OFFLU Swine Influenza Virus Tech Meeting
OIE HQs
Paris, France
27th – 28th February 2019

Ariel Pereda
Animal Health Program, INTA

Argentina/Guatemala/Colombia/Chile

South and Central America SIV Surveillance

Animal Influenza in Argentina

Wild Birds:

Instituto Virología, CICYyA, INTA

Dra. Agustina Rimondi / Valeria Olivera

Equine:

Instituto Virología, CICYyA, INTA

Dra. Maria Barrandeguy (OFFLU Equine Group)

Swine:

Grupo Sanidad Animal, EEA Marcos Juárez

Dra. Marina Dibarbora / Dr. Javier Cappuccio

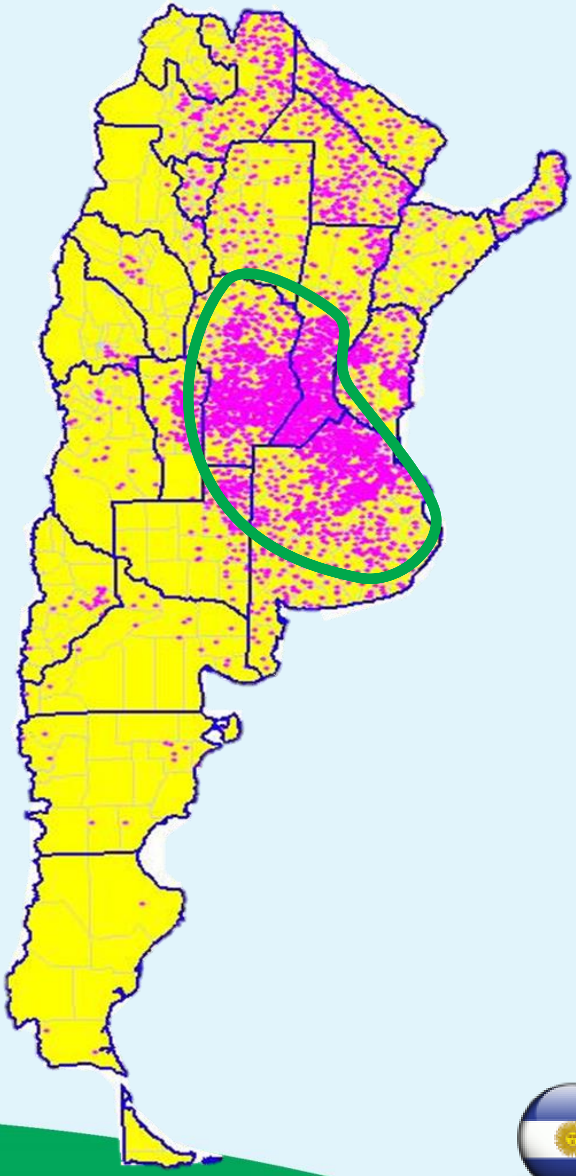
IAV in Swine Surveillance in Argentina

Nº sows: 962.881

24,7% Buenos Aires
22% Córdoba
15,1% Santa Fe
} 61,8%

Stratification

Nº sows	farm	Stock	Slaughter
< 250	59%	21%	3,5%
251-2000	30%	25%	17%
>2000	11%	54%	79,5%
Total	**100%**	**100%**	**100%**



Results

- Passive Surveillance

Period	Possitive Nasal Swabs /total (%)	Possitive Lungs /total (%)	Possitive Farms /total (%)
2015-2016	80/485 (16)	8/31 (26)	9/15 (60)
2016-2017	9/22 (41)	26/71 (36)	13/30 (43)
2017-2018	22/107 (20)	28/177 (16)	19/35 (54)
2018	21/167 (12)	18/133 (13)	12/37 (32)
Total	**132/781 (17)**	**80/412 (19)**	

Results

- Passive Surveillance

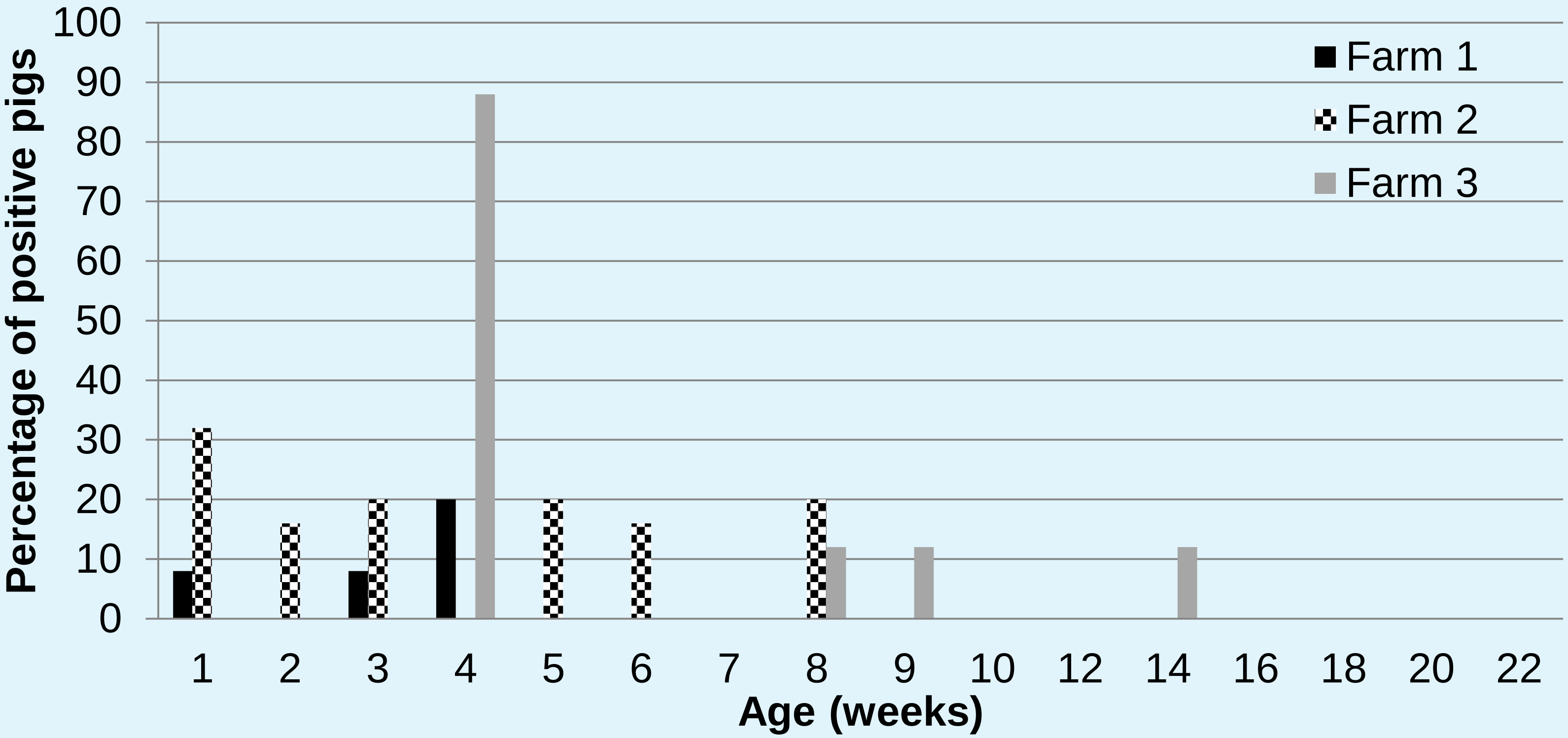
Subtype	Isolated (%)
1A.3.3.2 HA swine lineage (H1N1pdm09)	39 (66)
1B.2.1 HA swine lineage (H1N2 human-like)	12 (20)
H3N2 (human-like)	5 (8)
1B.2.1 HA swine lineage (H1N1 human-like pdm09)	2 (3)
1B.2.2 HA swine lineage (H1N2 human-like)	1 (1,7)
Total	**59**

Phylogenetic analysis of IAV isolates showed that Introductions of human viruses are not related to Brazilians or Chileans ones.

Argentina only imported breeding stock from Brazil (1,500 pig/year).

Results

- Longitudinal studies



Results

Longitudinal studies

Farm	Pig#	age (weeks) qRT-PCR positive	maximum difference (in days) between detection
#2	45	2-6	28
	59	1-5	28
	60	1-2-5	21
	61	1-2-5	21
	63	1-5	28
#3	12	4-9	35
	17	4-9	35
	28	4-8	38
	31	4-8	28
	35	4-8	28
	39	4-14	70
	34	4-14	70

NGS
UGA

Results

- Backyard pigs (n=228)

All negative (RRT-PCR/M)

HI

Region	Category	H1pdm09	H3
North	< 50 sows	4/10	1/10
	> 50 sows	0/0	0/0
Center	< 50 sows	9/10	4/10
	> 50 sows	18/19	1/19
South	< 50 sows	9/12	0/12
	> 50 sows	4/4	0/4
Total		44/55	6/55

IAV in Swine Surveillance in Guatemala

Celia Cordon-Rosales
Center for Health Studies
Universidad del Valle de Guatemala

- Guatemala is the largest swine producer in Central America (1.5 millions annually)
- 66% of production in commercial farms
- 34% backyard production
- 1.7% GDP – 15.8% agricultural gross domestic product

offlu
OIE FAO
network of expertise on animal influenza

UVG
UNIVERSIDAD
DEL VALLE

CENTRO DE
ESTUDIOS EN SALUD
INSTITUTO DE INVESTIGACIONES

Isolation and genetic characterization in Guatemala

- 2010-2011: Three pandemic H1N1 and one seasonal human-like H3N2 virus were isolated and sequenced.
    - All gene segment of the H1N1 viruses shared >98% sequence identity with the pandemic lineage.
    - The H3N2 was closely related to human viruses that circulated in Central America in 2010 (distinct to human seasonal vaccine lineage).

- 2016-2018: full genome amplification was performed directly from swabs in 140 RRT-PCR IAV-positive swabs and sequenced by NGS.
    - Only pandemic H1N1 subtype was identify. Data analysis is ongoing.
    - Other additional 141 RRT-PCR IAV-positive swabs samples are being amplified in order to submit them for NGS sequencing.

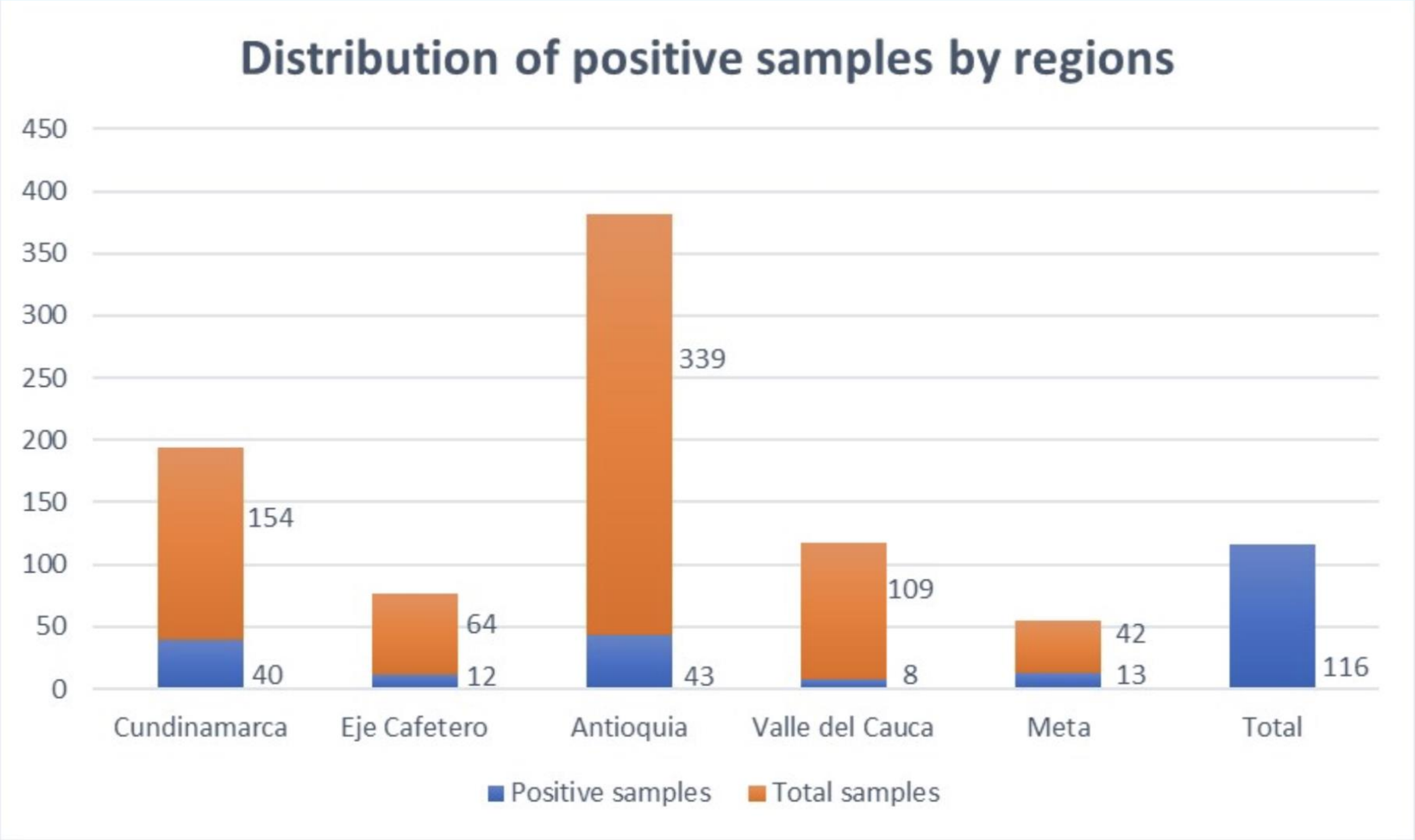
Main results and future projects

- Suveillance since 2010 in swine populations
  - Virological detection of IAV
    - 15.7% (2010), 11.7% (2011), 12% (2014) and 13.4% (2016-2018) of sampled pigs
    - Evidence of circulation of IAV of human origin in pigs
    - Phylogenetic analysis of sequences is pending
  - Serological detection of IAV
    - 10.6% (2010), 1.4% (2011) and 1% (2014)
    - Antibodies against viruses from different genetic cluster were detected

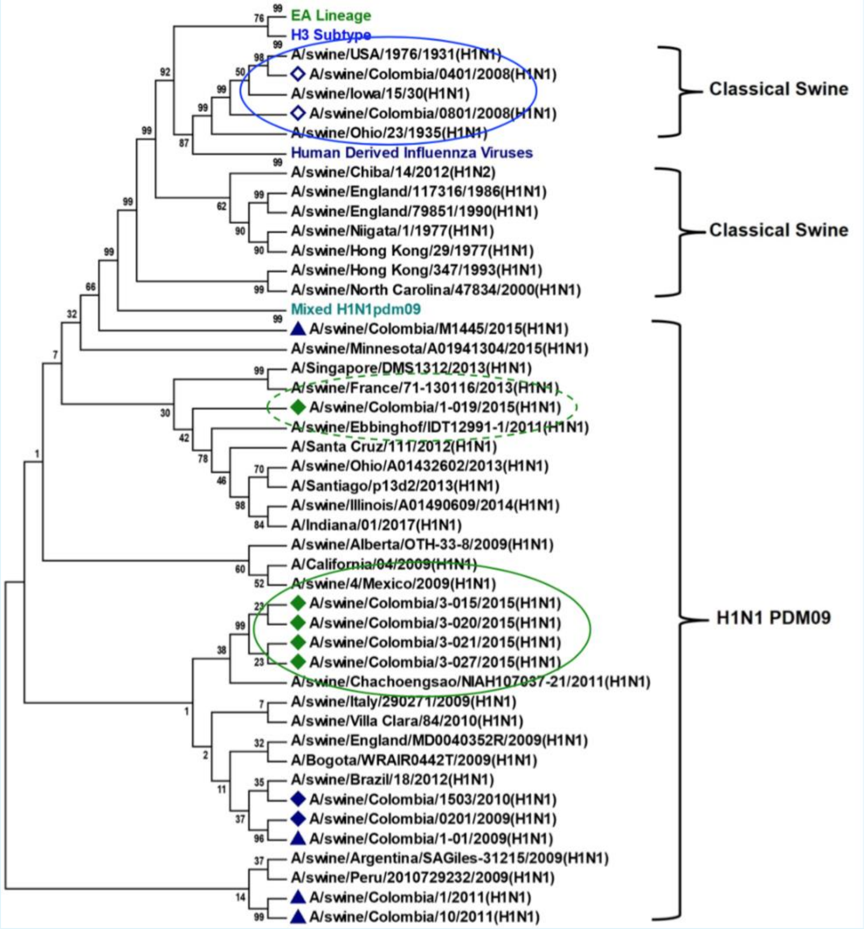
- Future projects include
  - 3rd nation-wide cross-sectional survey at commercial farms level to update information of circulating subtypes
  - Increase number of isolates for better understanding of the evolution and epidemiology of AIV
  - Contribute to establish a network of sentinel surveillance sites and its link with human disease

IAV in Swine Surveillance in Colombia

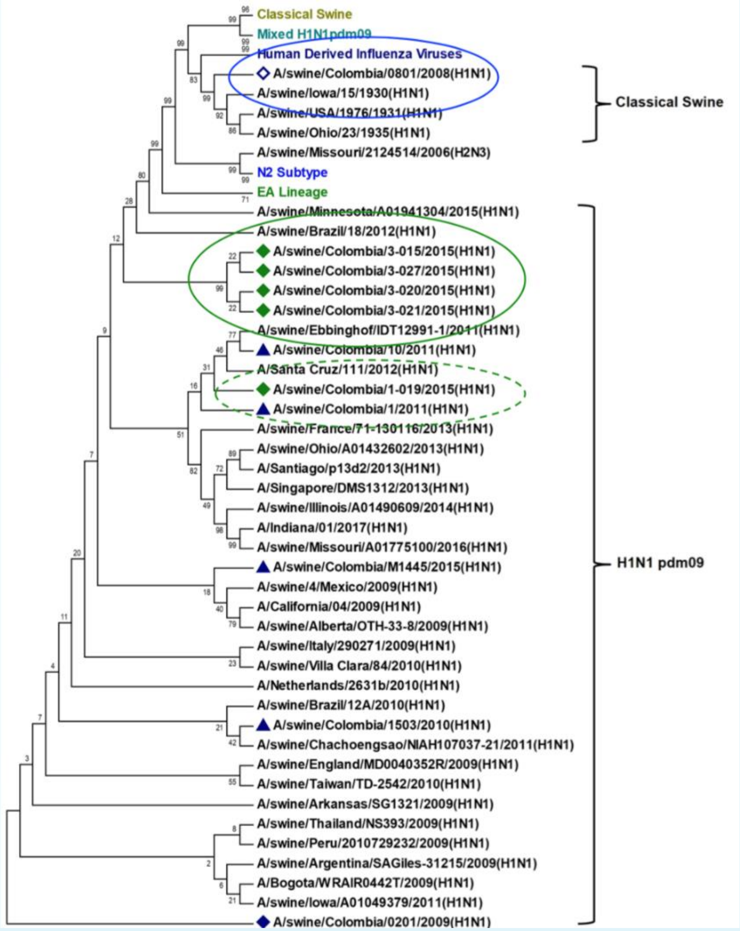
Gloria C. Ramirez-Nieto
Universidad Nacional



HA



NA



All samples isolated are related to H1pdm09
with more relation to pandemic Brazilian isolates

IAV in Swine Surveillance in Colombia

Maria Antonia Rincon Monroy
Instituto Colombiano Agropecuario ICA

Agreement

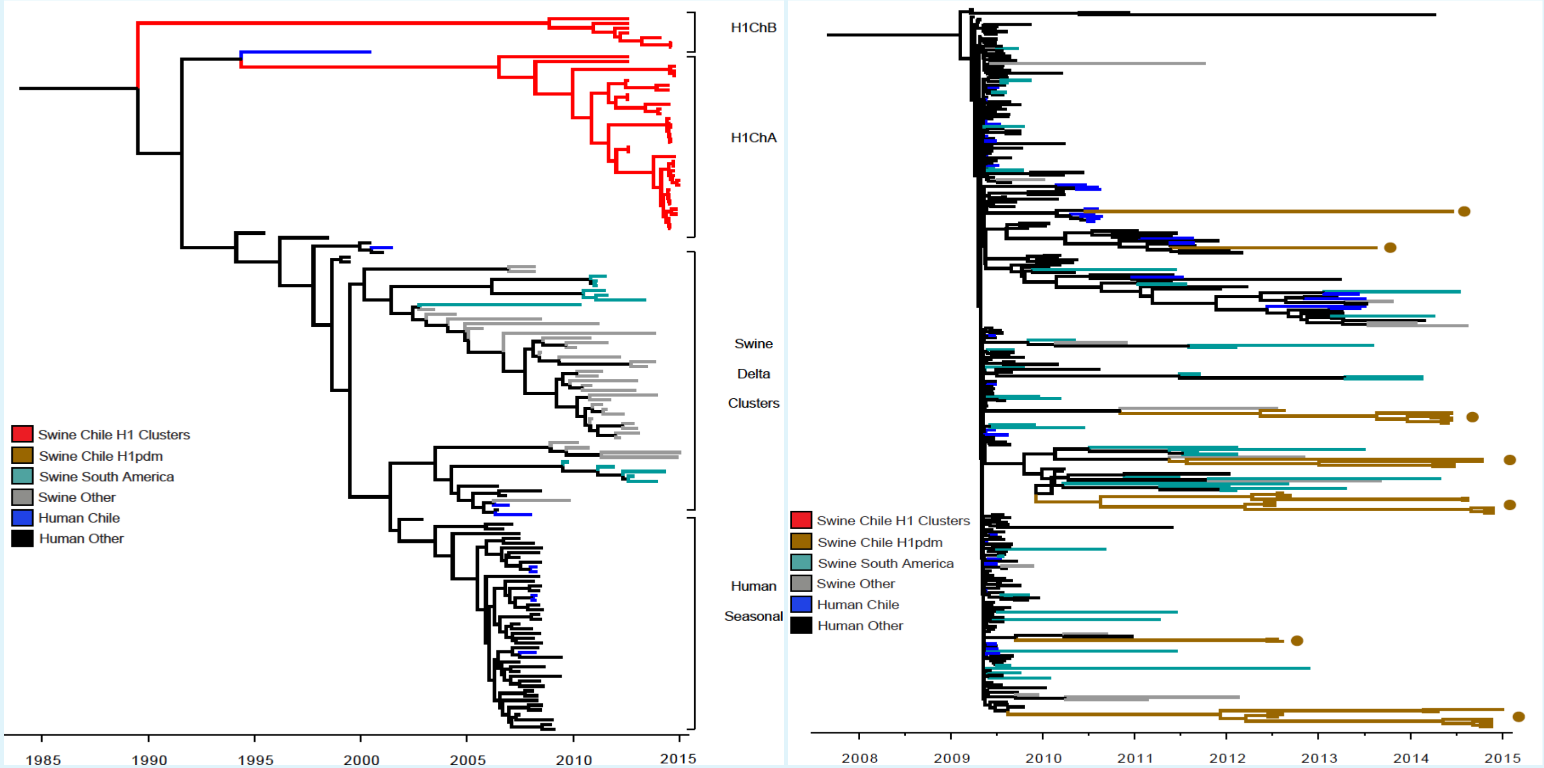
- PorkColombia
- Universidad de Wisconsin Madison
- CEIRS - Hospital St Jude

186 Farms (>100 sows) → Post weaned piglets (3-12 weeks) → Swabs & Oral Fluids (5/Farm)

RT-PCR M → 30,6% Positive → Positive samples to St. Jude for isolation and Characterization

IAV in Swine Surveillance in Chile

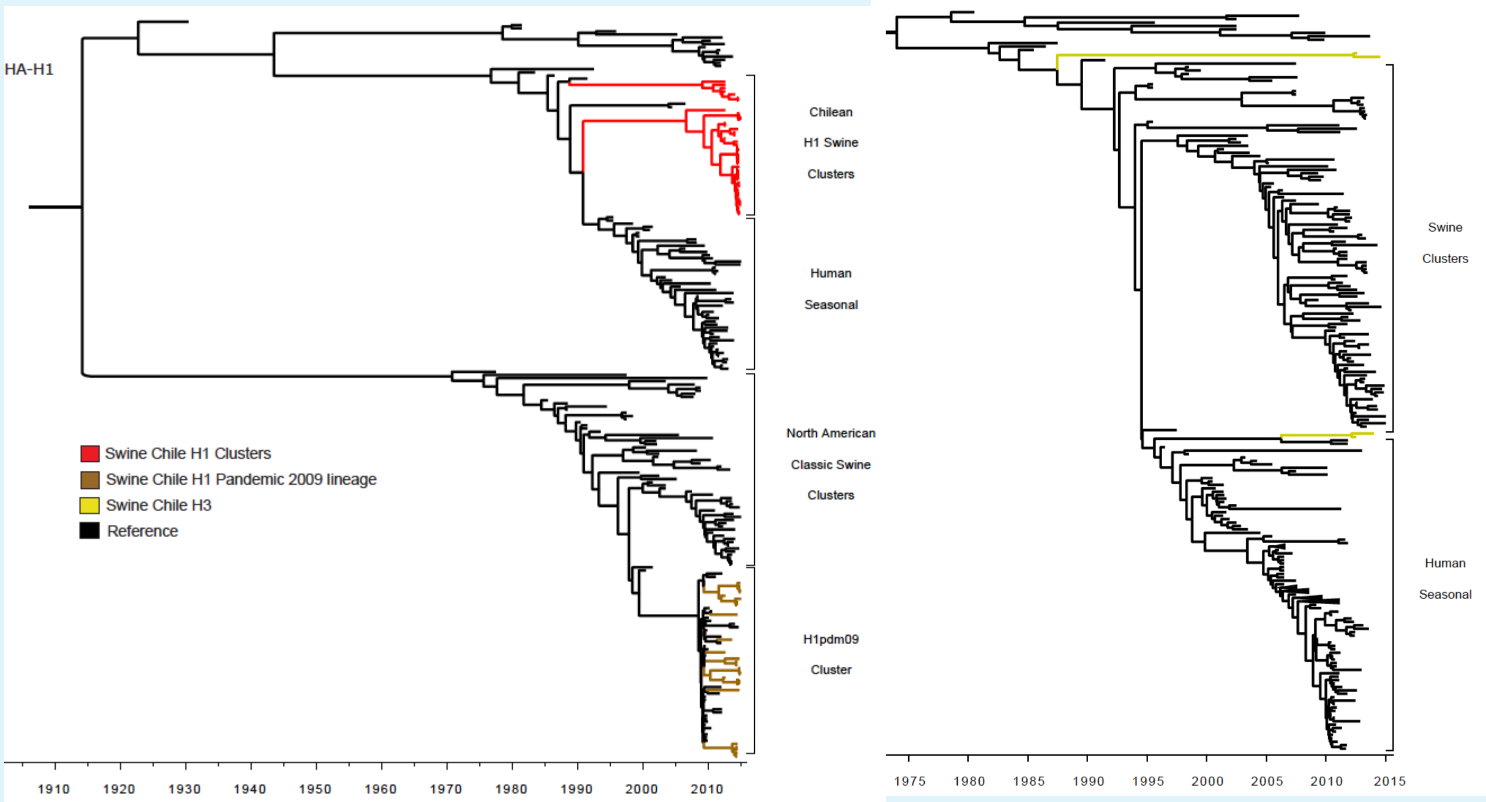
IDENTIFICATION OF HIGH DIVERSITY HUMAN DERIVED SWINE INFLUENZA VIRUSES



- **09H1pdm-like IAVs have been introduced at least 7 different introductions from human to swine**

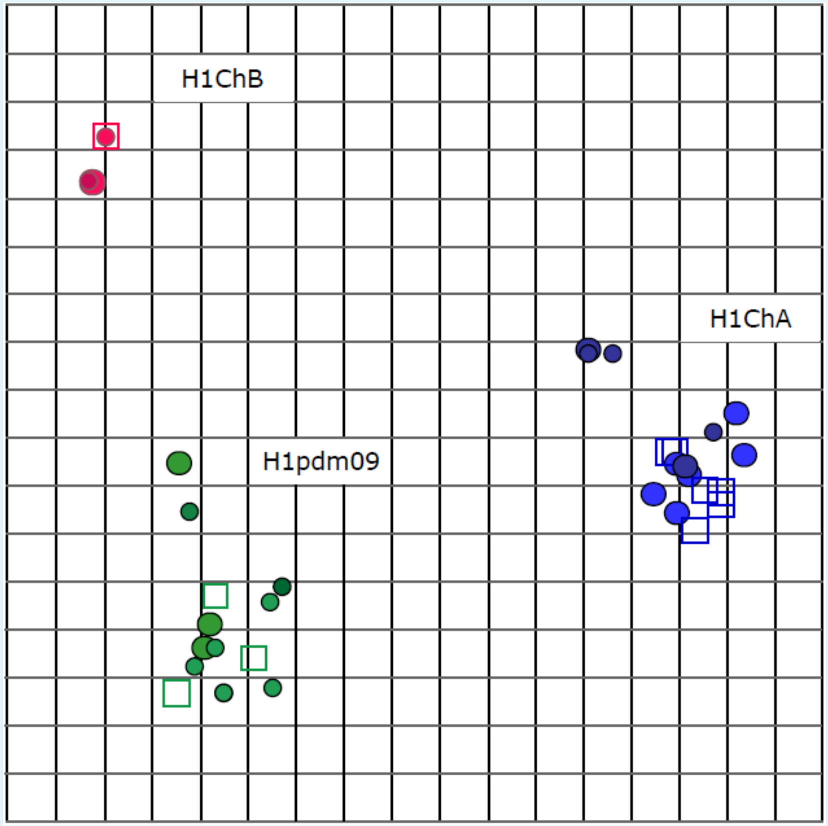
Multiple introductions of human seasonal IAVs results in high diversity and reassortment of swIAVs

Multiple introductions of human seasonal IAVs results in high diversity and reassortment of swIAVs



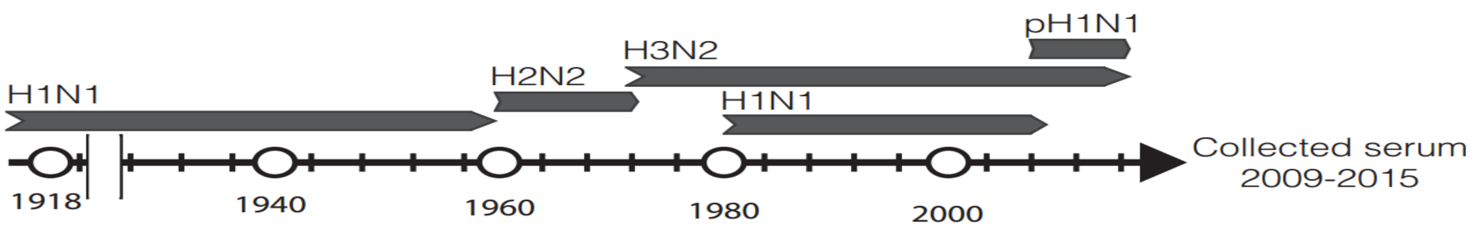
- **Maximum clade credibility tree reconstructed using 70 HA gene segment of influenza viruses collected from human and swine.**
- **TMRCA of cluster A estimated to be 1994 and of cluster B was estimated to as early as 1986.**
- **Molecular clock analyses for the H3 singletons was 1987 and 2006**

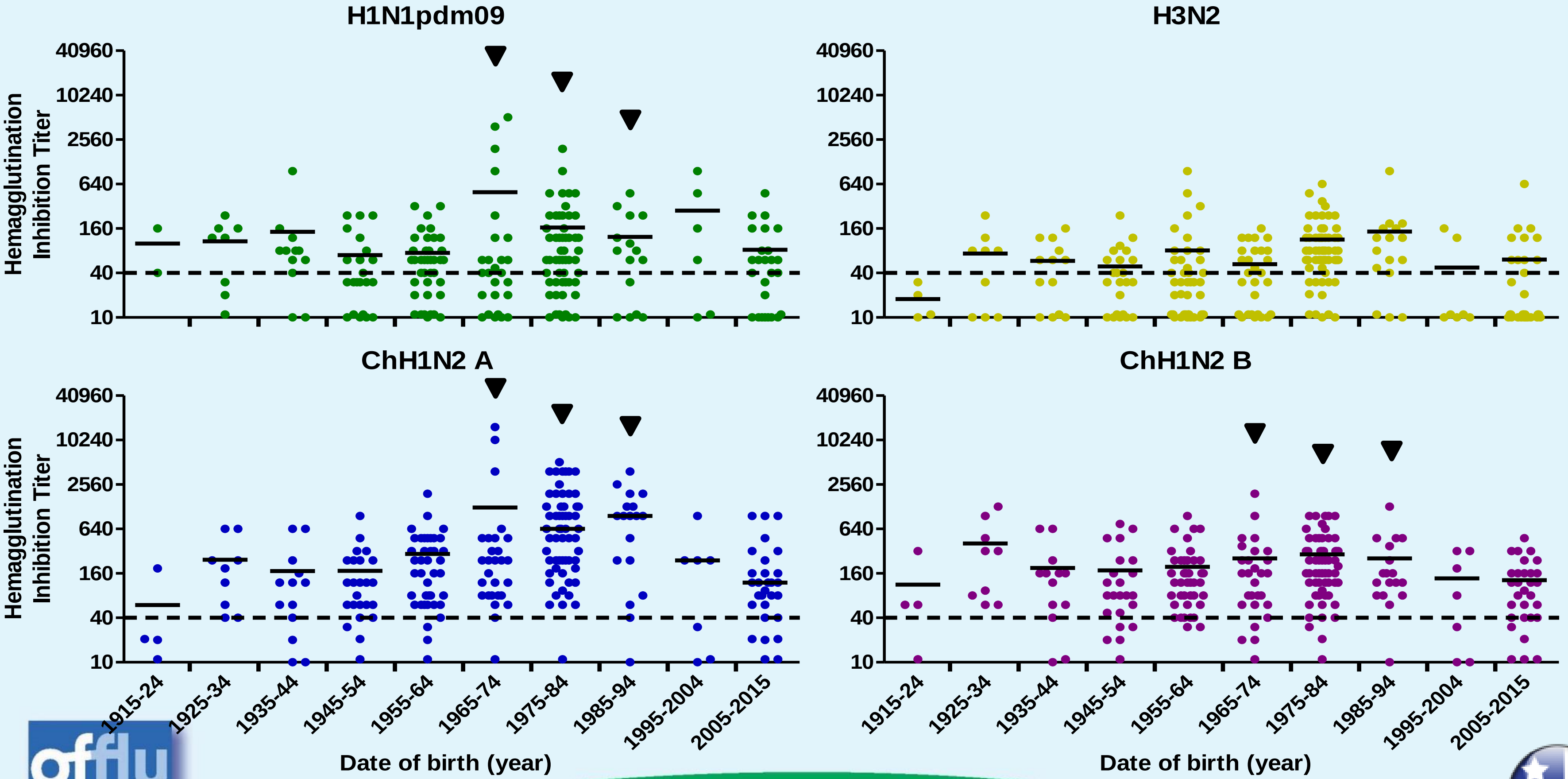
The novel swine H1ChA, H1ChB and A(H1N1)pdm09-like genetic clusters are antigenically distinct.



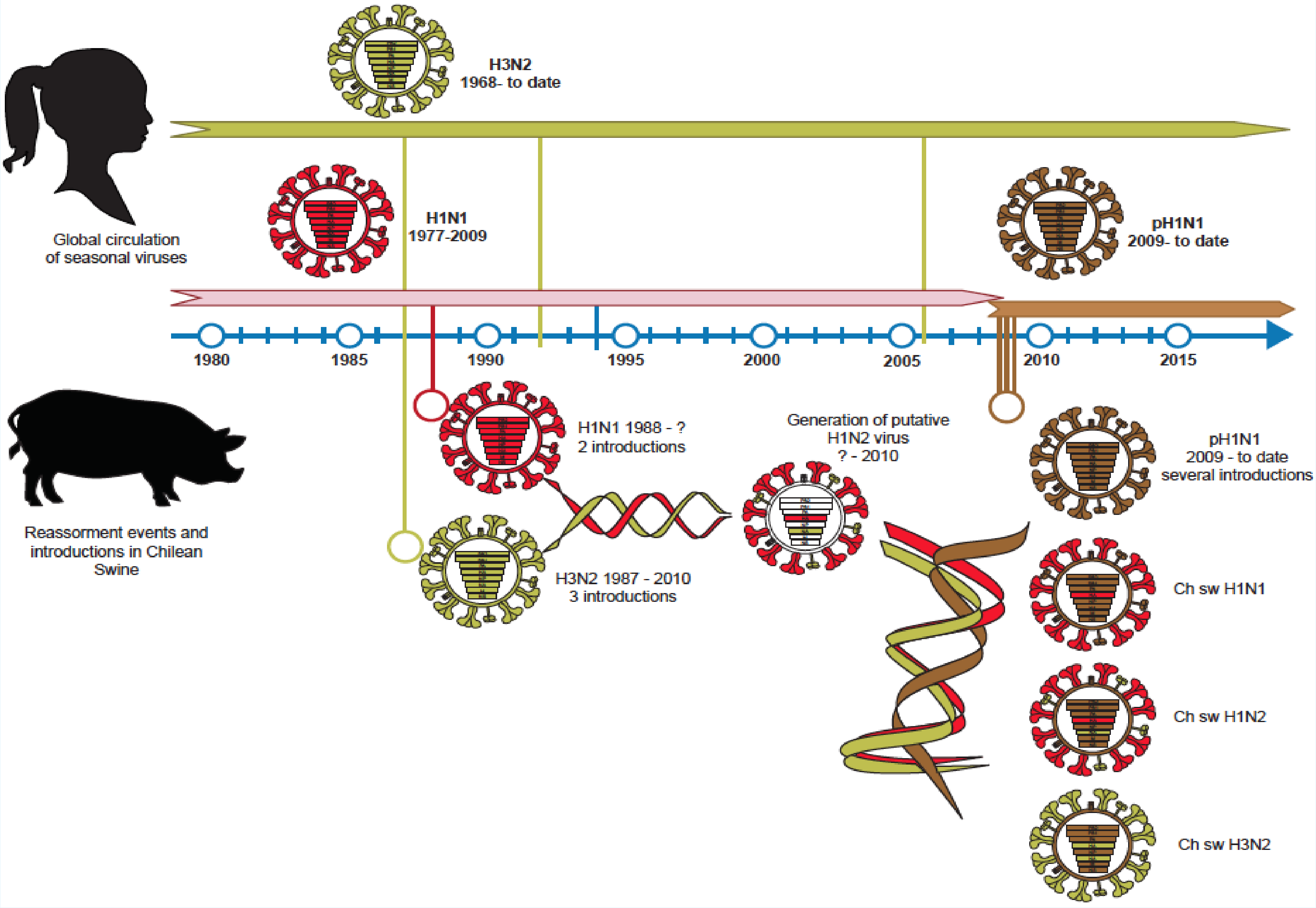
- Antigenic map constructed with Hemagglutination Inhibition (HI) titers from H1ChA, H1ChB and H1pdm09 clusters.
- Circles corresponding to antigens and squares corresponding to guinea pig antisera.

The general population has limited cross-protective antibodies against the H1ChA, H1ChB and swH3N2 viruses.





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



Global circulation
of seasonal viruses

H3N2
1968- to date

H1N1
1977-2009

pH1N1
2009- to date

Reassorment events and
introductions in Chilean
Swine

H1N1 1988 - ?
2 introductions

H3N2 1987 - 2010
3 introductions

Generation of putative
H1N2 virus
? - 2010

pH1N1
2009 - to date
several introductions

Ch sw H1N1

Ch sw H1N2

Ch sw H3N2

offlu
OIE FAO
network of expertise on animal influenza

Acknowledgements

Guatemala

Universidad del Valle de Guatemala

- Lucía Ortiz
- David Moran
- Celia Cordón Rosales

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

St. Jude Children´s Research Hospital

Colombia

Universidad Nacional

- Gloria Ramirez Nieto

ICA

- Maria Rincon Monroy

Chile

Universidad Católica

- Rafael Medina Silva

Univ. de Chile

- Victor Neira

Argentina

INTA

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