



Swine Influenza Viruses, a zoonotic threat with pandemic potential - Viet Nam, 2013

(EPT Plus Program)

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Overview

- The EPT Plus project document was approved by the Government of Vietnam (MARD) on 06 November 2012.
 - ✓ Project title: Surveillance and Characterization of Influenza Viruses posing Risk as the Next Global Pandemic.
 - ✓ Duration: September 2012 – September 2013
 - ✓ Budget: USD 200.000 funded by USAID

- **Study Design: Cross-sectional Study**
 - ✓ **Overall hypothesis:** Greater genetic diversity of influenza viruses exists in low bio-secure, open intensive swine systems where contact among birds, people and pigs is possible (multiple introductions) and large numbers of swine will be exposed to, amplify, and spread the virus

✓ **Objectives:** Characterize the influenza virus pool in Vietnam from **two swine production systems** and determine if greater genetic diversity exists in any of these production systems.

✓ **Study locations (12 provinces):**

- ❖ Six (06) provinces in the Red River Delta: Bac Ninh, Hai Duong, Hoa Binh, Nam Dinh, Ha Nam, Hai Phong
- ❖ Six (06) provinces in the Mekong River Delta: Vinh Long, Ben Tre, Binh Duong, Dong Nai, Soc Trang, Dong Thap

✓ Production systems for this study:

- ❖ Low bio-secure, medium sized **farrow-to-weaning** farms with 50-200 sows and about 500 pigs aged 4-12 weeks old (farm with 100-200 sows is preferable)
- ❖ Low bio-secure, medium sized **fattening** farms with 100-4000 pigs. These farm must have different age groups and not being all-in/ all-out production system.

✓ Samples:

- ❖ For each province (n=12), 02 farrow-to-weaning farms and 03 fattening farms will be sampled to give a total of 05 farms to be sampled.
- ❖ Pigs aged 4-12 weeks, sows and 8-16 weeks will be randomly sampled. Serum and nasal swabs will be collected.
- ❖ The single random sampling technique is used to select pigs in each farm.
- ❖ Sampling in 4 rounds:
 - ❖ The first 3 rounds: sampled as designed (60 farms)
 - ❖ The fourth round: **re-sampled positive farms**, and the negative farms will be replaced by the new farms.

✓ Sample size for the first 3 rounds (60 farms, 3600 swabs, 720 bloods) and **repeated in 4th** round

❖ For farrow-to-weaning farm (n=24):

- Pigs aged 4-12 weeks: 60 nasal swabs and 10 bloods
- Sows: 5 bloods

Total: 1440 swabs; 240 piglet bloods, 120 sow bloods

❖ For fattening farm (n=36):

- Pigs aged 8-16 weeks: 60 nasal swabs and 10 bloods

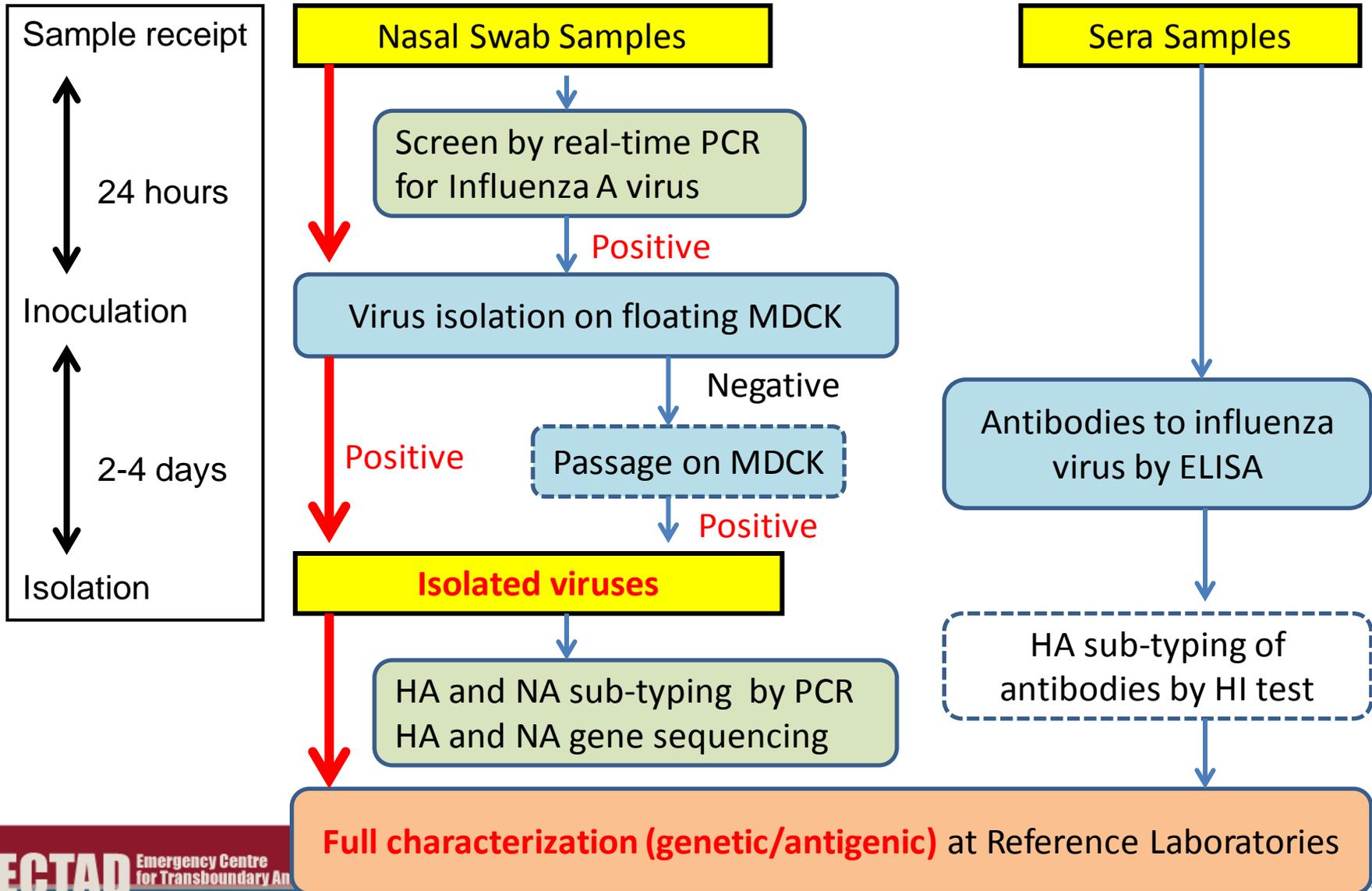
Total: 2160 swabs; 360 bloods

Remark: Calculation of 60 samples per farm would allow us with 95% confidence to detect at least 1 positive pig if the AI virus presented in the herds mentioned above (based on the assumption of virus prevalence at farm level is 5%)

✓ Testing

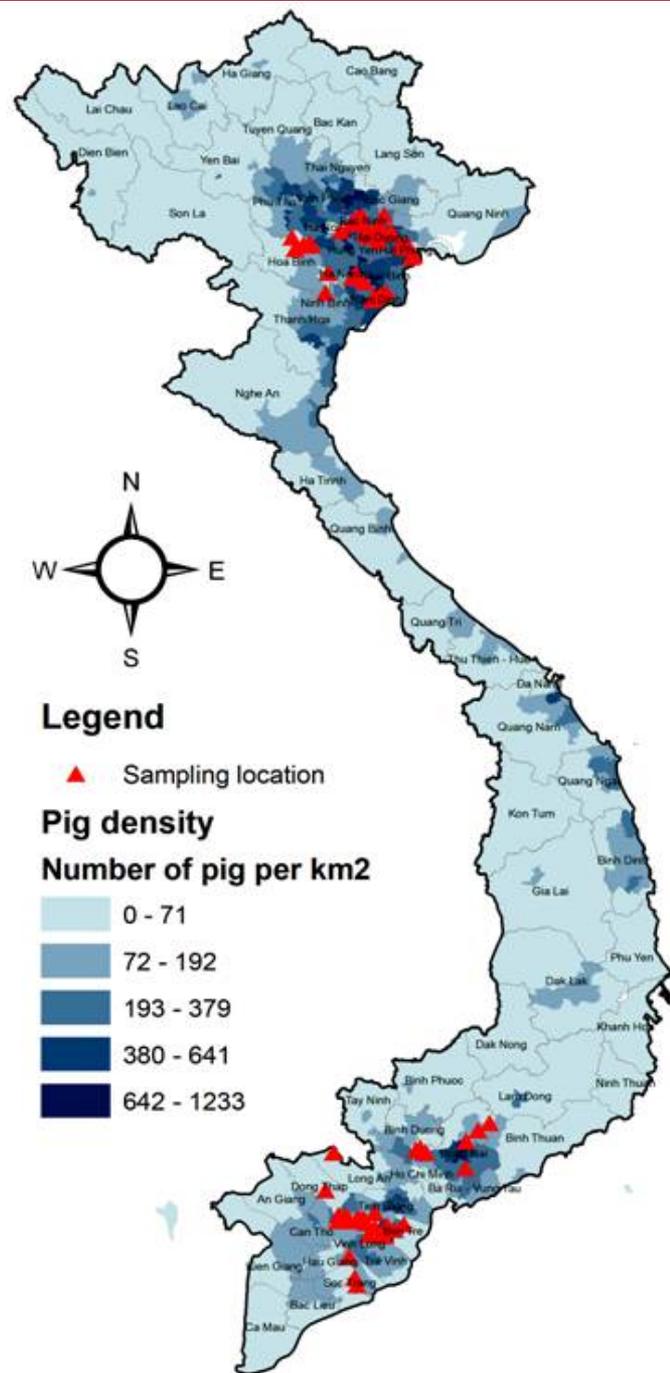
- ❖ NCVD (in Ha Noi) and RAHO6 (in Ho Chi Minh)
 - ❖ All samples were sent to Labs in the same day of collection for RRT-PCR analysis/ viruses isolation. Isolated viruses are sent to NCVD for further analysis of genetic characteristics.
 - ❖ Serum samples: ELISA
 - ❖ Swab samples: 5 swab samples will be pooled for M gene testing, RRT – PCR applied for single swab in (+) pool, then follow by virus isolation.
- ✓ Questionnaires: applied to all selected farms. All detailed information related to farms and farms' owners will be collected. Face-to-face interview is applied to the farm owners/ technicians.

Laboratory Testing Flowchart



Study location

- 12 Provinces:
 - 06 in the North:
Bac Ninh, Hai Duong,
Hai Phong, Hoa Binh,
Ha Nam, Nam Dinh
 - 06 in the South:
Dong Thap, Vinh
Long, Dong Nai, Ben
Tre, Binh Duong, Soc
Trang



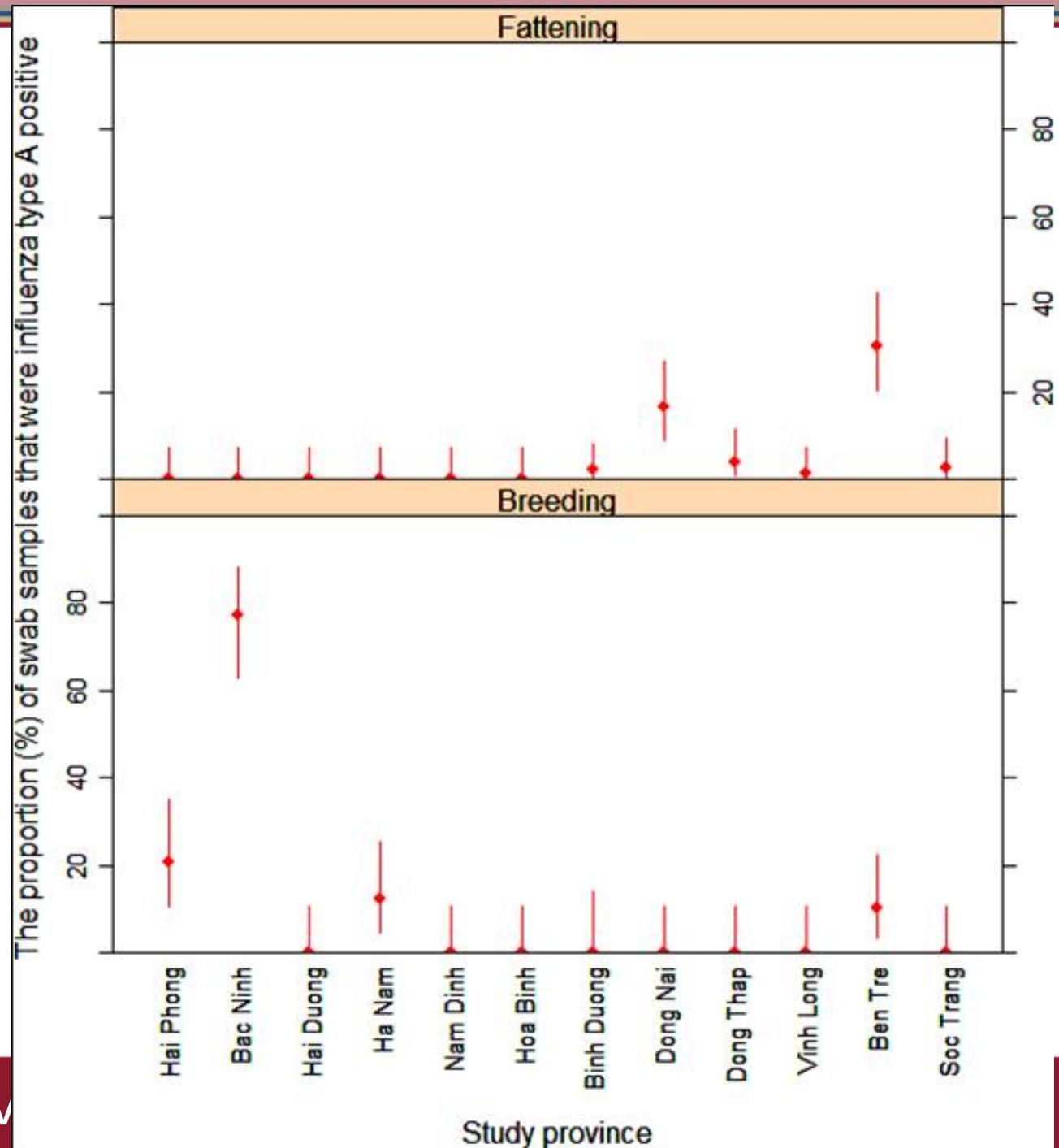
Results (1)

- A total of 7,200 nasal swab samples and 1,434 serum samples were collected at random from 88 pig farms (32 breeding farms and 56 fattening farms) over one year period.
- 5 swab samples will be pooled for M gene testing, therefore 1,440 swab pools and 1,434 serum samples tested.

Results (2)

- The overall prevalence of influenza type A virus infection in pigs was 6.94% (95% CI 5.69 - 8.38).
- Fifteen out of 120 (12.5%) study farms had at least one pig was positive with influenza type A virus.
- The prevalence of influenza type A virus infection in pigs at breeding farms is 10.28% (95% CI 7.90 - 13.09), significant higher than the one recorded for fattening farm (χ^2 test statistic = 13.7754, df = 1, p-value = 0.0002).
- The prevalence of influenza type A virus infection in pigs at fattening farms 4.79% (95% CI 3.48 - 6.43).

The proportion (%) of nasal swab samples that were positive with influenza type A virus stratified by production type of pigs (breeding and fattening).



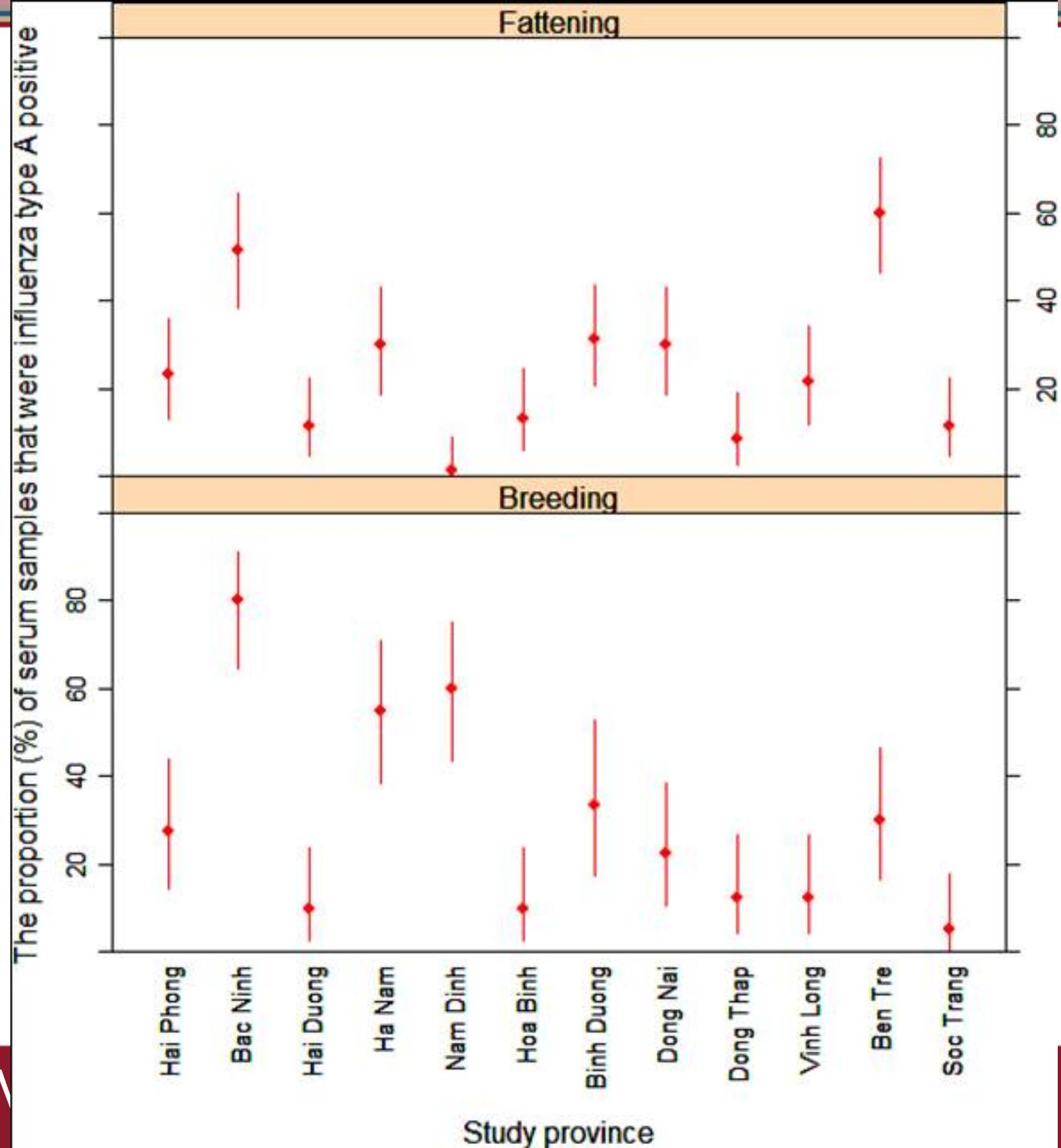
Results (3)

- 12.5% study farms had at least one pig positive with influenza type A virus. The highest prevalence of influenza virus infection at farm level is 30.83% (95% CI 22.73 - 39.91).
- 75% study provinces had influenza type A virus circulated in their pig population.

Results (4)

- The sero prevalence of influenza in fattening and weaned pigs was 26.76% (95% CI 24.26 - 29.36), the highest sero prevalence was 63.00% (95% CI 52.76 - 72.44). All 12 study provinces had pigs with sero positive.
- The sero prevalence of influenza in weaned pigs was 29.91% (95% CI 25.80 - 34.29), slightly higher than that of 24.73% (95% CI 21.63 - 28.03) recorded for pigs at fattening farms (χ^2 test statistic = 2.2428, df = 1, p-value = 0.1342).
- The sero prevalence of influenza in sows was 58.80% (95% CI 52.30 - 65.10), much higher than that of fattening pigs (χ^2 test statistic = 41.7478, df = 1, p-value < 0.0001).

The proportion (%) of serum samples of fattening pigs and weaned pigs that were positive with influenza type A virus stratified by breeding and fattening farms



Results (5)

- All swab samples (n = 106) that were positive or suspect with influenza type A viruses were used for virus isolation and identification.
- A total of 6 samples in 5 provinces were positive with H1N2 and H3N2 viruses
- All positive samples were also sent to Macrogen lab (Korea) for sequencing.
- Phylogenetic analyses indicated that swine influenza viruses in Viet Nam belong to the North American strain.

Conclusion (1)

- High proportion of pigs with sero-conversion to SIVs in Viet Nam (26.76% sero-positive) indicates that many pigs exposed to SIVs which circulated previously on the pig farms.
- Lower proportion of pigs shedding the SIVs (6.9% RRT-PCR positive) would be explained that those pigs might get a new infection in the farm.
- The infected pigs would continue to shed the SIVs to others and pose a risk to infect humans, especially those in close contact with pigs.

Conclusion (2)

- H3N2 and H1N2 were found in 06 farms from 05 provinces would directly pose the risk to pigs and human that in contact within/ between farms
- Possible concurrent infection with seasonal influenza viruses or Highly Pathogenic Avian Influenza (H5N1, H5N6) may result in new virulent strains with human pandemic potential.
- Swine influenza virus monitoring should continue to timely detect emerging viruses with potential pandemic potential and prevent such events



Thank you for your attention

