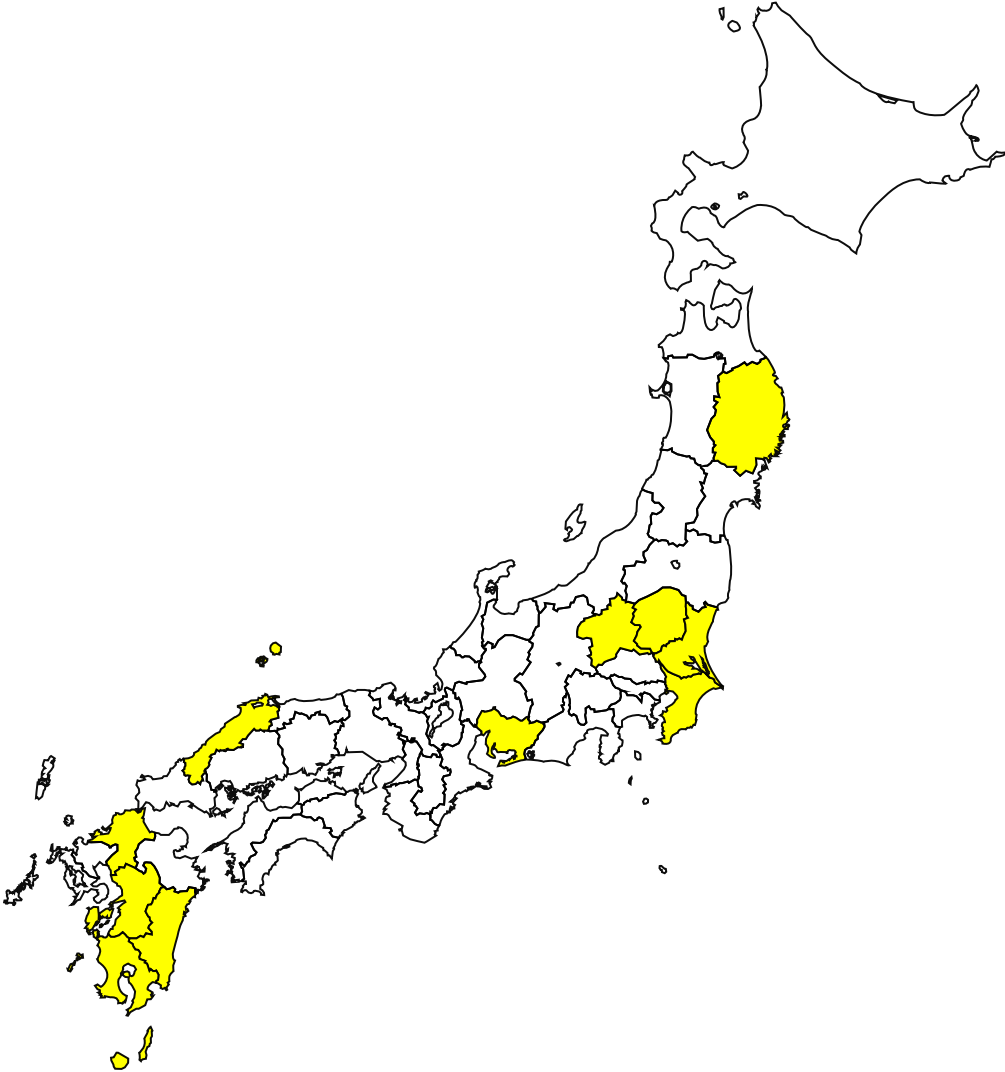
Genetic background of Japanese IAVs-S

- IAVs-S are circulating all over Japan including
 - H1 (derived from A(H1N1)pdm09): detected frequently
 - H1 (derived from Human strain 1970s～): majority
 - H3 (derived from Human strain 1999-2000～): not detected since 2023
- Reassortment between A(H1N1pdm09) virus and endemic H1N2 and H3N2 IAVs-S
 - almost all of internal genes of Japanese strains are already replaced by A(H1N1pdm09) viruses

Surveillance activities

- Since April 2024...

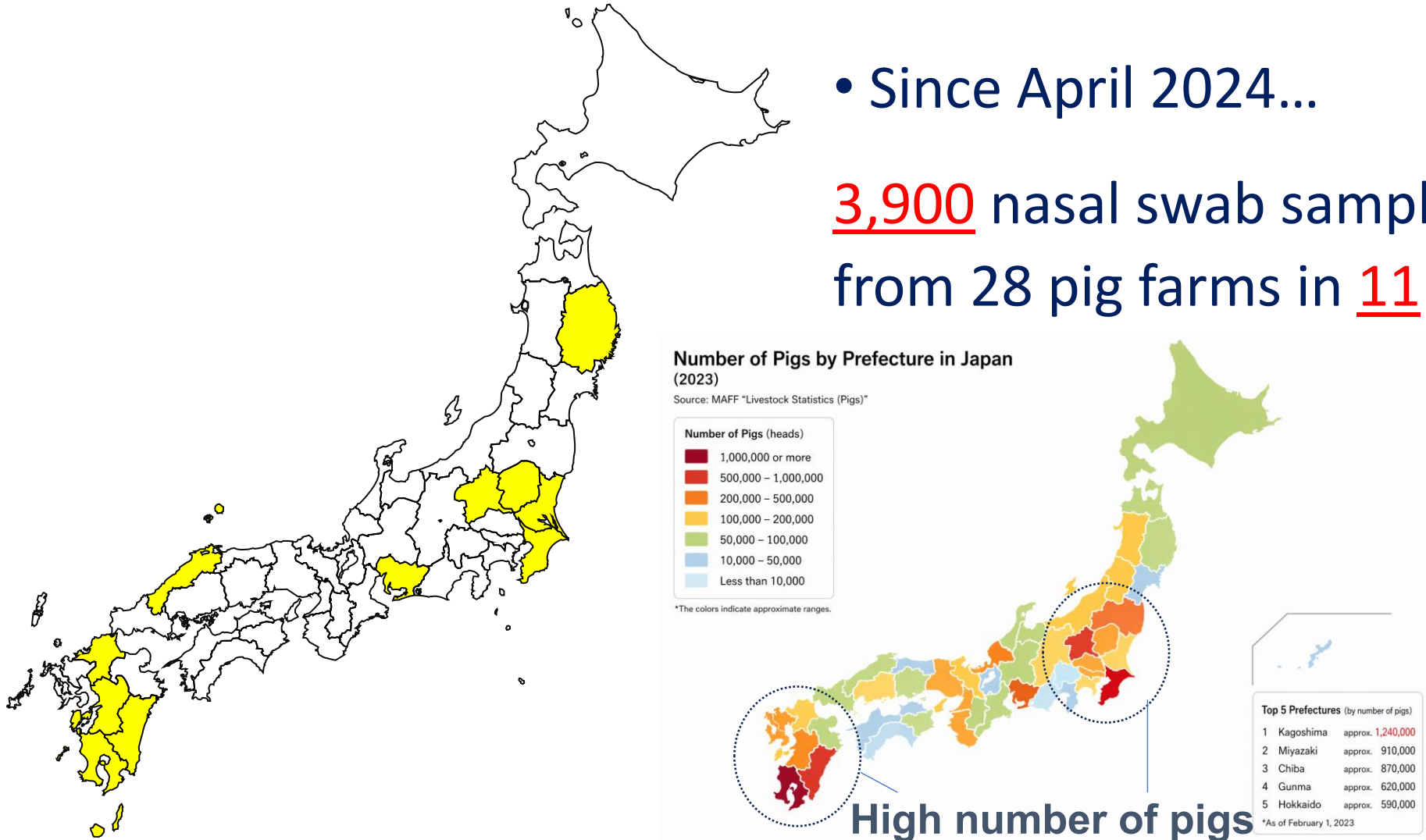
3,900 nasal swab samples were collected from 28 pig farms in 11 prefectures in Japan.



Surveillance activities

- Since April 2024...

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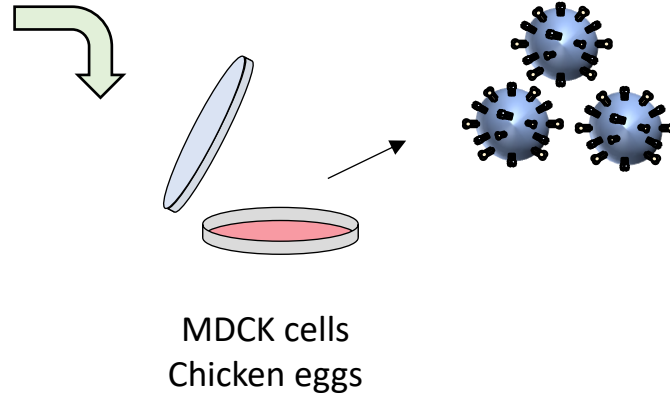


Surveillance activities

1. Virus isolation (periodic surveillance)



Weaning pigs

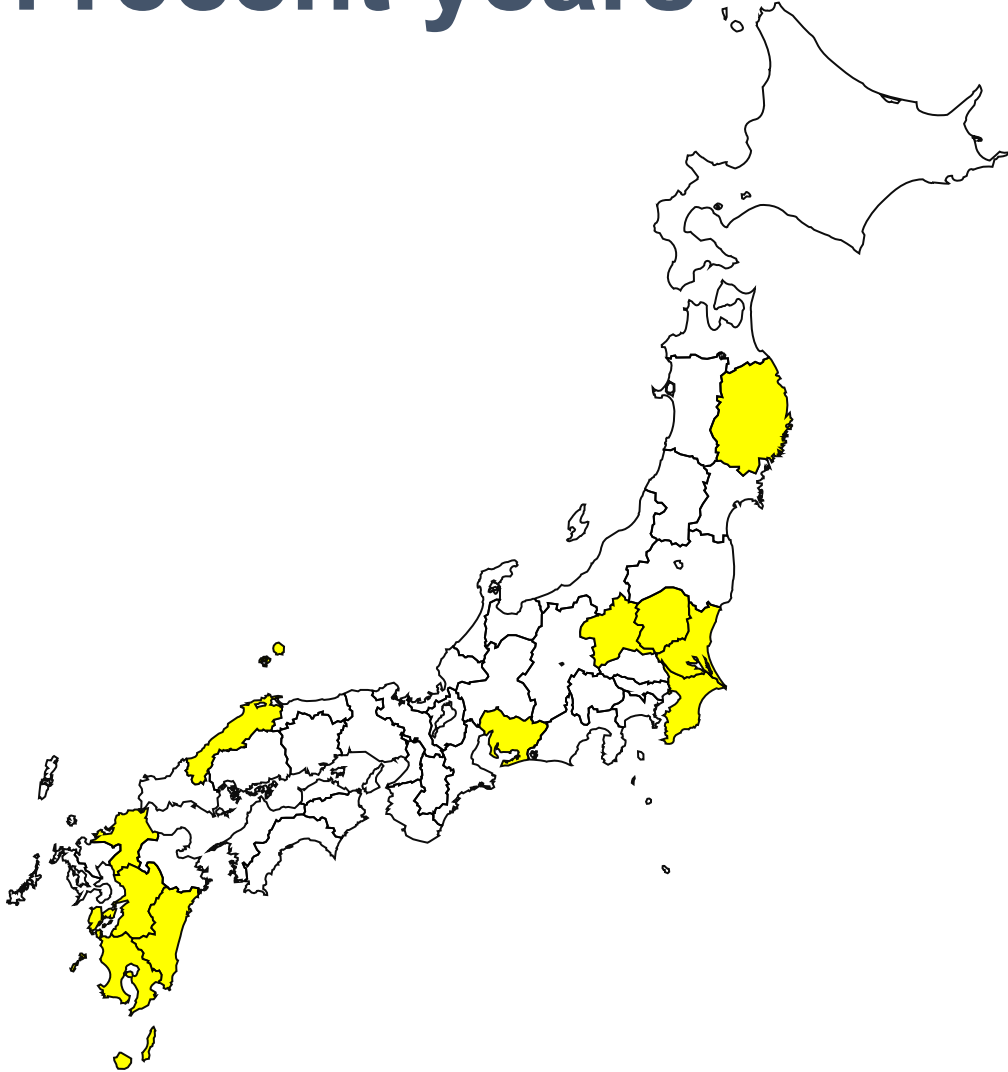


2. Full-genome sequence of isolated IAVs-S



- Identification of subtypes and genotypes
- Phylogenetic analysis

Genetic characters of Japanese IAVs-S in recent years



- Since April 2024...

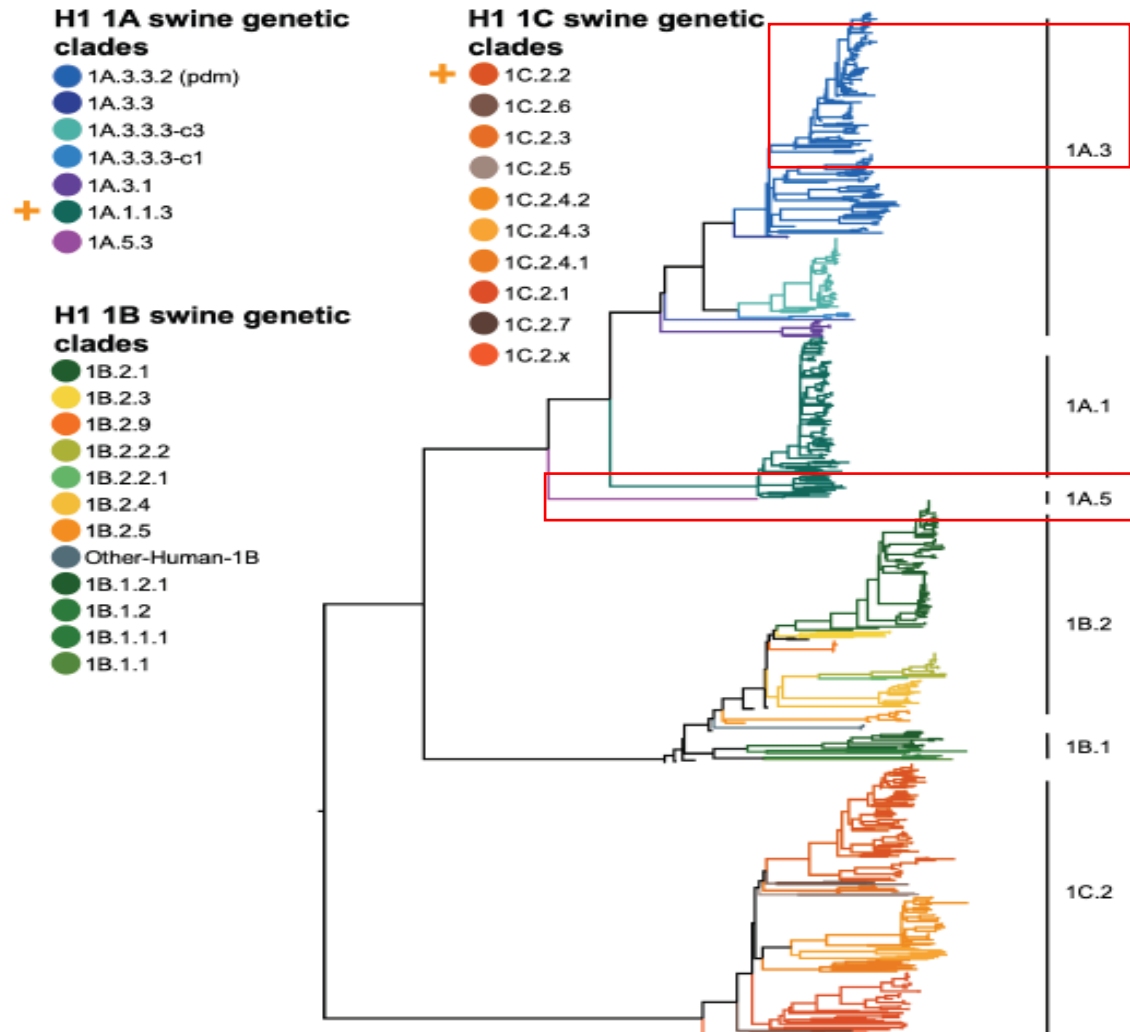
3,900 nasal swab samples were collected from 28 pig farms in 11 prefectures in Japan.

340 strains were isolated (**8.7%**)

- 96 A(H1N1)pdm09 and 244 1A.5.1 HAs

The phylogenetic trees on HA gene

Contemporary Global H1 swine IAV: genetic diversity

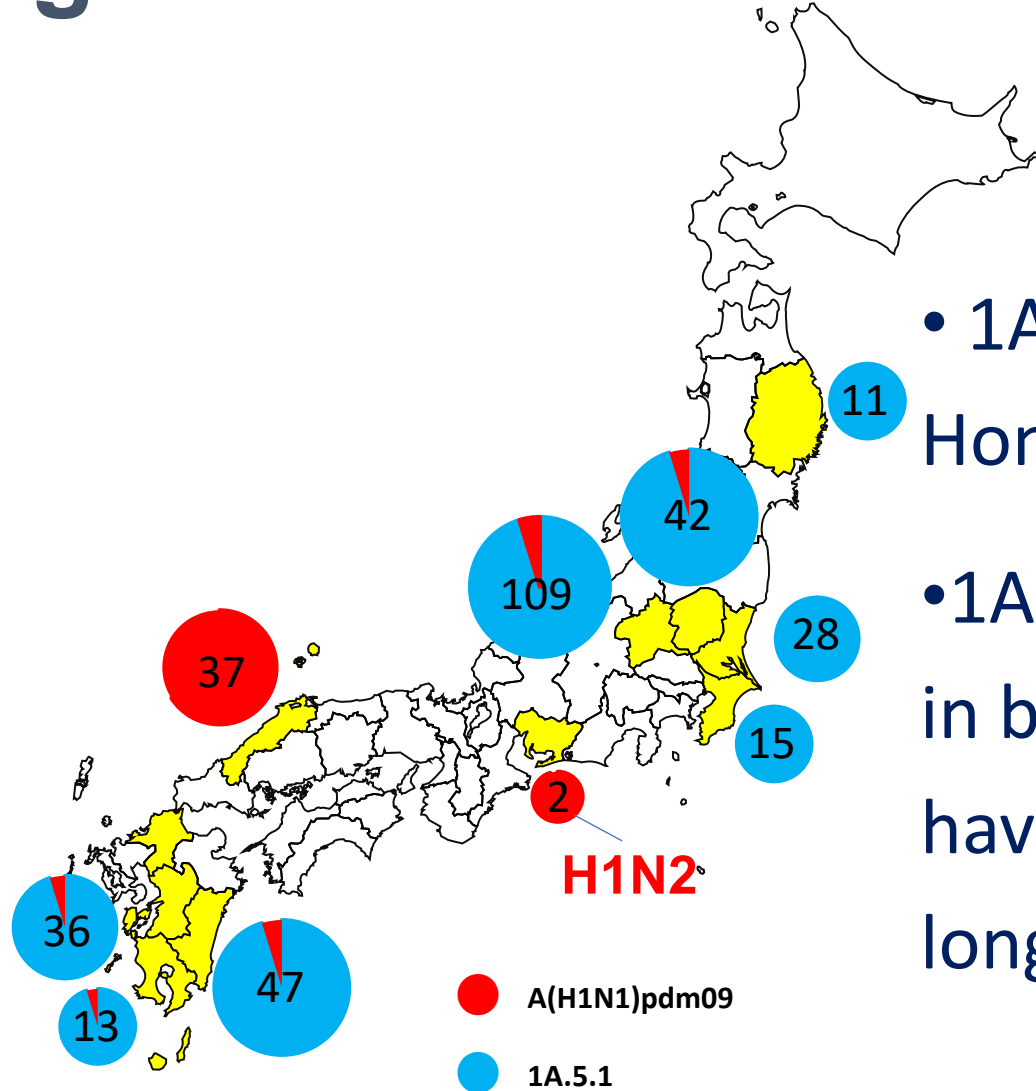


96 1A.3.3.2 HA IAVs-S however...
2 IAVs-S possess N2 NA

244 1A.5.1 HA IAVs-S however...
1 IAV-S possess N1 (pdm) NA

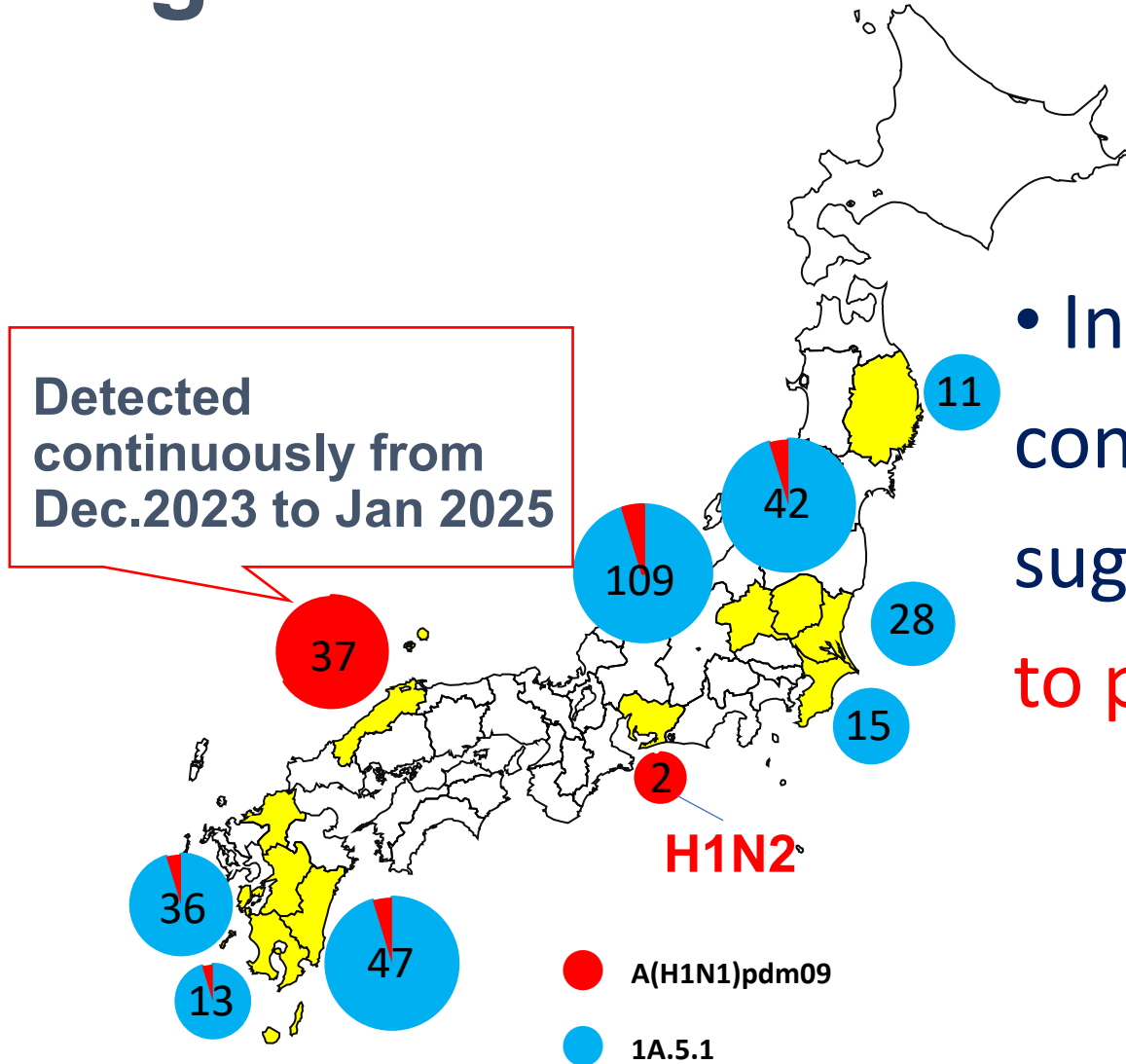
→ **Reassortment** between
H1N1(pdm)09 and endemic H1N2
has continuously occurred.

Geographical relationship with the HA genes



- 1A.5.1 HA IAVs-S are now **major** in Honshu and Kyushu.
- 1A.3.3.2 HA IAVs-S are **minor** but detected in both areas. They are **sporadic** as they have not been continuously detected as long as 1 year. However...

Geographical relationship with the HA genes



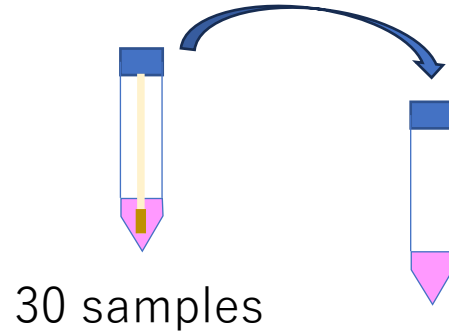
- In one case, 1A.3.3.2 derived IAVs-S are continuously circulating at a farm, suggesting the **adaptation from human to pigs?**

Recent studies

1. Virus isolation (periodic surveillance)

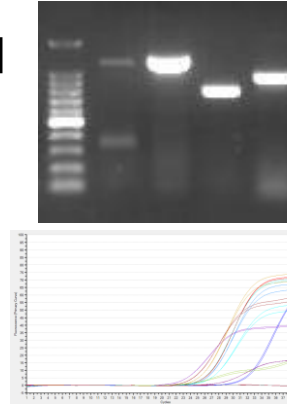


Weaning pigs



5 samples/1 pool

DNA/RNA
extraction



Detection of respiratory pathogens including **PRRSV**, **PCV2**, **PRCV**, and other bacteria.



- Identification of subtypes and genotypes
- Phylogenetic analysis

Summary

- Two genotypes (H1 1A.5.1; H1 1A.3.3.2) are circulating in Japan.
- H1 1A.5.1 IAVs-S are most isolated recent years.
- While almost H1 1A.3.3.2 IAVs-S are sporadically isolated throughout Japan, In one case, apparent adaptation to pigs are found.
- I am now interested in the impact of IAVs-S on PRDC, so now started working on the detection of other pathogens such as PRRSV, PCV2, and PRCV.

Thank you

