Swine Influenza in South and Central America

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INTA
Lack of surveillance activity in Latin America

Viral sequences available in public databases:
- 54 HAs from Latin America
- 47 from south America
- Only 10 full genomes (from Argentina, Brazil, Colombia)
- Only partial data from Chile
- Is the 5th largest swine meat exporter in the world (still growing).

- Chile’s geographical barriers and strict livestock control policies have prevented the introduction of foreign pathogens.

- IAV has been detected consistently in Chilean production farms since 2009.
Swine Surveillance Sites

- Site 1
- Site 2
- Site 3
- Site 4
- Site 5

Species: Domestic Swine

Samples: Nasal swabs, oral fluids, sera
Positivity of analyzed swine samples per year.

**Sera 2013**
- Positive: 9%
- Negative: 91%
- n = 278

**Nasal Swabs 2013**
- Positive: 14%
- Negative: 86%
- n = 59

**Oral Fluids 2013**
- Positive: 7%
- Negative: 93%
- n = 129

**Sera 2014**
- Positive: 41%
- Negative: 59%
- n = 440

**Nasal Swabs 2014**
- Positive: 43%
- Negative: 57%
- n = 478

**Oral Fluids 2014**
- Positive: 47%
- Negative: 53%
- n = 120
Longitudinal serological studies from an industrial farm in the Central Region of Chile.

A. Activity against NP (Farm 1)

B. Activity against pH1N1 HA (Farm 1)

C. Activity against Chilean H1N2 HA
Cross-sectional serological studies in 2 industrial farms in different Chilean regions.

- Data indicate at least to swine influenza viruses circulate in most swine farms in Chile.
- The pdmH1N1 2009 predominates, followed by an H1N2 strain, followed by H3N2 which is only sporadically found.
We have only recently generated a total of:
- 67 H1
- 2 H3,
- 24 N1
- 27 N2
Conclusions

• SIV are endemic with multiple strains co-circulating in Chilean swine.

• Current analyses suggests multiple introduction of human IAV into swine populations since the late 80’s – early 90’s and after the 2009 H1N1 pandemic.

• Identified strain's include: SwH3N2, pH1N1-like, SwH1N2, and an H1N2 containing a classical swine Hemagglutinin (cSwH1) and N1 derived from the pH1N1 strain

• Additional phylogenetic analyses are ongoing to further characterize the time of introduction and the reassortment events that gave rise to the Chilean swine IAVs.
Animal influenza surveillance in Guatemala, 2006-2014
CRIP surveillance in pigs – Guatemala (UMD-UVG)

Animal-human interface

- Two nation-wide cross-sectional surveys. Years 2010, 2011
  Evidence of circulation of IAV of human origin in pigs.

Human-animal contact may be important for the epidemiology of swine IAV in Guatemala

- Cross-sectional surveys in pigs from peridomestic smallholdings in proximity to health centers with human ILI surveillance (2 sites, 200 samples/site/yr). Years 2012, 2014
- Influenza A virus monthly prevalence (2012):
  - rRT-PCR: Santa Rosa 19% (95% CI: 14%, 23%), in Quetzaltenango 14% (95% CI: 12%, 16%)
  - ELISA: Santa Rosa 0%, in Quetzaltenango 9% (95% CI: 7%, 11%)
  - Swine farmed with domestic waterfowl may have higher risk of being infected with influenza A: Santa Rosa prevalence risk ratio (PRR): 5, 95% CI: 2.5, 9.7; Quetzaltenango PRR: 1.9, 95% CI: 0.9, 3.8. Müller et al. In prep.
Surveillance in pigs – Guatemala (CDC-UVG-UGA)

Animal-human interface

- Longitudinal study in backyard pigs (years 2013-2014)
- Two rural communities in proximity to wetlands with migrating waterfowl during winter
- Influenza A virus monthly prevalence (April-August 2013):
  - rRT-PCR: 0 - 6% (swine) and 0 - 2% (ducks)
  - ELISA: 1 - 6% (swine) and 0 - 4% (ducks)
- Antigenic response against pandemic H1N1 was detected in one pig suggesting IAV interspecies transmission.
- A cluster of influenza A seropositive households was observed may indicate suggest recent influenza virus transmission in this location.

Müller, Ortiz, Cordon-Rosales et al. In prep.

Influenza A circulates in co-habiting backyard swine and ducks in wetlands in Guatemala
<table>
<thead>
<tr>
<th>CIP</th>
<th>Year</th>
<th>N samples</th>
<th>Lung</th>
<th>Positive</th>
<th>Nasal swabs</th>
<th>Positive</th>
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<tbody>
<tr>
<td>051</td>
<td>2010</td>
<td>27</td>
<td>8</td>
<td>1 (12.5)</td>
<td>19</td>
<td>0 (0)</td>
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<tr>
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<td>2011</td>
<td>499</td>
<td>38</td>
<td>12 (31.6)</td>
<td>461</td>
<td>37 (8)</td>
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<tr>
<td></td>
<td>2012</td>
<td>2313</td>
<td>39</td>
<td>19 (48.7)</td>
<td>2274</td>
<td>58 (2.6)</td>
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<tr>
<td></td>
<td>2013</td>
<td>166</td>
<td>61</td>
<td>28 (45.9)</td>
<td>105</td>
<td>68 (64.8)</td>
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<tr>
<td></td>
<td>2014</td>
<td>55</td>
<td>55</td>
<td>4 (7.3)</td>
<td>0</td>
<td>0 (0)</td>
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<tr>
<td>112</td>
<td>2014</td>
<td>545</td>
<td>110</td>
<td>20 (18.2)</td>
<td>435</td>
<td>32 (7.4)</td>
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<td>2015</td>
<td>869</td>
<td>32</td>
<td>7 (21.9)</td>
<td>837</td>
<td>116 (13.9)</td>
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<td>Total</td>
<td></td>
<td>4474</td>
<td>343</td>
<td>91 (26.6)</td>
<td>4131</td>
<td>311 (7.5)</td>
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Nasal swabs: pooled processed
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<tr>
<th>Granja</th>
<th>Edad de obtención de aislamientos (días)</th>
<th>Nombre del aislamiento</th>
<th>Subtipo</th>
<th>Nº acceso GenBank</th>
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<tr>
<td>1</td>
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<td>A/swine/Argentina/CIP051-A232/2012</td>
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<tr>
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</table>
Sw EA
Hn seasonal
Sw ARG
H1N1pdm09
Sw γ
Sw γ2
Sw β
Sw α
Sw δ
Continuous survey of SIV in pig farms

H3N2 → rH1N1δ → rH3N2 → rH1N2 δ2 → rH1N2 δ2 → H1N1 pdm → H1N1 pdm
SMALL-SCALE / FAMILY OF PIG FARMING

90% pig productive units

57 farms - 622 samples

<table>
<thead>
<tr>
<th>Tipo de establecimiento</th>
<th>% animales (positivos/total)</th>
<th>% establecimientos (positivos/total)</th>
<th>% animales (positivos/total)</th>
<th>% establecimientos (positivos/total)</th>
</tr>
</thead>
<tbody>
<tr>
<td>50 a 100 Madres</td>
<td>39,06 (150/384)</td>
<td>93,1 (27/29)</td>
<td>2,08 (8/384)</td>
<td>17,24 (5/29)</td>
</tr>
<tr>
<td>10 a 50 Madres</td>
<td>32,35 (77/238)</td>
<td>60,71 (17/28)</td>
<td>0,42 (1/238)</td>
<td>3,57 (1/28)</td>
</tr>
</tbody>
</table>
Conclusions 2014 - 2015

- **H1N1 pdm**: Predominant Subtype in Argentina
- **rH1N2 δ2**: Continuous circulation in non related pig farms
- **rH3N2**: Serological evidence of circulation
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