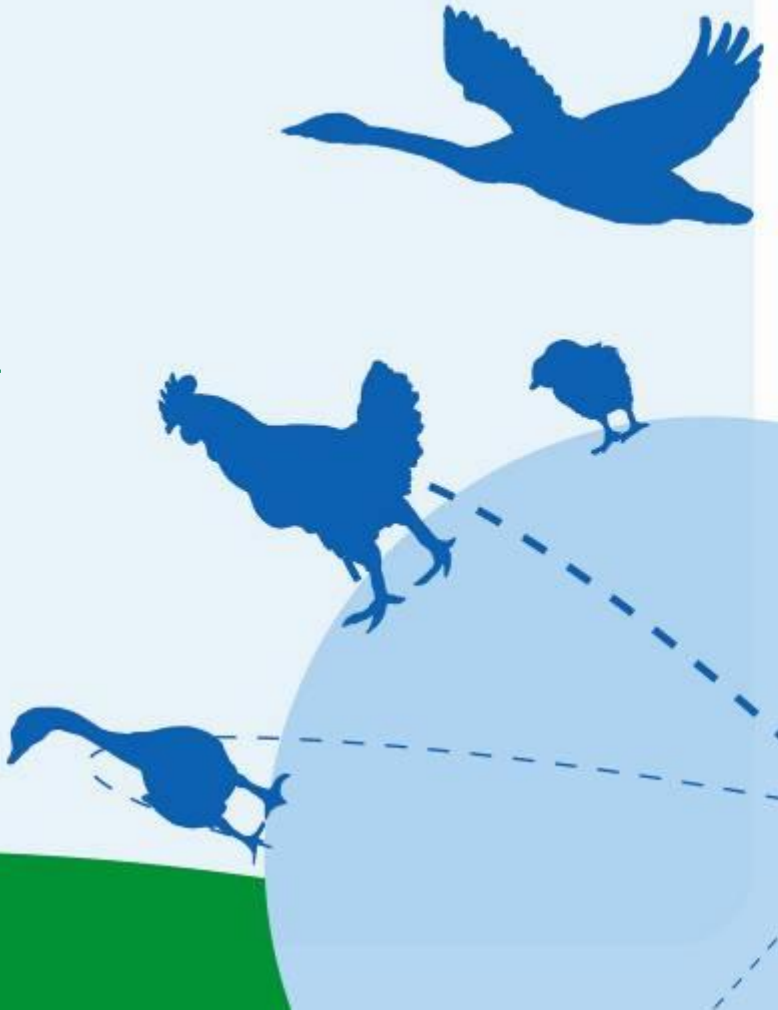
OFFLU virtual SIV group meeting
9 December 2020

Ariel Pereda

INTA - Argentina

SIV surveillance in Latin America



Groups contacted w/ SIV surveillance records in the regions

- Mexico
  - Centro de Investigación en Alimentación y Desarrollo
- Chile
  - Universdad de Concepción
  - Universidad Católica de Chile
  - Universidad de Chile
- Colombia
  - Universidad Nacional de Colombia
- Guatemala
  - Universidad del Valle de Guatemala
- Argentina
  - National Institute of Agriculture Technology

Guatemala

Influenza A Virus surveillance in swine in Guatemala, 2016-2020

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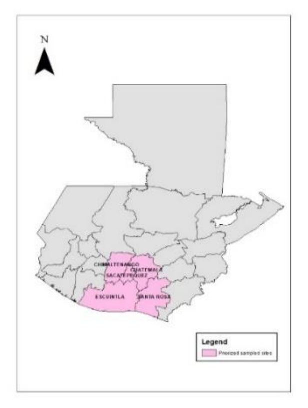
CENTRO DE ESTUDIOS EN SALUD · CES ·
INSTITUTO DE INVESTIGACIONES

The University of Georgia

CRIP IAV in swine populations –Guatemala:2018



Samplig site

- Farms in Chimaltenango, Escuintla, Guatemala, Sacatepéquez y Santa Rosa (high prevalence in previous surveys)
- Nasal swabs prioritizing animals with clinical like-flu signs (nasal secretion, ocular secretion, cough and / or sneezing).
- Antibodies tested in samples from Classical Swine Fever survey across the country.

Results:

A) Selected farms on the prioritized departments:

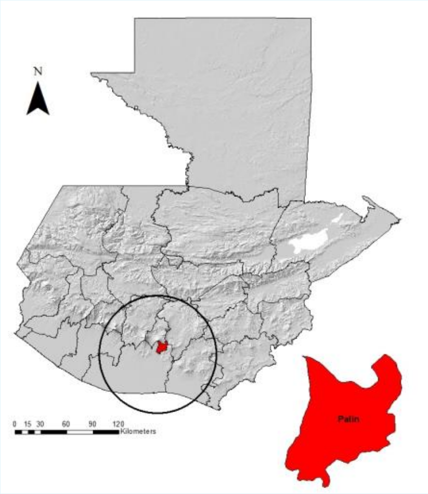
- 6.8% (36/524) swabs tested IAV-positive by RRT-PCR.
- 15.8% (83/523) serums tested Antibodies-positive by ELISA.
- 2.7% (16/523) individual positive for AIV in PCR and ELISA .

B) National surveillance of Classical Swine Fever Serum Survey:

- Total of 1,024 sera receive and 368 processed by pools (2-6 samples/pool) or individually
- 10.0% (37/368) were positive by ELISA

Swine IAV infection rate in Guatemalan swine populations has ranged from 6-12% during the last 10 years. Antibody prevalence seems high in 2018 (16%)

CRIP IAV surveillance in swine – Guatemala: 2016-2018



Samplig site

- Active surveillance in Escuintla, Southern region of Guatemala
- Nasal swabs collected weekly from sick animals (rectal temperature, sex, respiratory signs)
- Age of sampled pigs ranged from 6 to ≥24 weeks (and sows when possible)
- Pigs were tattooed to avoid re-sampling

Results:

- 12% (251/2094) swabs tested IAV-positive by RRT-PCR
  - Two high infection periods were detected trough the surveillance period
- All samples were identified as H1N1 by NGS (H1 swine clade 1A.3.3.2)
  - Phylogenetic analysis on HA and NA genes revealed samples are clearly separated from other sequences of human and swine A/H1N1pdm09 viruses circulating in Central America within the same time frame and in the previous 7 years.
- 10 amino acids mutations were present in HA1 relevant sites

Guatemalan viruses represent a unique group of sequences, suggesting independent evolution from other A(H1N1)pdm09 viruses circulating in Central America and whose zoonotic risk remains to be determined.

Argentina

Influenza A Virus surveillance in swine in Argentina

Javier Cappuccio, Marina Dibárbora, Daniel Pérez

Subtypes characterized in Argentina (2008-2015):

- 59 isolates:
  - 39 H1N1pdm09
  - 13 H1N2 human like
    - 12 1B.2.1 HA swine lineage and 1 1B.2.2 HA swine lineage)
  - 5 H3N2 Human like
  - 2 H1N1 human like (1B.2.1 HA swine lineage)

Contract Year	Nasal Swabs +/Total (%)	Lungs +/Total (%)	Farm +/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)
2018-2019	43/258 (17)	19/187 (10)	15/49 (30)
2019-2020	6/26 (23)	21/124 (17)	7/27 (26)
2020-2021 (dec)	6/6 (100)	23/131 (17)	9/30 (30)

Farms Locations

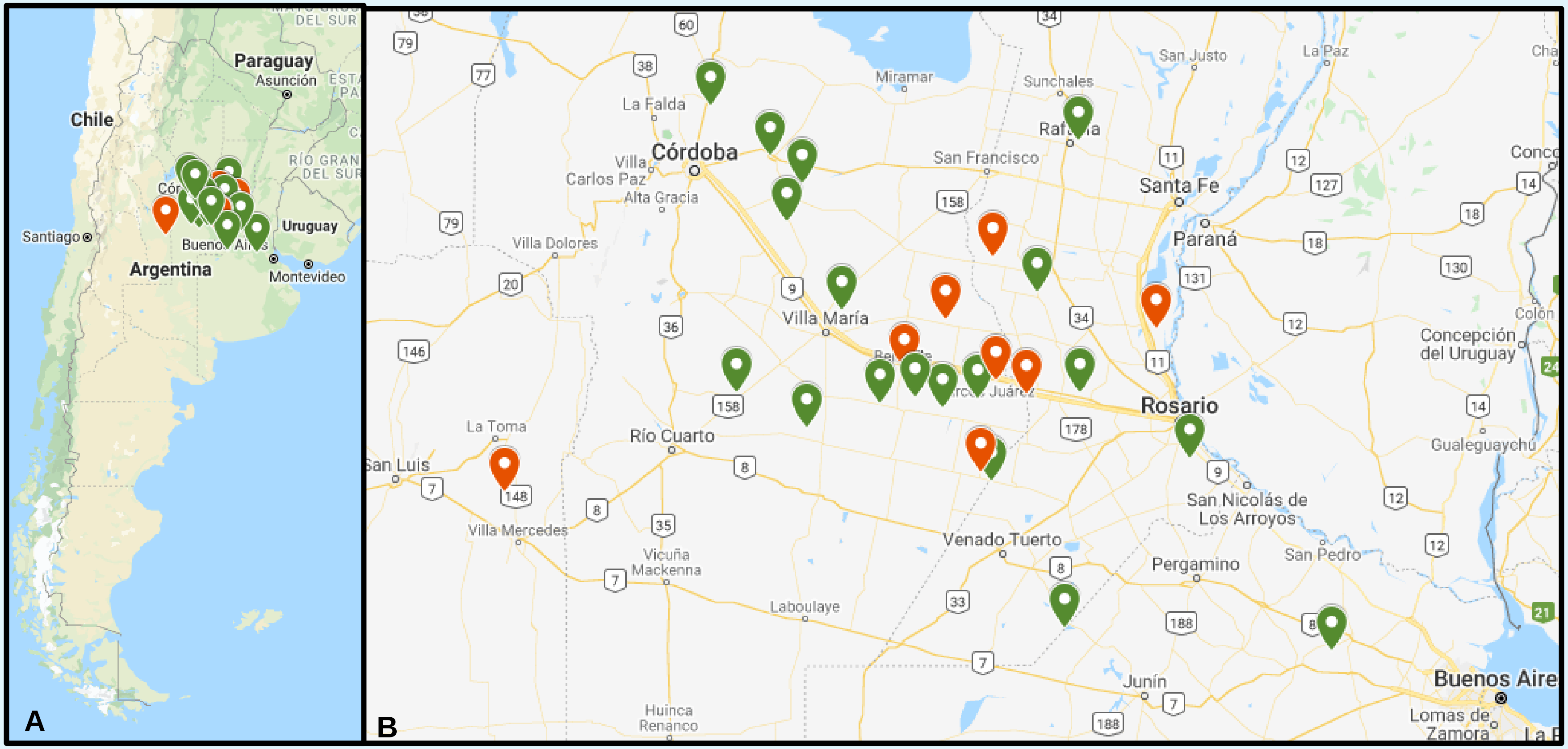


Figure JC01. Location of farms analyzed in this period. **Red dots represent positive influenza A farms by RRT-PCR (n=7). Green dots represent negative influenza A farms by RRT-PCR (n=27).**

Province	Positive	Negative	Total
Cordoba	4	11	15
Buenos Aires	0	1	1
San Luis	1	0	1
Santa Fe	2	6	8
Unknown	0	2	2
Total	7	20	27

Table JC01. Number of positive and negative farms analyzed by province.

Type of sample	Positive	Negative	Total
Nasal swab	6 (4)	20 (13.3)	26 (17.3)
Lung	21 (14)	103 (68.7)	124 (82.7)
Total	27 (18)	123 (82)	150 (100)

***Table JC02. Number of positive and negative samples by type of sample*. Percentage are presented between brackets**

130 RNA´s form these samples were sent to UGA for full length sequencing

Thanks for your kind attention