OFFLU swine influenza virus meeting
27 – 28 March 2017
FAO Headquarters, Rome, Italy

Ariel Pereda
Instituto de Patobiología
INTA - ARGENTINA

Swine Influenza in South and Central America

Chile
Guatemala
Colombia
Argentina

South and Central America SIV Surveillance

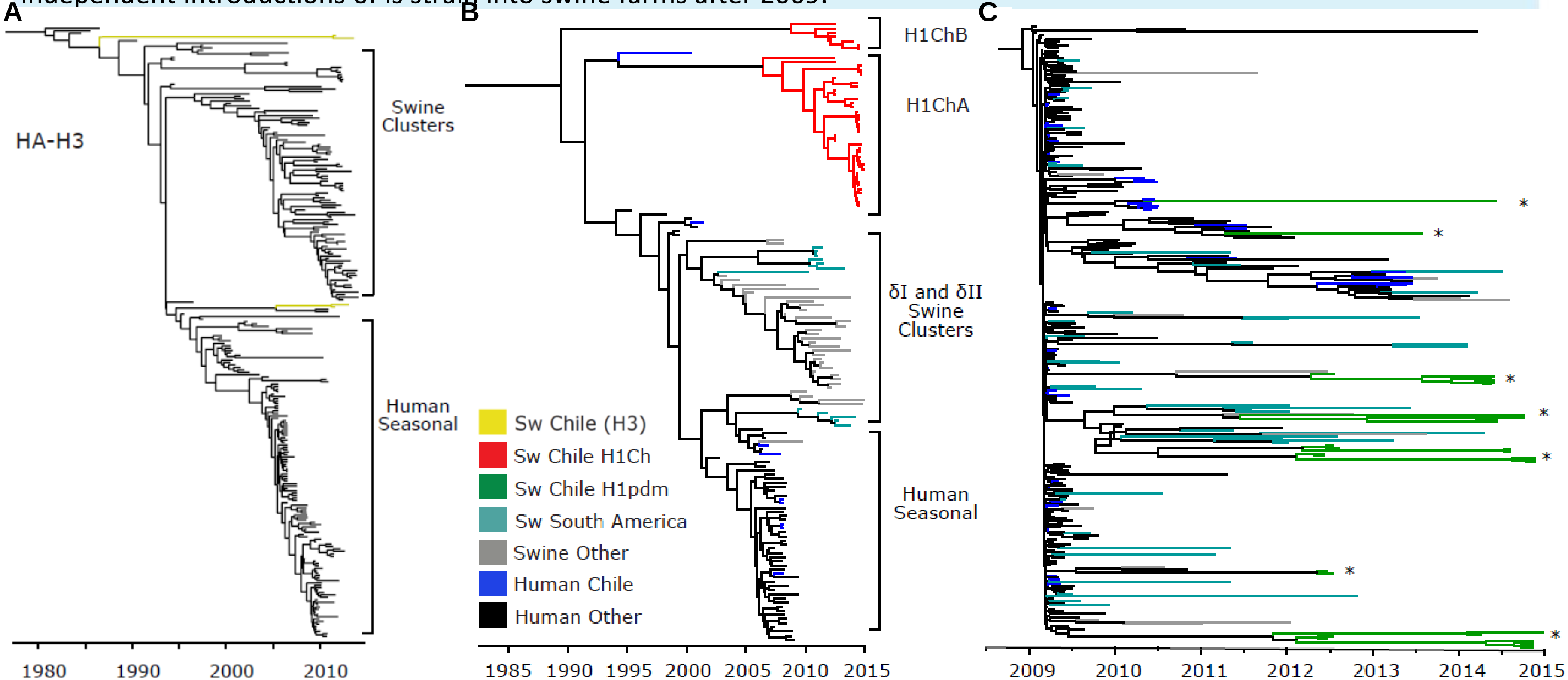
Chile

Multiple introductions of human seasonal IAV results in high diversity and reassorment of SwIAV

A. The H3 viruses were closely related to 2 human-like H3 IAVs that are different from the North American clusters. The time to most recent common ancestor (TMRCA) was estimated as early as 1987 and 2006, respect..

B. Phylogenetic analyses of H1 viruses revealed 3 clusters of swIAV, a H1pdm cluster and two unique Chilean clusters. TMRCA of cluster A estimated to be 1994 and of cluster B was estimated to as early as 1986.

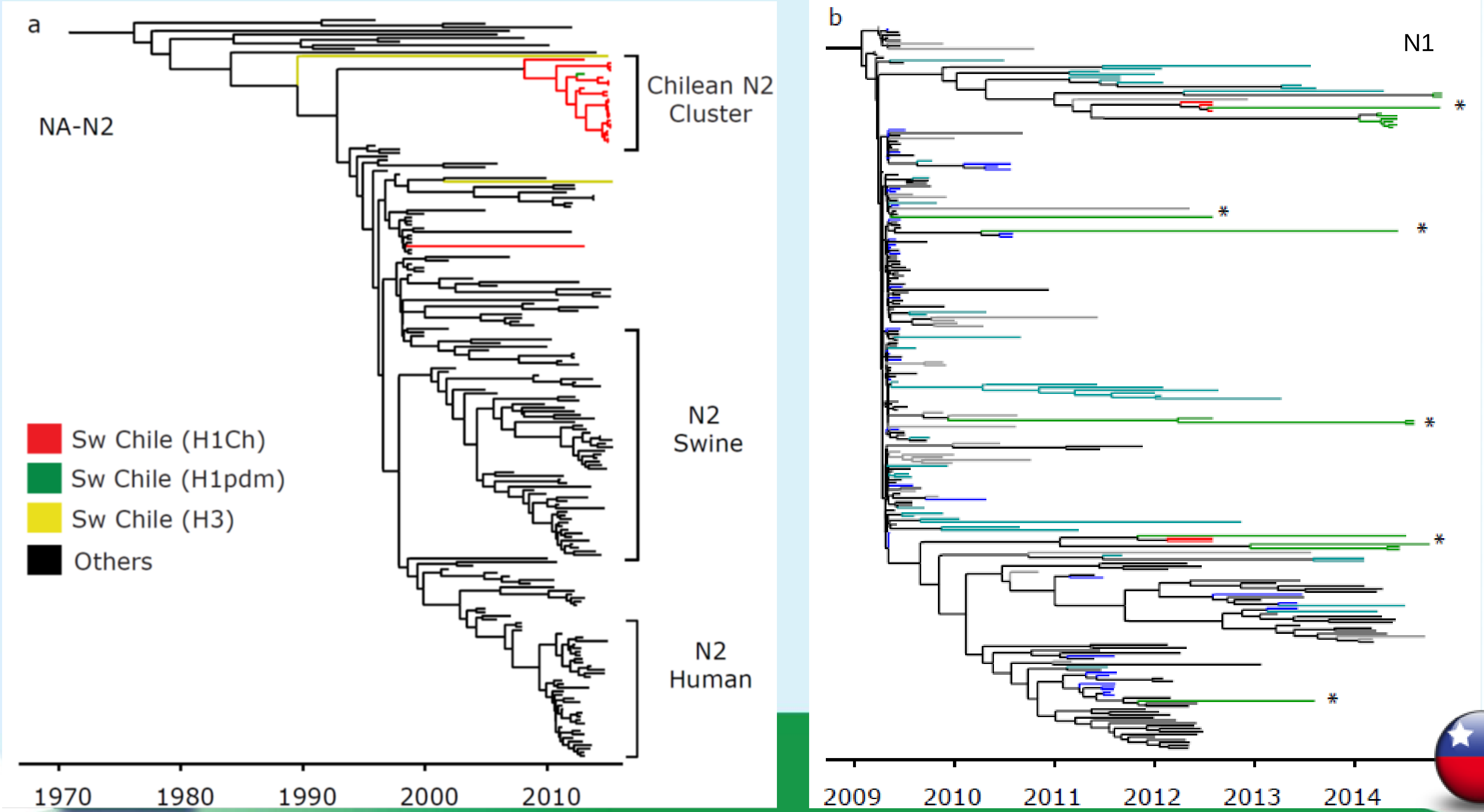
C. The H1pdm cluster shows these viruses interleaved with different swine and human viruses, suggesting at least 7 independent introductions of is strain into swine farms after 2009.



Multiple introductions of human seasonal IAV results in high diversity and reassortment of SwIAV

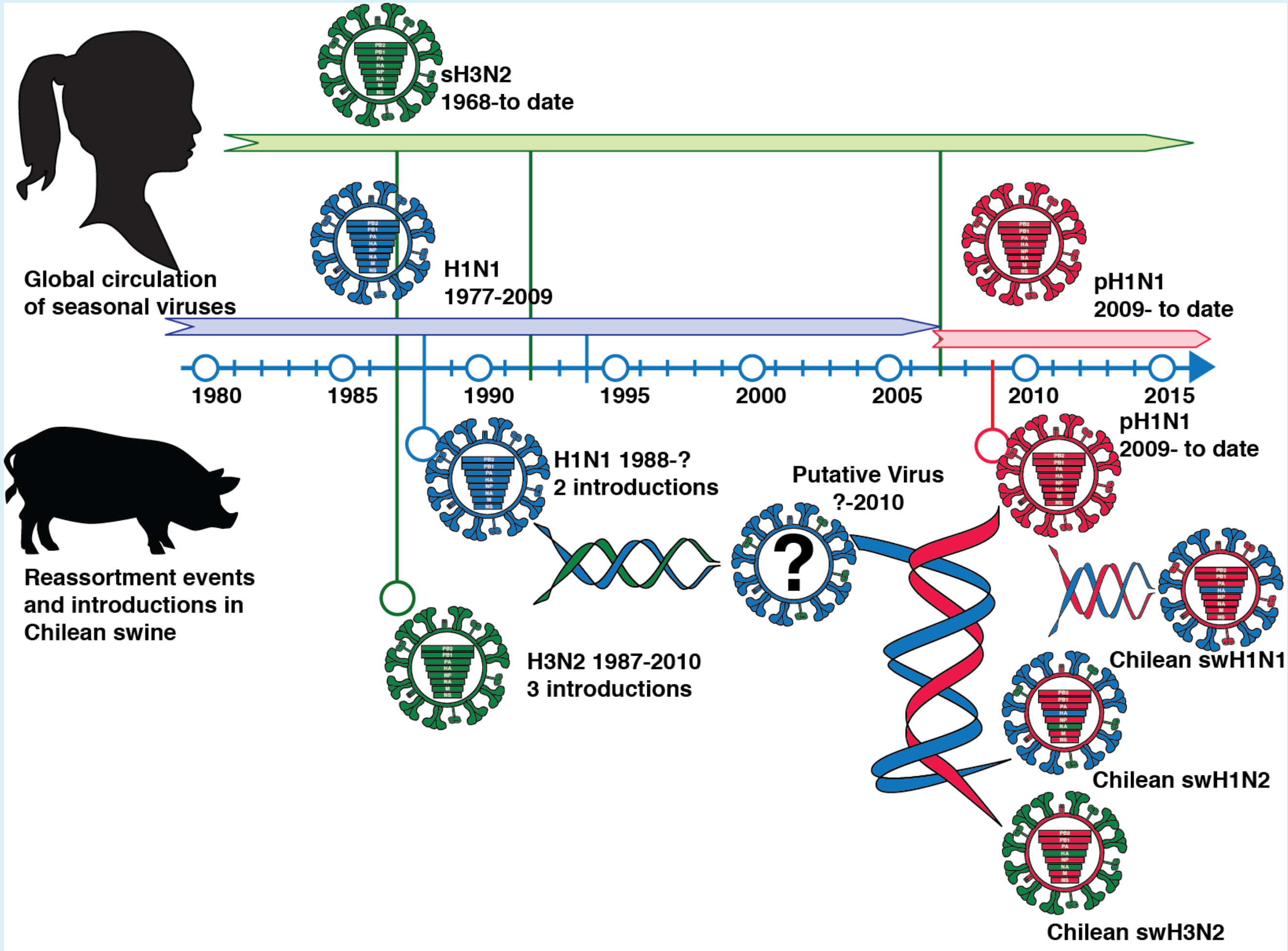
a. Phylogenetic tree of NA sequences from N2 subtype IAV from Chilean H1 (red), H1pdm (green), and H3 (yellow) viruses. The N2 group mainly in a monophyletic cluster that is unique to Chile. The introduction of this N2 in the swine population dates to May 1992 (95%HPD December 1988 - July 1994).

b. Phylogenetic analysis of N1pdm subtype reveal 6 independent introductions of the N1 segment (green, and asterisk) into the swine population.



Model of circulation, reassortment and viral diversity of SwIAV in Chile

Human seasonal H1N1 and H3N2 viruses were likely introduced into the swine population in Chile sometime during the late 1980s to mid 1990s, generating increased reassortment and diversity since the 90s.

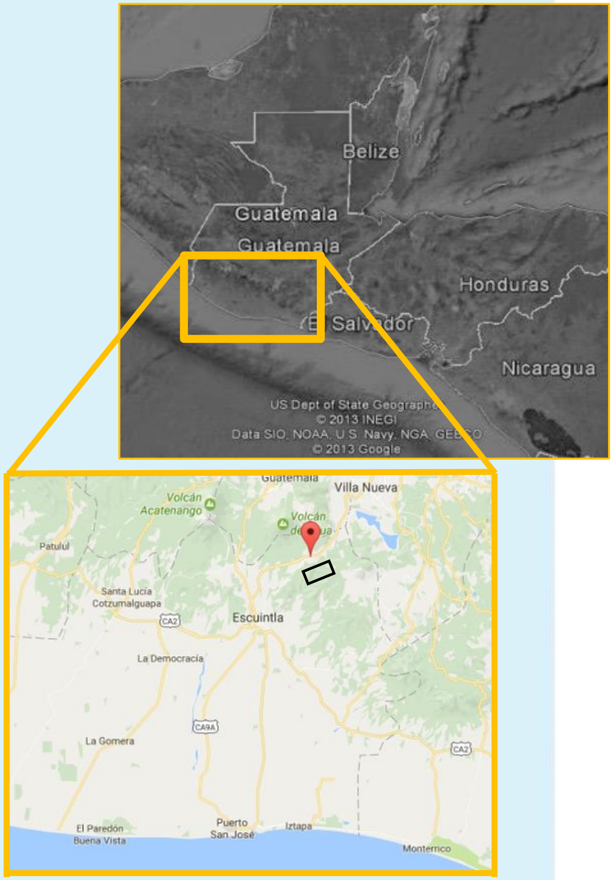


GUATEMALA

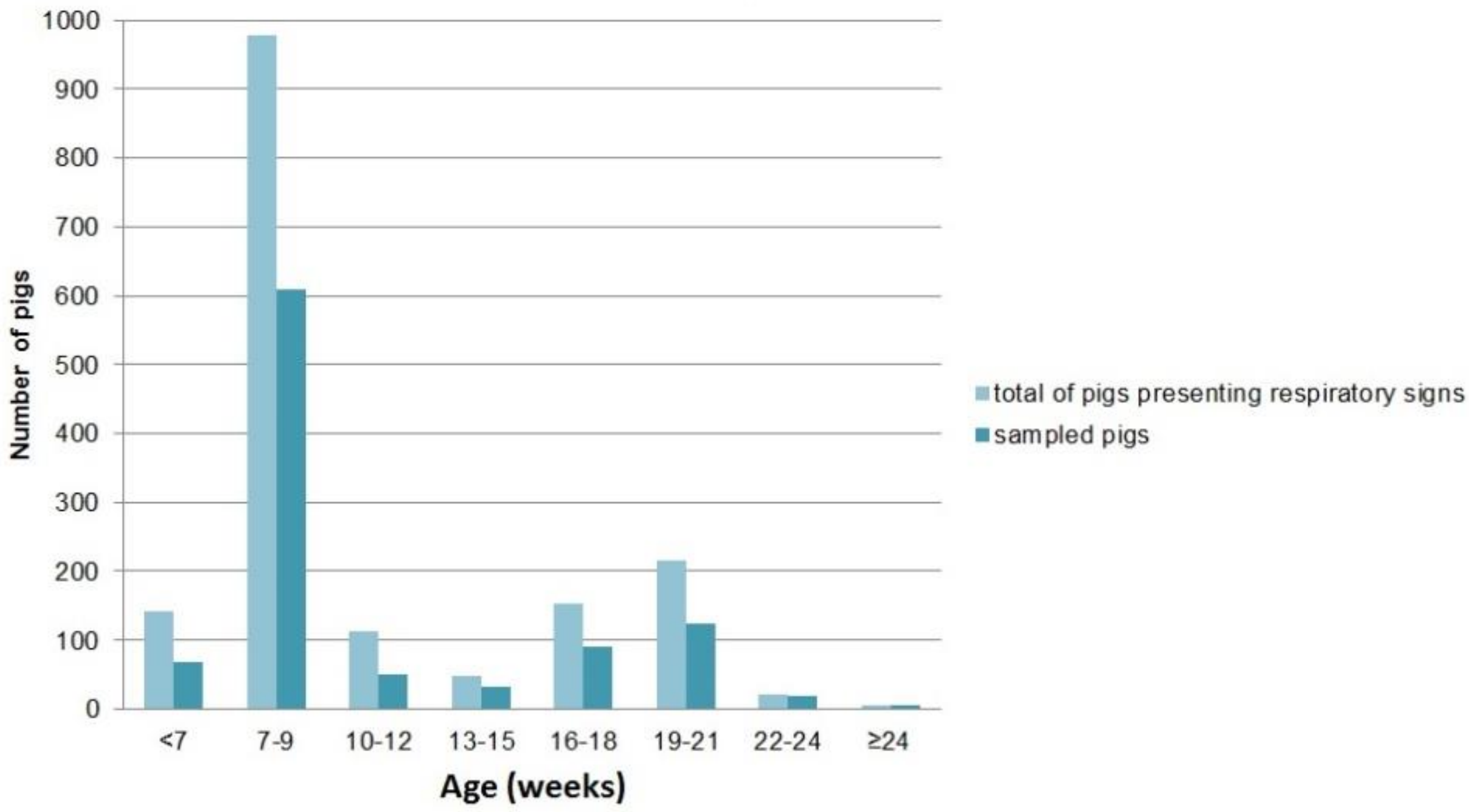
CRIP surveillance in pigs (UGA-UVG)

Active surveillance in a commercial farm:

- A pilot surveillance of swine influenza is being conducted in Escuintla (Southern region of Guatemala):
  - Only pigs showing respiratory signs are being sampled twice per week.
  - Age of sampled pigs ranges from 6 to ≥24 weeks.
  - Rectal temperature, sex and respiratory signs of each sampled pig is being recorded.
- To date, a total of 997 nasal swabs were collected from May 2016 to February 2017.

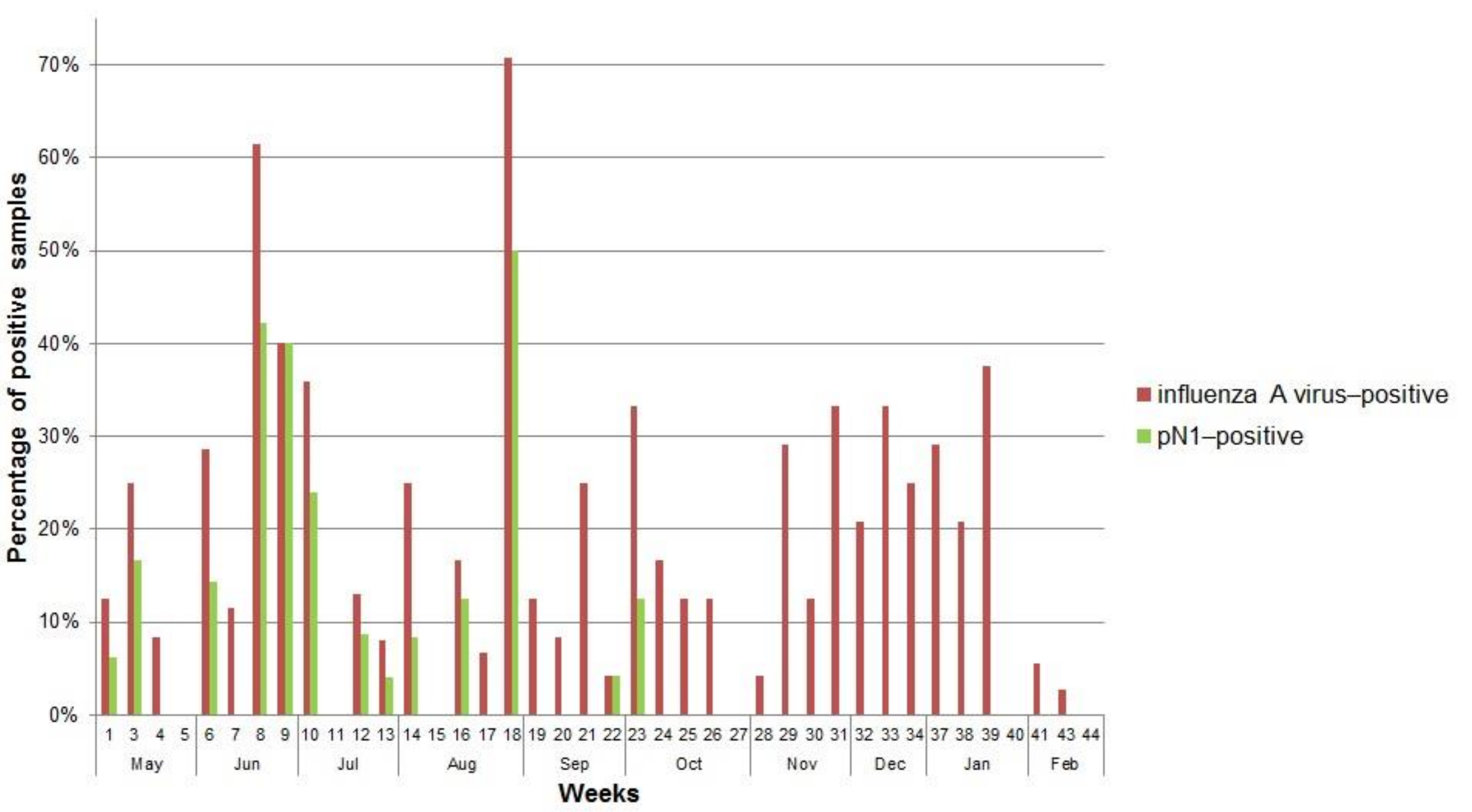


Preliminary results showing the total of pigs presenting respiratory signs, by age group in a commercial farm in Escuintla, Guatemala, May 2016-February 2017



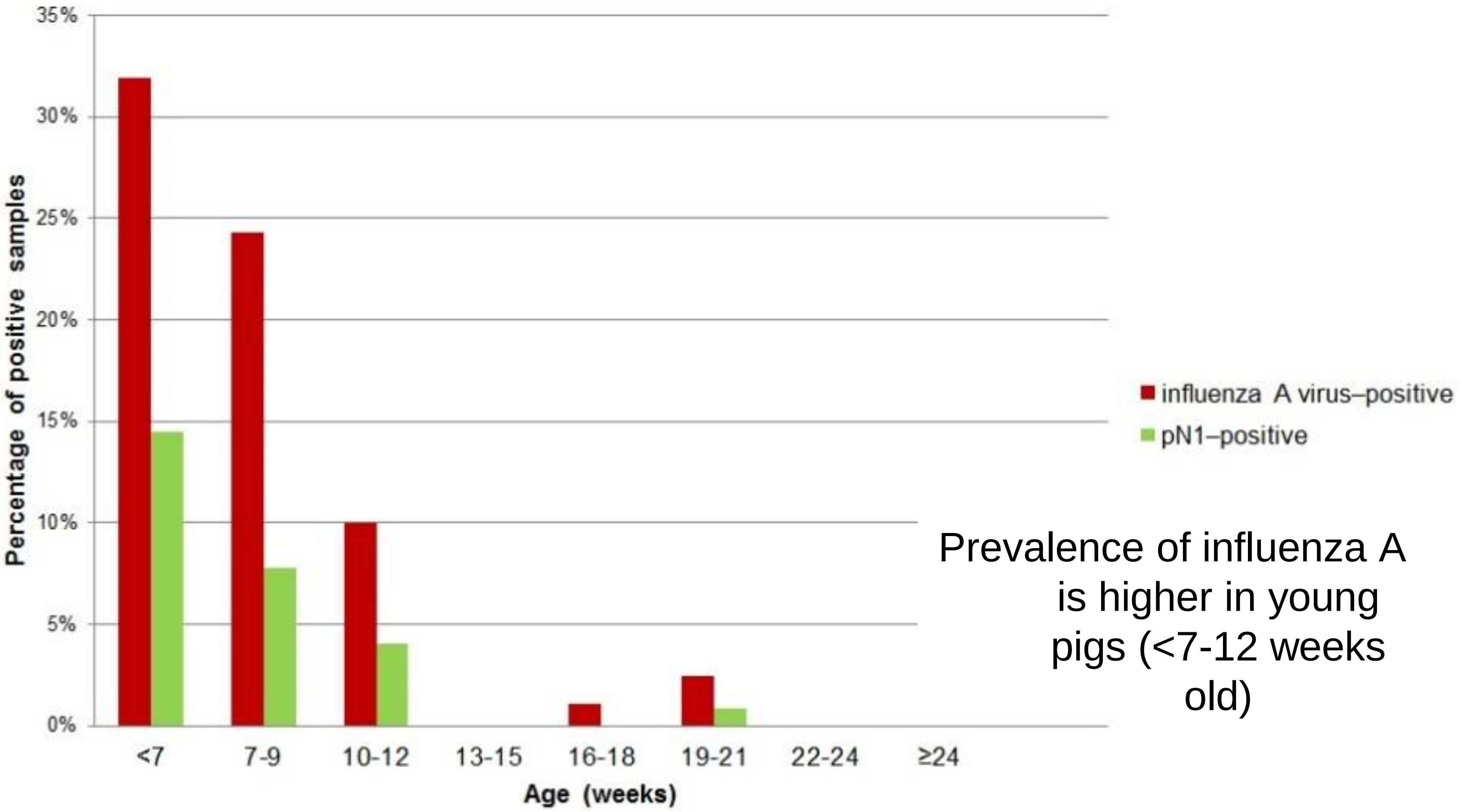
Approximately 60% of pigs presenting signs has been sampled for influenza A and pN1 detection. Pigs between 7-9 weeks present more number of pigs with respiratory signs.

Preliminary results showing the percentage of influenza A virus and pN1 positive samples by RRT-PCR, in a commercial farm in Escuintla, May 2016 to February 2017



Influenza A has been detected throughout the period; however pN1 has been detected only from May to September 2016. All influenza A-virus positive samples by RRT-PCR are being cultured in MDCK cells; viral isolates will be sequenced by NGS.

Preliminary results showing the age distribution influenza A and pN1 positives by RRT-PCR, in a commercial farm in Escuintla, Guatemala, May 2016 to February 2017



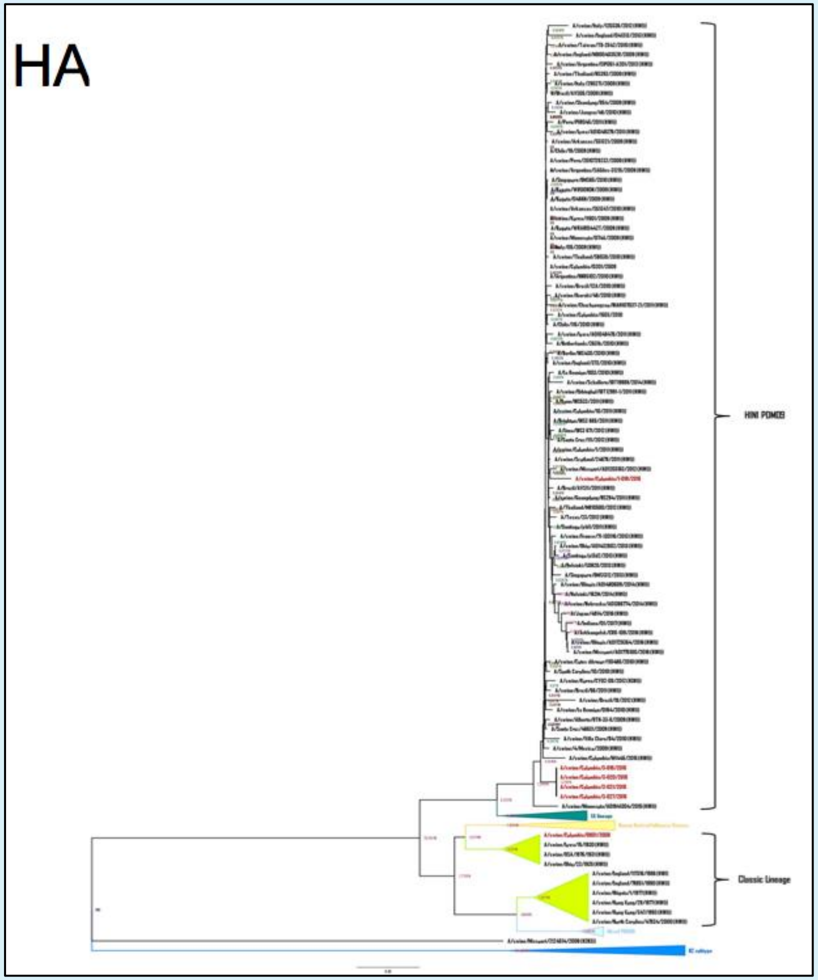
Prevalence of influenza A is higher in young pigs (<7-12 weeks old)

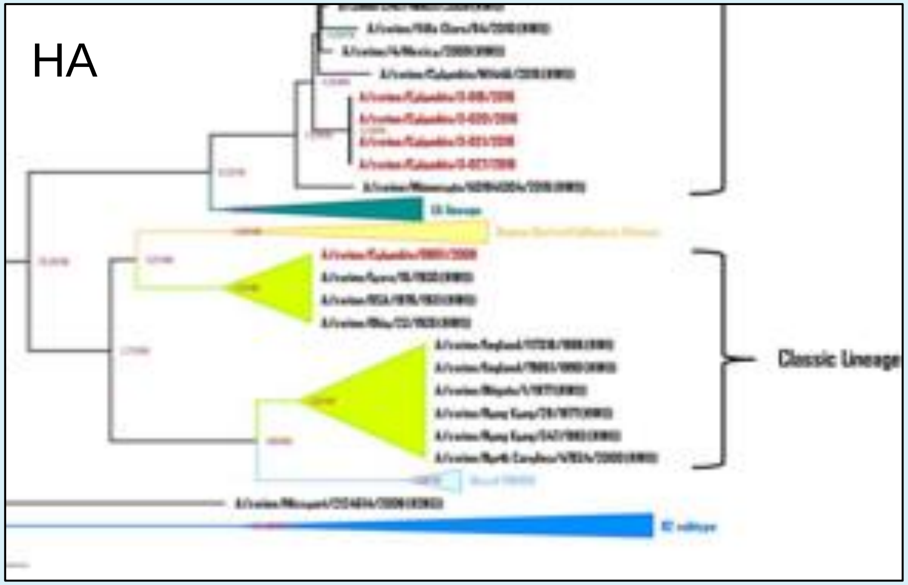
Preliminary results show 19% (186/997) of influenza A detected by RRT-PCR and 33% (62/186) for pN1 in influenza A-positive samples.

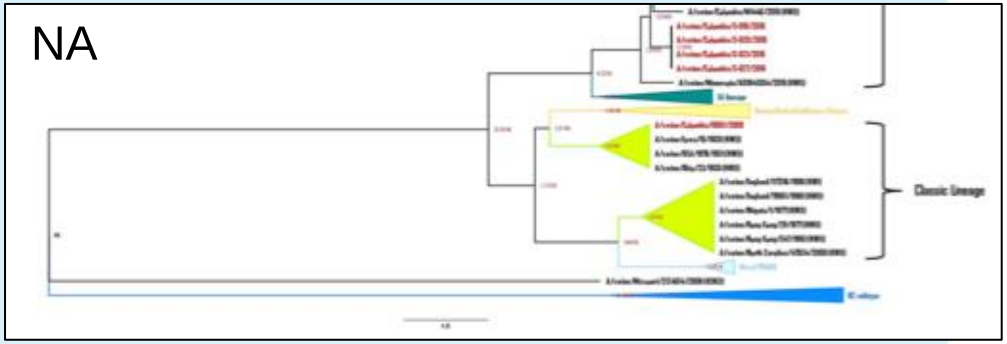
COLOMBIA

Region	Samples
Antioquia	341
Cundinamarca	154
Valle del Cauca	109
Meta	42
Eje Cafetero	64
Tolima	10
Chocó	10
Huila	10
Santander	10
Atlántico	20
Nariño	20
Total	790

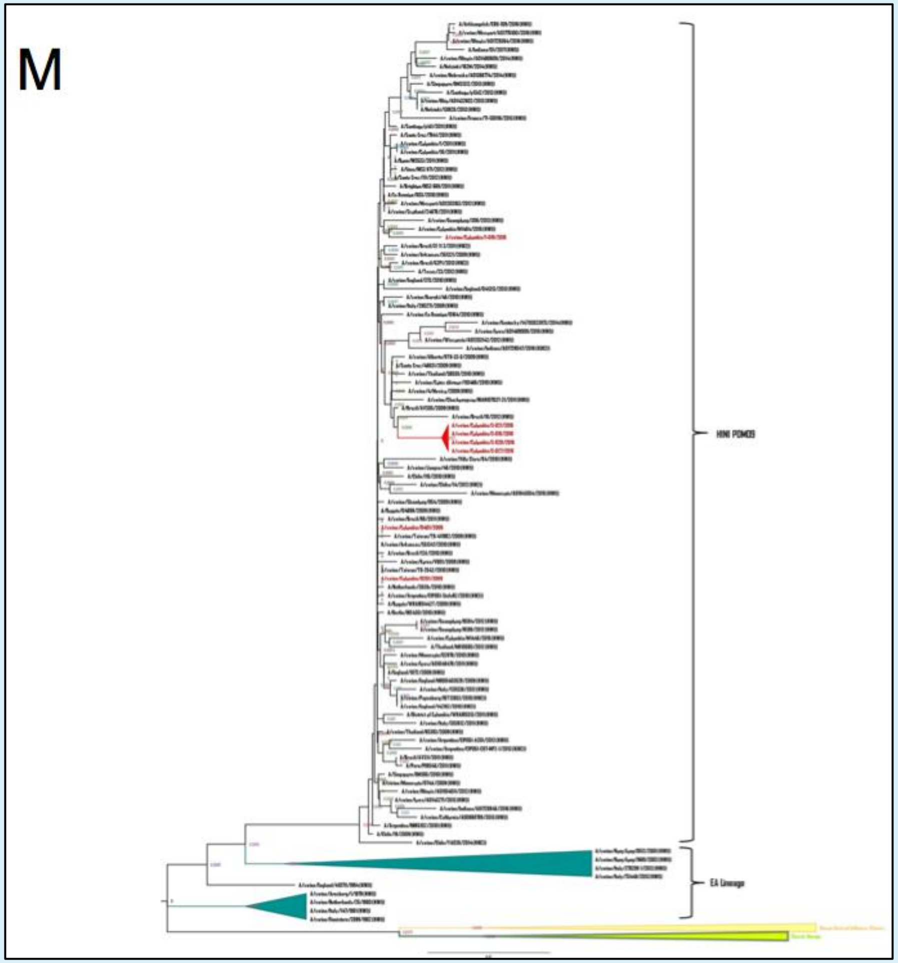
5 isolates


HA
H1N1 PDM09
Classic Lineage

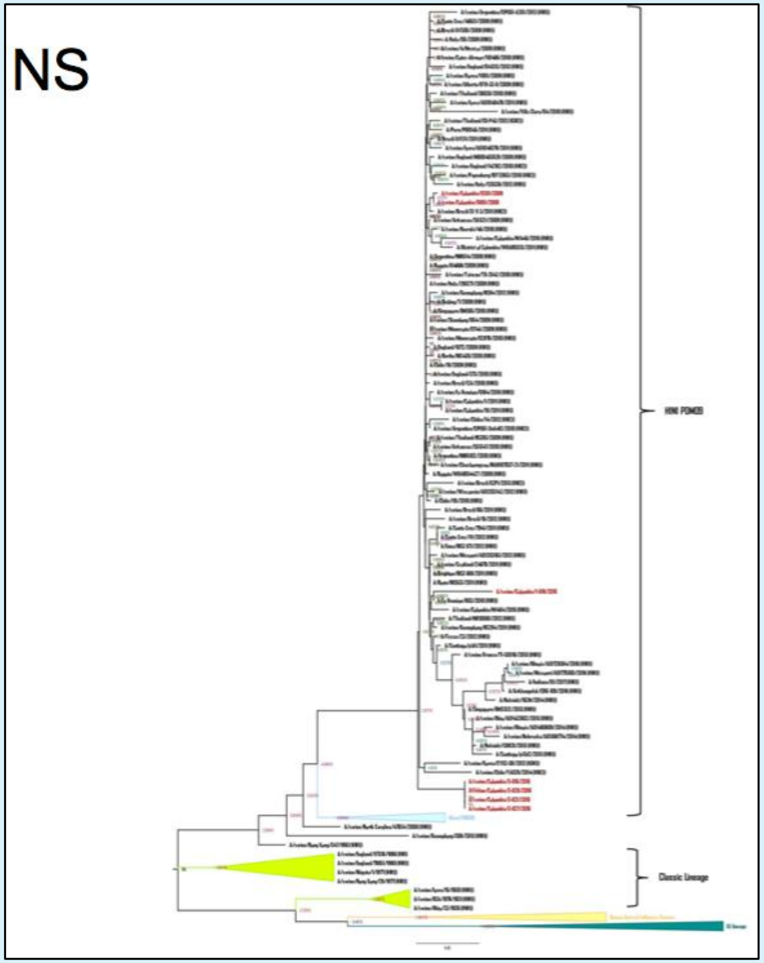

HA
Classic Lineage


NA
Classic Lineage

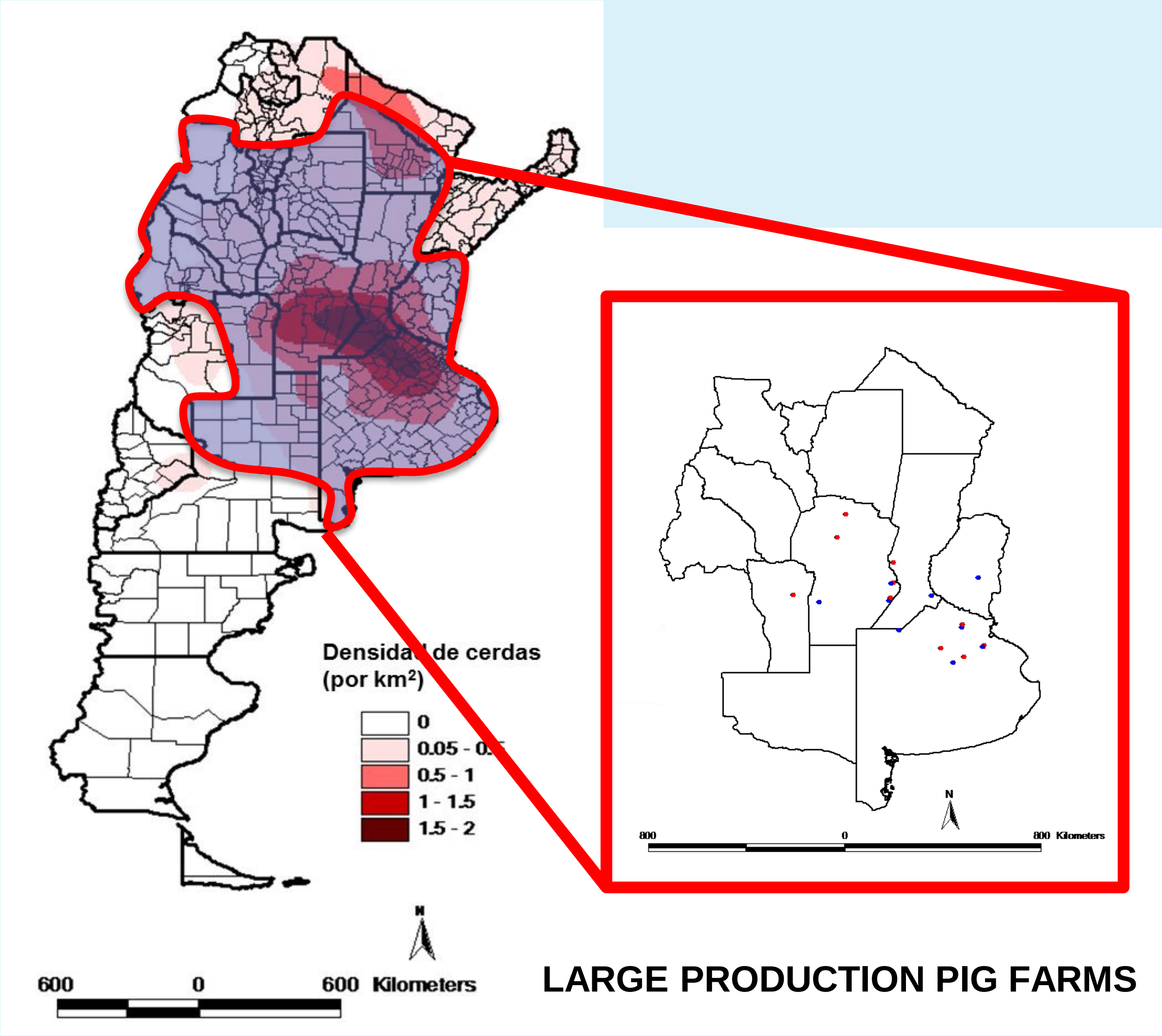
M



NS



ARGENTINA



LARGE PRODUCTION PIG FARMS

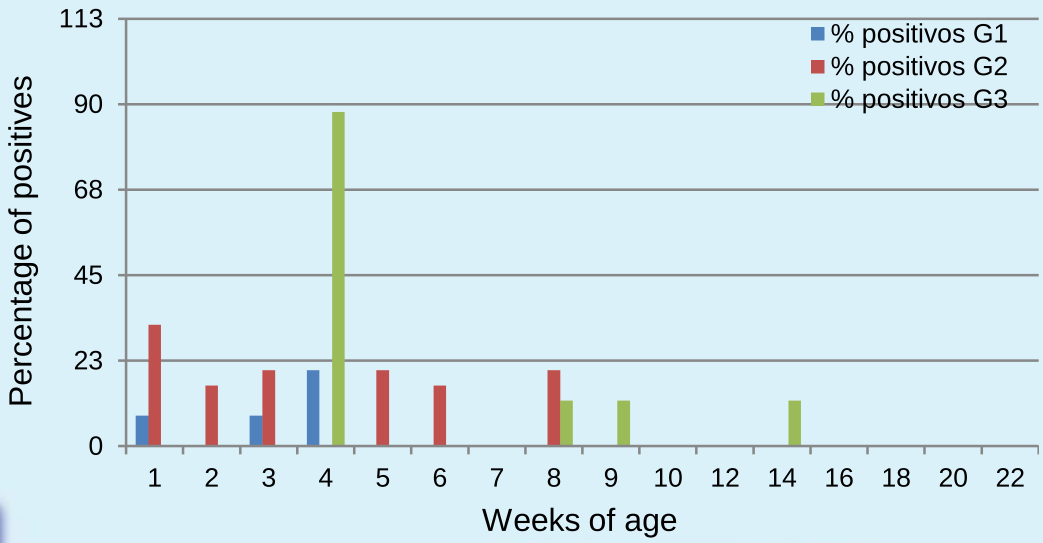
Passive surveillance

2015: 869 samples – 91 RRT-PCR positives — 11 isolates

2016: 110 samples – 35 RRT-PCR positives — ¿? isolates

Active surveillance – 3 longitudinal studies

400 samples/farm (total 1200) – 284 RRT-PCR positives — ¿? isolates



(50)

NGS
UGA/CEIRS

Ag Cartography
USDA - UC

Conclusions

- SIV´s are endemic with multiple strains co-circulating in Central and South America
- Pandemic viruses seems to be predominant in the region
- There are some examples of reassortment in the region
- In some cases there is a potential evidence of antigenic drift
- Additional phylogenetic analyses are ongoing to further characterize these isolates, study the reassortment events and, in some cases, select which of them could be further characterized by antigenic cartography

Acknowledgements

Guatemala

Universidad del Valle de Guatemala

- **Lucía Ortiz**
- **David Moran**
- **Celia Cordón Rosales**

Colombia

Universidad Nacional

- **Jairo Jaime Correa**
- **Victor Vera Alfonso,**
- **Juan Miguel Florez Ramos**
- **Gloria Ramirez Nieto**

Chile

Universidad Católica

- **Marco Saavedra**
- **Karla Tapia**
- **Tamara Garcia**
- **Raveen Rathnasinghe**
- **Rafael Medina Silva**

Univ. de Chile

- **Victor Neira**
- **Bárbara Brito**
- **Garcia**

USA

University of Georgia (UGA)

- **Daniel R. Pérez**
- **Lucas Ferreri**

Icahn School of Medicine at Mount Sinai

- **Adolfo García Sastre**

University of Minnesota

- **Montserrat Torremorell**

Argentina

INTA

- **Marina Dibárbora**
- **Valeria Olivera**
- **Javier Cappuccio**
- **Ariel Pereda**