OFFLU Swine Influenza Virus Regional Meeting

20th October 2018
XXIX Brazilian Virology Congress and XIII Mercosul Virology Meeting
Gramado, RS, Brazil

Rejane Schaefer

Embrapa Suínos e Aves
Concórdia, Santa Catarina

Brazil

Created in June 13th, 1975

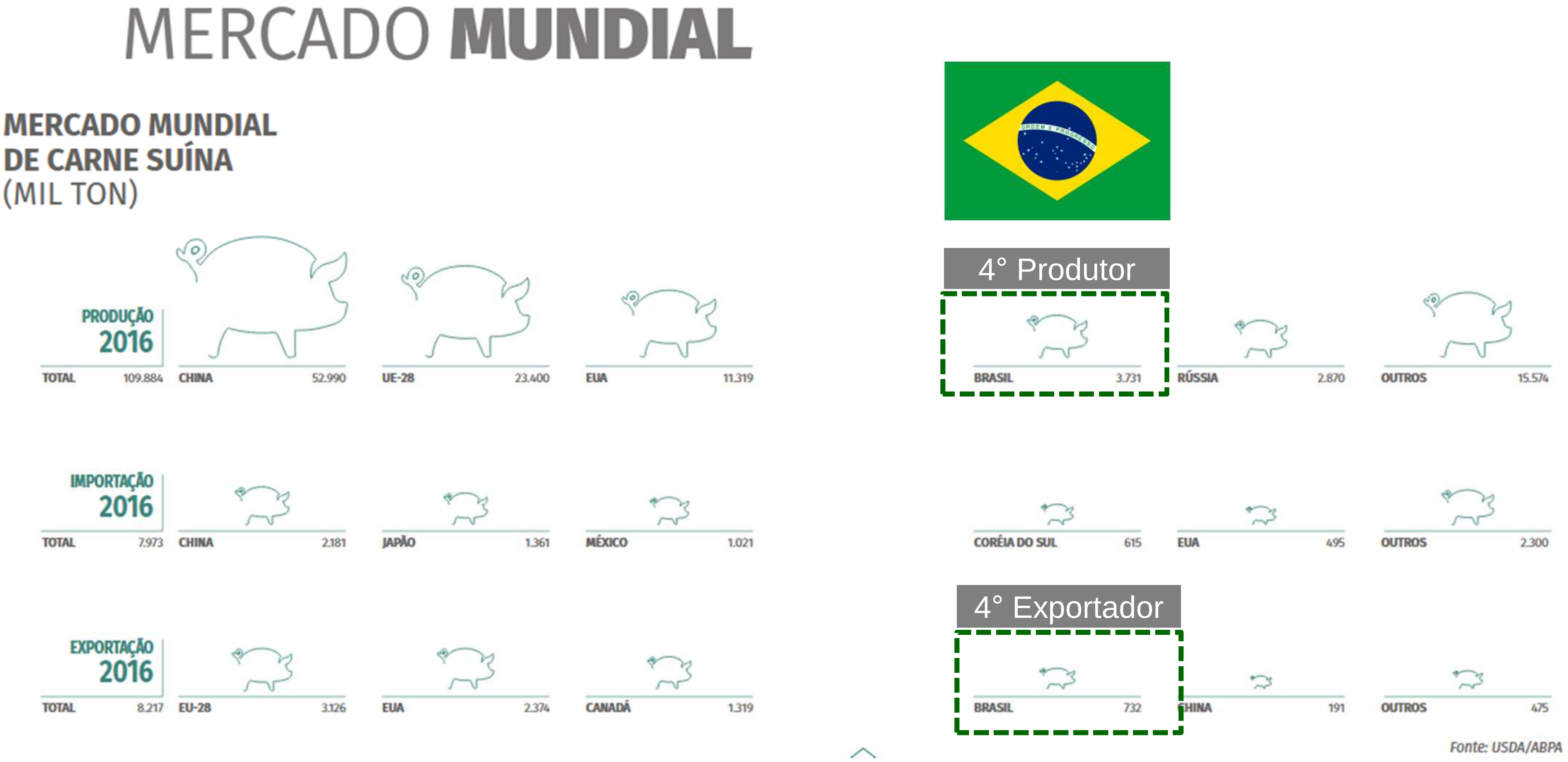
- Land area: 520 acres
- 205 employees / 48 researchers
- 5 thematic areas (swine production, poultry production, swine health, poultry health and environment)

Introduction

Swine Health Research Group:

- 5 veterinarians: virologists (3), pathologist (1), immunologist (1)
- Bioinformatician (1)
- 2 laboratory technicians
- Influenza Project: Molecular and antigenic characterization of IAV in swine, development of diagnostic tests, vaccine trials, disease prevention and control.

Brazil: 4th largest swine producer and exporter (ABPA, 2017)



MERCADO MUNDIAL

MERCADO MUNDIAL DE CARNE SUÍNA (MIL TON)

4° Produtor

4° Exportador

	TOTAL						
PRODUÇÃO 2016	109.884	CHINA 52.990	UE-28 23.400	EUA 11.319	BRASIL 3.731	RÚSSIA 2.870	OUTROS 15.574
IMPORTAÇÃO 2016	7.973	CHINA 2.181	JAPÃO 1.361	MÉXICO 1.021	CORÉIA DO SUL 615	EUA 495	OUTROS 2.300
EXPORTAÇÃO 2016	8.217	EU-28 3.126	EUA 2.374	CANADÁ 1.319	BRASIL 732	CHINA 191	OUTROS 475

Fonte: USDA/ABPA

Swine influenza in Brazil

Limited data of influenza in pigs before 2009 (studies based in serology analysis with no further genomic characterization)

1974: Virus isolation, 3 month-old pig, Minas Gerais (Cunha et al., 1978)

1996-1999: HI, Southern Brazil, 16.7% H3N2, 8.45% H1N1 and 2.2% human H1N1 *(Brentano et al., 2002)*

2005-2006: RT-PCR/ M gene, Santa Catarina, no virus isolation *(Schaefer et al., 2008)*

2006: HI, São Paulo, 85.29% H1N1 and 91.17% H3N2 *(Mancini et al., 2006)*

2009: HI, Minas Gerais, 44.5% H1N1, 10.1% H3N2 and 38.3% human H1N1 *(Rajão et al., 2012).*

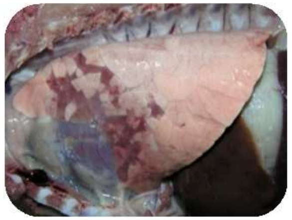
Swine influenza in Brazil

Since 2009:

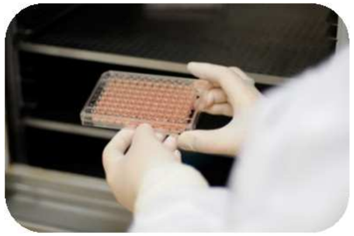
- Frequent outbreaks of acute respiratory disease in pigs caused by H1N1pdm
- Currently, influenza seroprevalence in pig herds is estimated in 78.1%
- H1N1pdm, human seasonal origin H1N2 and H3N2 circulate in swine in several Brazilian states
- All H1N2 and H3N2 viruses sequenced so far have the internal gene segments derived from H1N1pdm.

Data on Isolation and genetic characterization of FLUAVs detected in swine in Brazil

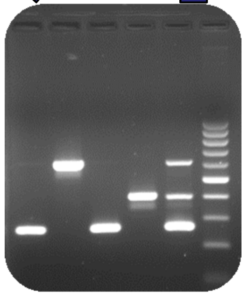
Workflow



RNA sample screened by RT-qPCR



VI on ECE/ or MDCK cells



IAV subtyping by RT-PCR

HI test

Genetic sequencing ABI 3130xl /Ion Torrent

Genotypes of IAV found in pigs in Brazil

Subtype	Year of isolation	PB2	PB1	PA	HA	NP	NA	M	NS	sw clade classif (IRD)	Total
H1N1	2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016	pdm	pdm	pdm	pdm	pdm	pdm	pdm	pdm	1A3.3.2 (npdm)	45
H1N2	2011, 2013, 2014, 2015, 2016	pdm	pdm	pdm	huH1 2002	pdm	huN2 1998	pdm	pdm	1B2.2 (delta like)	18
H1N1	2011, 2014, 2015	pdm	pdm	pdm	huH1 2006	pdm	huN1 2006	pdm	pdm	Other-Human-1B.2 (delta 2)	3
H3N2	2011, 2014, 2015, 2016	pdm	pdm	pdm	huH3 1998	pdm	huN2 1998	pdm	pdm		13

H1pdm (H1N1): Multiple separate human-to-swine transmissions of H1N1pdm have occurred since 2009.

H1s (H1N2): Transmission of human seasonal H1N2 viruses to pigs occurred in the early 2000s (2002-2003).

H1s (H1N1): Transmission of human seasonal H1N1 into swine approx in 2006.

H3 (H3N2): Introduction of human H3N2 virus into swine in Brazil during late 1990s.

N2 (H1N2 and H3N2): Two different introductions of N2 segment from huH3N2 viruses into swine (late 1990s).

*NELSON M.I.; SCHAEFER R. et al. Emerging Infectious Diseases. v.21, n.8, 2015. SCHMIDT C. et al. Genome Announc. 2(6):e01319-14. 2014. RAJÃO D.S. et al. Influenza and Other Respiratory Viruses. v.7, n.5, 2013.

Ongoing and Future projects

- Continue to monitor influenza in pigs.
- Increase sequencing capabilities and the phylogenetic analysis of Brazilian swine influenza virus sequences.
- Antigenic characterization of Brazilian swine influenza viruses using antigenic cartography.
- Test vaccine protocols.

Contribution of you team to the group

- Share data, protocols, virus and serum samples.
- Creation of a database of reference sera and viruses from Latin America.
- Exchange of researchers for training

Conclusions

- Great IAV genetic diversity has been detected in swine in Brazil following the introduction of pandemic H1N1 virus in 2009.

- New HA and NA segments of human seasonal virus origin persist at higher rates than the internal genes, which are replaced through reassortment by circulating swine viruses, particularly H1N1pdm.

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