OFFLU Swine Influenza Virus Regional Meeting

20th October 2018

XXIX Brazilian Virology Congress and XIII Mercosul Virology Meeting

Gramado, RS, Brazil

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Guatemala

UVG UNIVERSIDAD DEL VALLE DE GUATEMALA

CENTRO DE ESTUDIOS EN SALUD

INSTITUTO DE INVESTIGACIONES

Introduction

- 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

Swine IAV in Guatemala

Year	Type of study	Results
2010	USAC Vet school • Swine IAV serological survey among commercial and backyard pig populations • Whole country (2155 samples) • HI assay	• H1N1: 20.6% commercial, 41% backyard • H3N2: 6.59% commercial, 17% backyard
2010-2011	CES-UVG • Two nationwide swine IAV surveys • Virological and serological assays	• Swine IAV: 15.7% of sampled pigs (30.6% of herds) in 2010 and 11.7% (24.2% of herds) in 2011 • Seropositivity: 10.6% (16.1% of herds) in 2010 and 1.4% (3.1% of herds) in 2011
2012, 2014	CES-UVG • Cross-sectional surveys in pigs from peridomestic smallholdings in 2 sites • 200 samples/site/year • Virological and serological assays	• Swine IAV: 16.5% (2012) and 12% (2014) of sampled pigs • Seropositivity: 4.5% (2012) and 1% (2014) of sampled pigs
2016-2018	CES-UVG • Two-years active swine IAV surveillance in a commercial farm (southern region of Guatemala) • 2,094 nasal swabs (weekly collection) • Virological assays	• Estimated prevalence among pigs with respiratory signs was 11.1% • Only pandemic H1N1 was identified by RRT-PCR or sequencing

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 for last period
  - Serological detection of IAV
    - 10.6% (2010), 1.4% (2011) and 1% (2014)
    - Antibodies against viruses from different genetic cluster were detected

- Commercial farms, animal health status and age are potential risk factors associated with IAV infection and exposure.

- 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

Contribution of the team to the group

- Consolidate surveillance in pigs in Guatemala and support other countries in the region.
- Share isolates for regional studies.
- Network with animal and human health authorities.
- Provide training to regional stakeholders.

Conclusions

- Need to develop a sustainable model for IAV surveillance in swine populations with the participation of multiple stakeholders.

- Surveillance data needs to inform producers and health authorities for the control of influenza to prevent and mitigate animal and human diseases.

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Department of Population Health, University of Georgia

- Daniel R. Perez
- Lucia Ortiz
- Lab members

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- David Orellana
- Pablo Ola
- Veterinary epidemiologists
- Field technicians

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- Adolfo Garcia-Sastre
- Ana Silvia Gonzalez-Reiche

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USA

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Who are we?

- Rajao/Perez lab at UGA
  - Daniel R. Perez, Professor
  - Daniela Rajao, Assistant Professor
  - 3 undergraduate students, 4 graduate students, 4 post-docs, 1 lab manager/NGS coordinator
  - Lab is member of the Center for Research on Influenza Pathogenesis (CEIRS-NIAID-NIH)

Center for Research on Influenza Pathogenesis

- **Adolfo Garcia-Sastre**, *PI*, ISMMS NY, P. Palese, N. Bouvier, F. Krammer, R. Albrecht, A Fernandez-Sesma, M. Shaw, H. van Bakel
- *D. Perez, U. Georgia*
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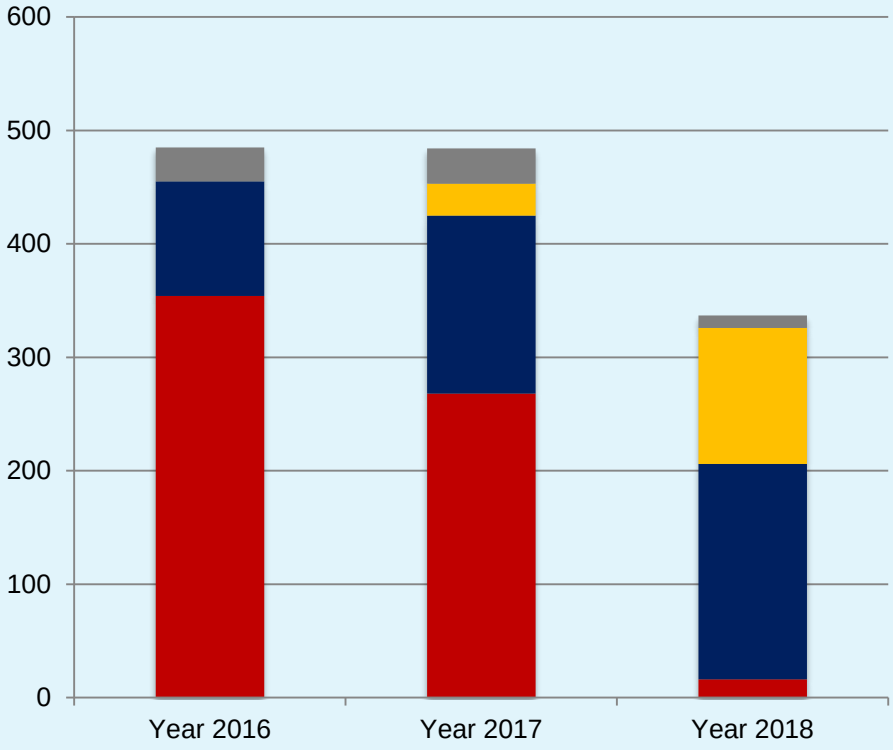
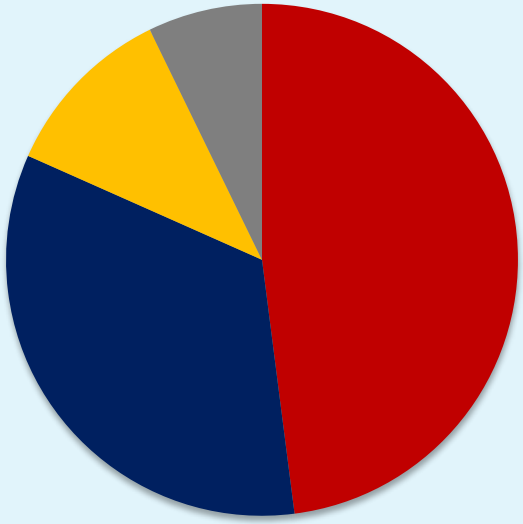
What do we do?

- Support surveillance activities in Argentina and Guatemala through FFS agreements
- Surveillance activities support avian and swine influenza surveillance
- Provide virus characterization support and NGS sequencing capacity to collaborators in Argentina and Guatemala (but not limited to only these two countries)
- Antigenic characterization and Vaccine development (emphasis on swine and avian influenza)

DIGS – NGS sequencing capacity

A summary of all NGS activity in the Rajao/Perez lab sequencing core since its initiation reflects the an annual sequencing capacity of almost 500 samples.





Validation Other Lab Genomes Surveillance Genomes

DIGS: Distributed Influenza Genome Sequencing

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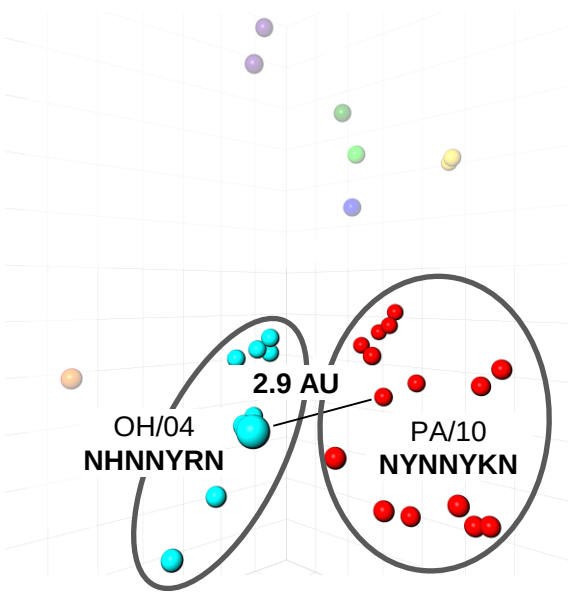
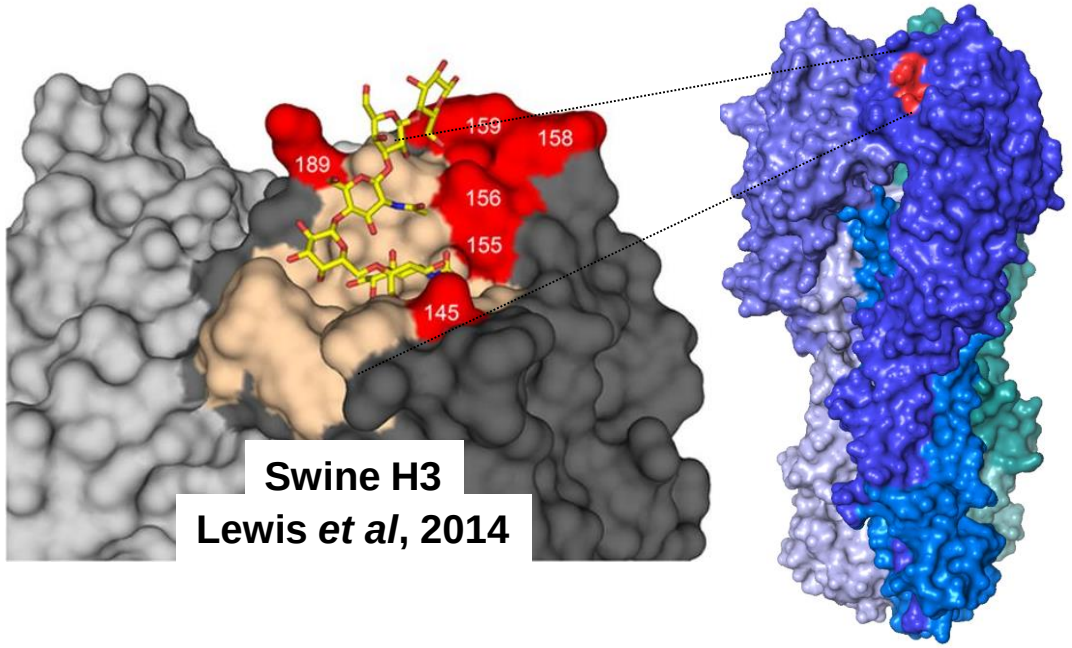
Substitutions in key positions on the HA recapitulate antigenic properties (HI profile) of swine H3 influenza viruses

Collaboration with Amy Vincent and Nicola Lewis



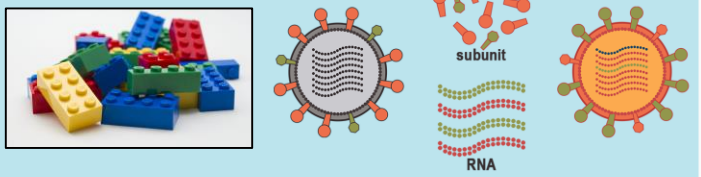
Abente, Santos et al, 2016

A/turkey/Ohio/303153/2004 (H3N2)
OH/04 – swine-origin TRIG virus



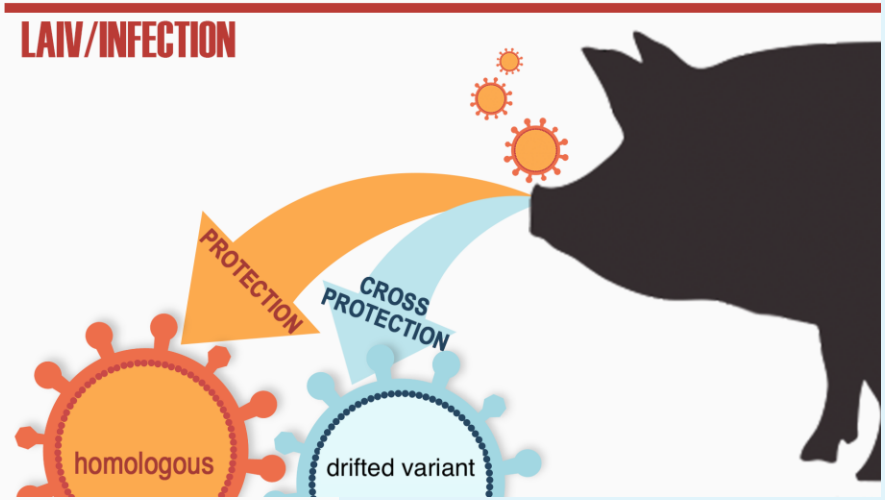
Swine H3
Lewis *et al*, 2014

VACCINE PLATFORMS FOR INFLUENZA IN SWINE



	WIV	VECTORED	LAIV
Delivery route	IM	IM/IN	IN
HI response	+++	++	+
Antibody secreting cells	++	+	+
Memory B cells	+	+	+
Nasal IgA	-/+	-/+	+++
NA antibody	+++	-/+	++
CD4 T cells	++	++	+++
CD8 T cells	-	+	+
Cross protective immunity	-/+	+	++
VAERD	yes	-/+	no

LAIVs have the potential to provide a multidimensional response (humoral – IgA and IgG - and cellular) unparalleled by any other vaccine approach.



From Vincent, Perez, et al 2017, Vet. Micro.

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LAIV vs Adjuvanted-WIV vaccine against challenge with contemporary, antigenically drifted H3N2 IAV-S – Study design

Collaboration with Eugenio Abente and Amy Vincent at NADC, USDA-ARS and Daniela Rajao at UGA

	Groups	Vaccine WIV/LAIV (antigenic cluster)	Challenge virus (antigenic cluster)	Number of pigs per group
STUDY 1	**NV-NC**	No vaccine	No challenge	8
	NV-IN/13	No vaccine	IN/13 (red)	8
	OH/04WIV-IN/13	OH/04WIV (cyan)	IN/13 (red)	8
	OH/04LAIV-IN/13	OH/04LAIV (cyan)	IN/13 (red)	8
STUDY 2	**NV-NC**	No vaccine	No challenge	5
	NV-IA/14	No vaccine	IA/14 (green)	10
	IA/14WIV-IA/14	IA/14WIV (green)	IA/14 (green)	10
	IA/14LAIV-IA/14	IA/14LAIV (green)	IA/14 (green)	10
	NV-NY/11	No vaccine	NY/11 (red)	9
	IA/14WIV-NY/11	IA/14WIV (green)	NY/11 (red)	10
	IA/14LAIV-NY/11	IA/14LAIV (green)	NY/11 (red)	10

NV, non-vaccinated. NC, non-challenged.

If you like to know the outcome of these studies, please check the paper by Abente, Rajao *et al*, 2018, JVI

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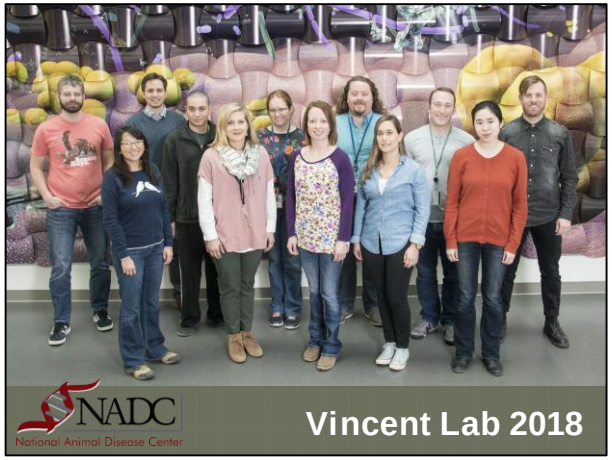
Contribution to the group

- Biological and antigenic characterization of viruses
  - Currently producing recombinant viruses for N2 antigenic characterization
- NGS sequencing capacity open to anyone
  - Moving on to nanopore technology and protocols to perform sequencing on site and produce results in real time
- Reverse genetics support
  - Virus is not needed, only sequence

Acknowledgements



NIH National Institute of Allergy and Infectious Diseases

CRIP

CEIRS
NIAID Centers of Excellence for Influenza Research and Surveillance

GEORGIA POULTRY FEDERATION

Crystal Loving

USDA ARS

Present (and *past*) members of the Rajao/Perez Lab:

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