OFFLU swine influenza virus meeting
27 – 28 March 2017
FAO Headquarters, Rome, Italy

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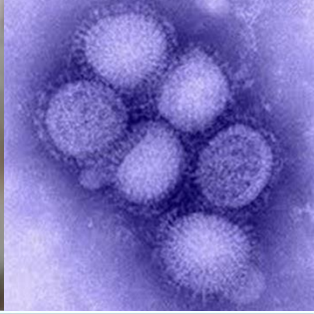
Embrapa Swine and Poultry
Concordia, SC

BRAZIL

Swine influenza in Brazil



<u>Since 2009</u>:

- Frequent outbreaks of H1N1pdm in pigs associated with respiratory illness.

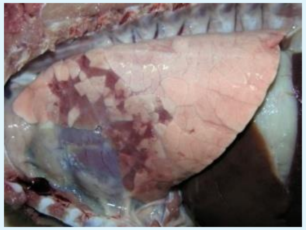
<u>Since 2011</u>:

- Human-like H1N2 and H3N2 FLUAVs detected in swine in seven Brazilian states (RS, SC, PR, SP, MG, MT and MS).
- H1N2 and H3N2 viruses have the internal gene segments of H1N1pdm origin.

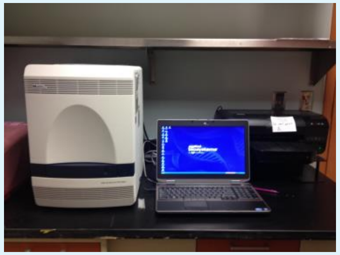
Isolation and genetic characterization of FLUAVs detected in swine in Brazil from 2009 to 2016.

Sampling and methods

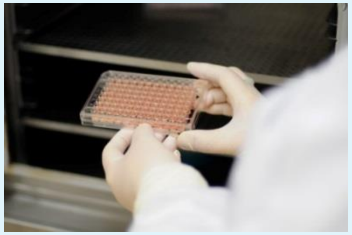
1952 nasal swabs



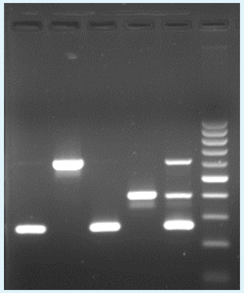
165 lung tissue samples



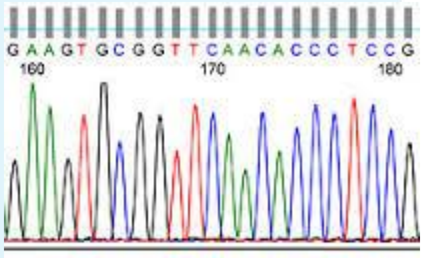
RNA Sample screened via RT-qPCR for FLUAV



RT-qPCR + samples Inoculated for VI on ECE/ or MDCK cells



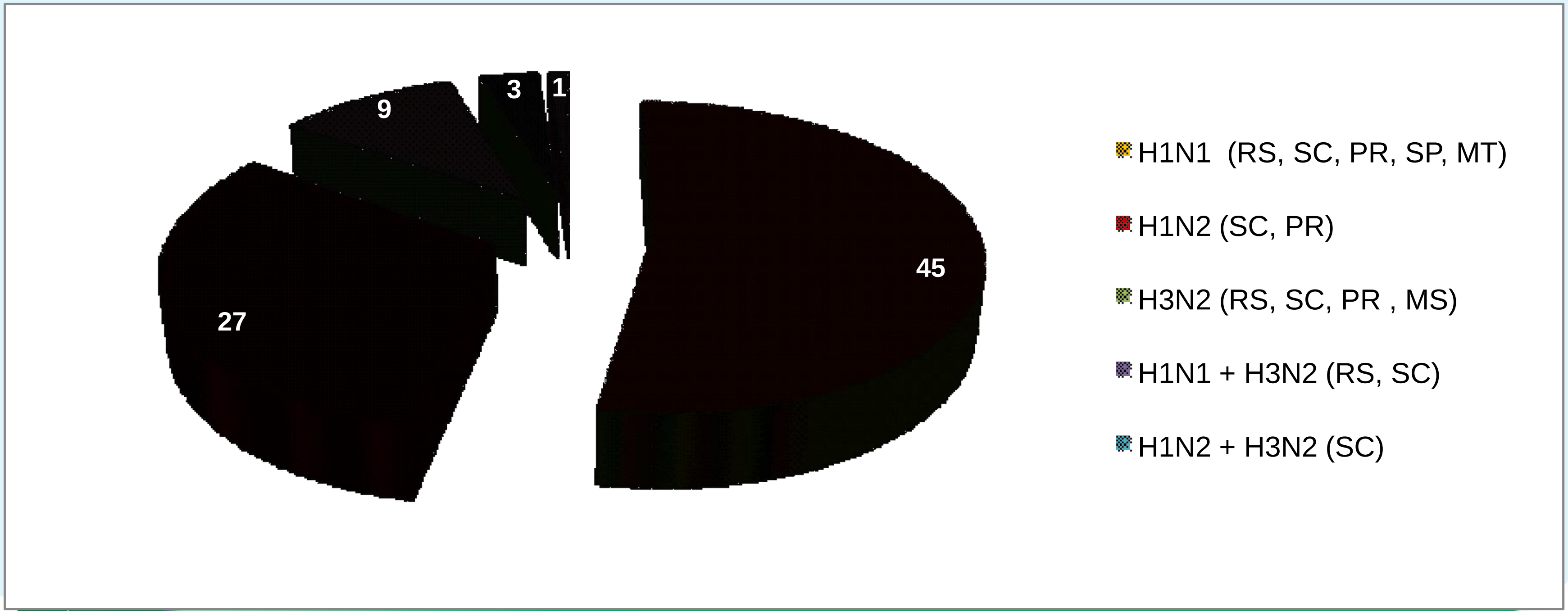
FLUAV subtyping by RT-PCR



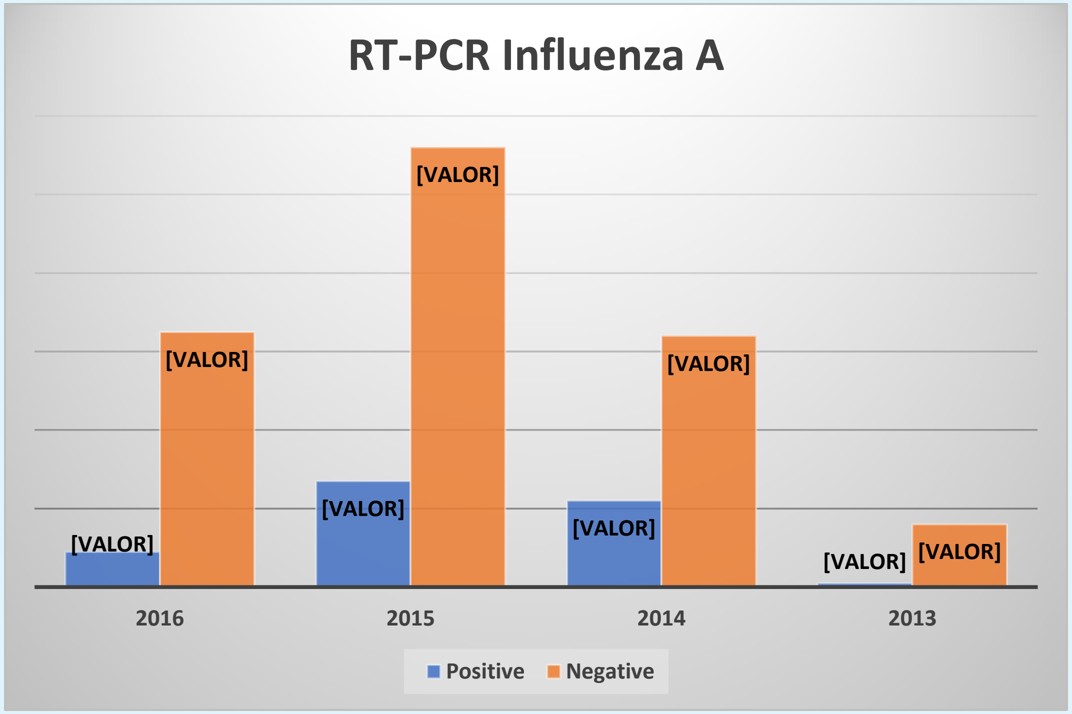
Genetic sequencing

Results

ASSAY	NO. SAMPLES
FLUAV RT-qPCR	306/2117 (14.45%)
Virus isolation	162/295 (54.91%)
FLUAV Subtyping	85/162



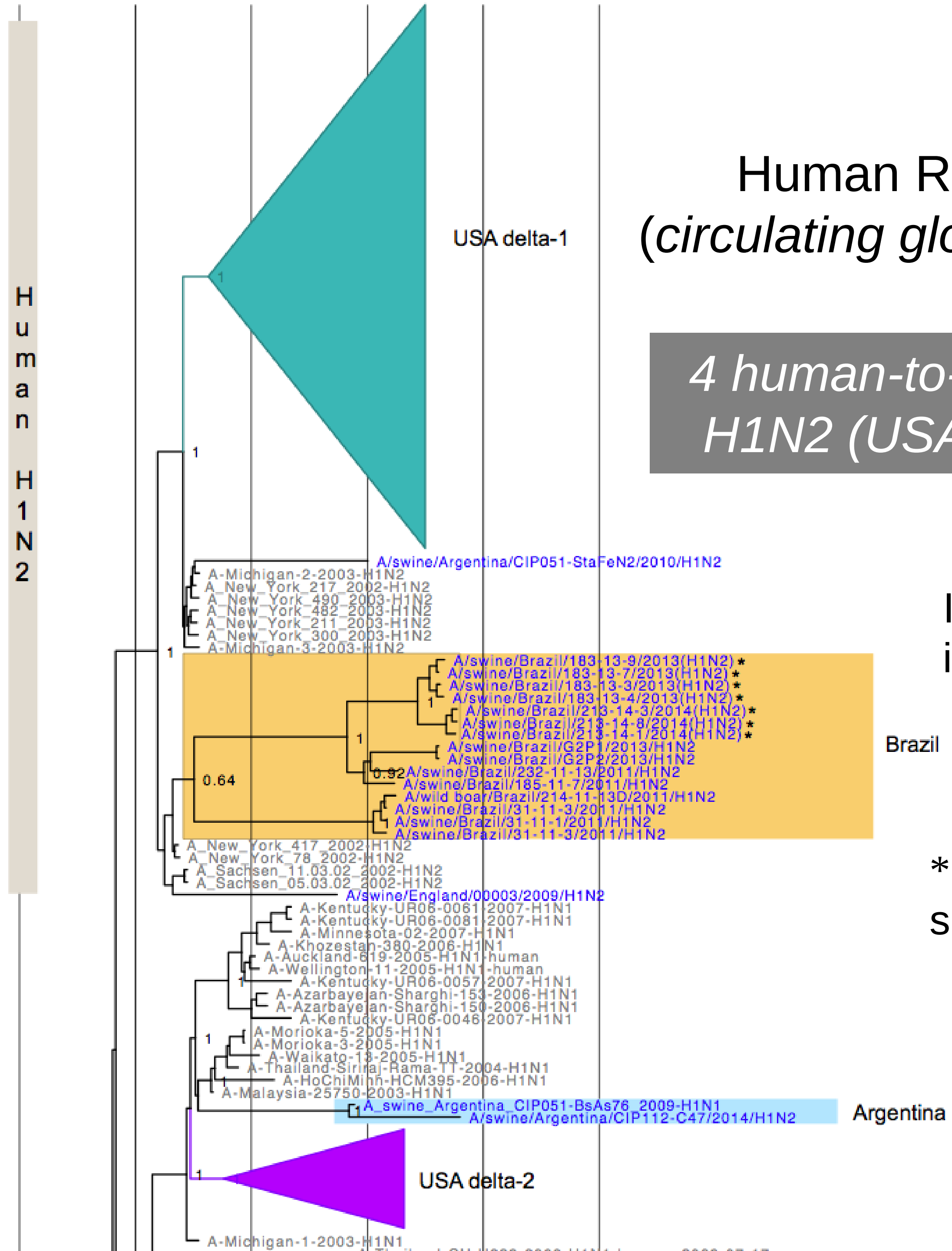
Results


RT-PCR Influenza A
[VALOR]
[VALOR]
[VALOR]
[VALOR]
[VALOR]
[VALOR]
[VALOR]
[VALOR]
2016
2015
2014
2013
Positive
Negative

Results

- Partial and complete gene sequences were generated for 58 FLUAVs.
- Sequence analysis of gene segments H1s, H1pdm, H3, N1 and N2.

HA (H1) segment



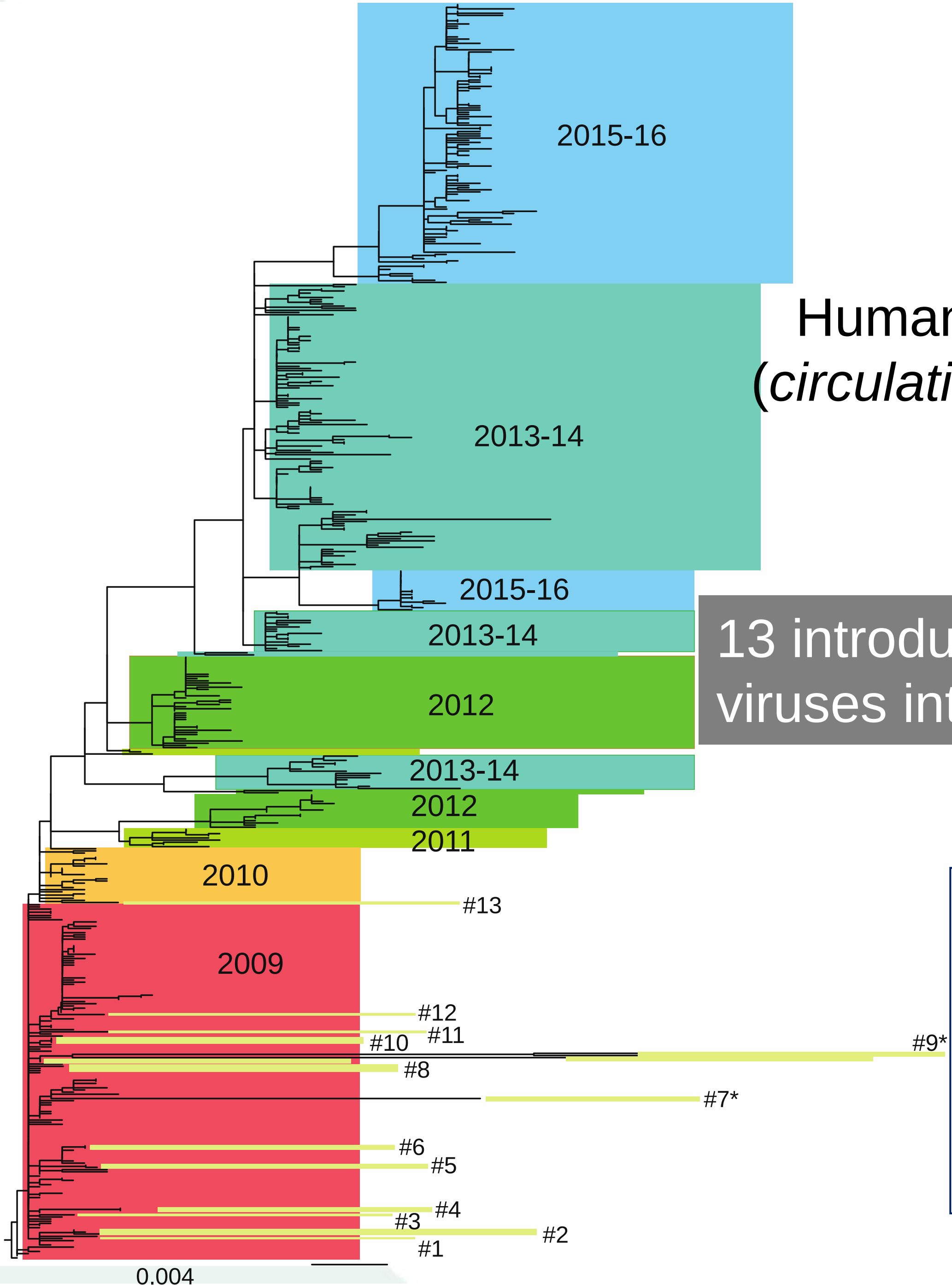
Human Reassortant H1N2 lineage
(*circulating globally in humans 2001-2003*)

4 human-to-swine transmission events of H1N2 (USA, Argentina, Brazil, England)

Introduction of human H1N2 viruses into Brazil swine (approx 2003)

* Viruses collected in 2013-2014 are a sub-clade of the Brazil lineage

HA (H1) segment

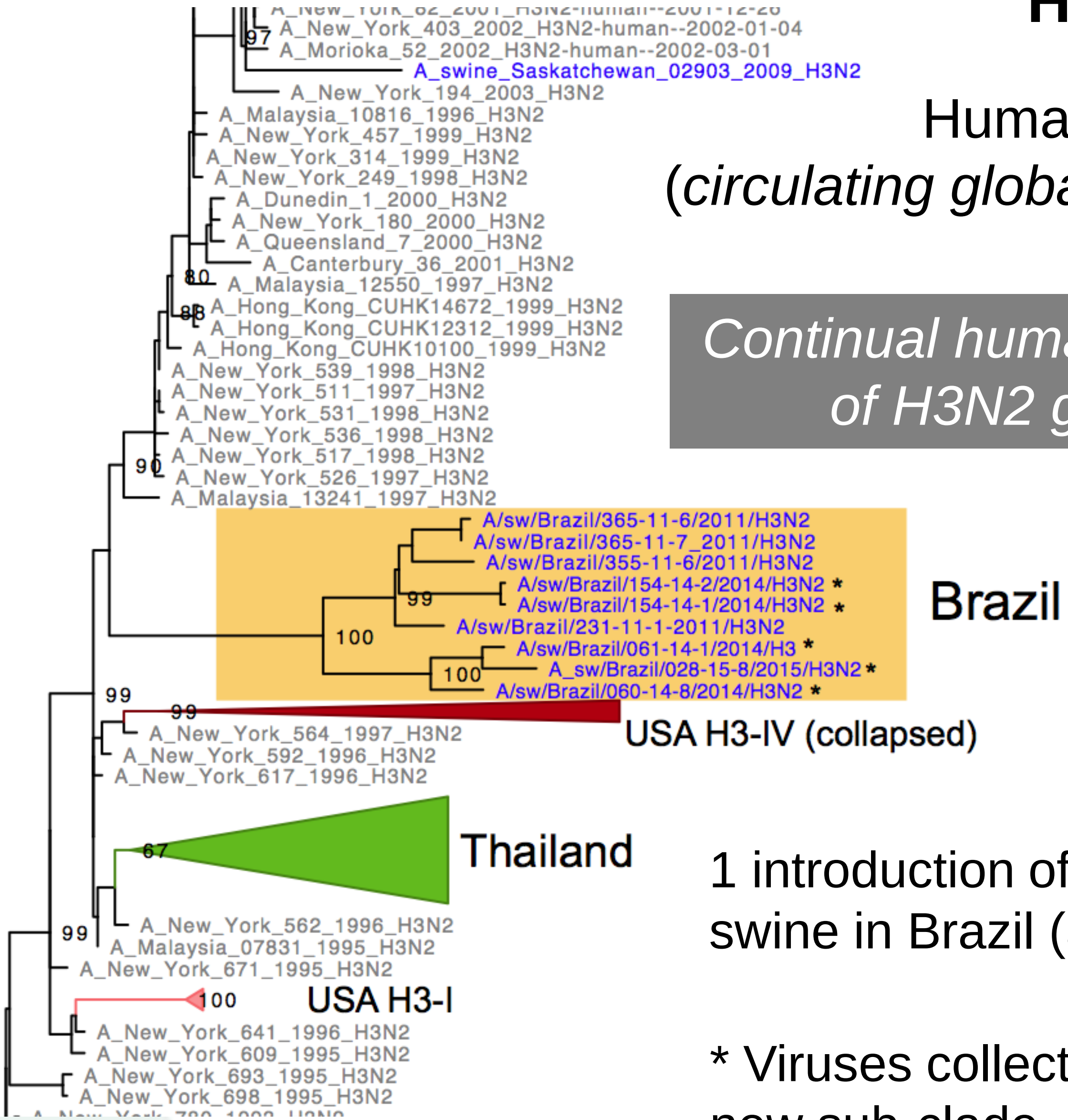


Human 2009 Pandemic H1N1 Lineage
(*circulating globally in humans 2009-2016*)

13 introductions of human pandemic H1N1 viruses into swine in Brazil since 2009

* Viruses collected in 2014 in swine in Brazil were introduced from humans during the 2009 pandemic wave and have been circulating in pigs ~5 years

HA (H3) segment



Human H3N2 lineage
(*circulating globally in humans 1968-2016*)

Continual human-to-swine transmission of H3N2 globally since 1970s

1 introduction of human H3N2 viruses into swine in Brazil (approx 1996)

* Viruses collected in 2014-2015 are a new sub-clade

NA (N2) segment

Human H3N2 lineage
(*circulating globally in humans 1968-2016*)

Continual human-to-swine transmission of H3N2 globally since 1970s

2 introductions of human H3N2 viruses into Brazil swine (approx 1998)

* Viruses collected in 2013-2015 are in clade 1; no evidence of transmission of clade 2 since 2011

NA (N1) segment

Novel introduction of human N1 into swine in Brazil (approx 2006)

Human H1N1 lineage
(*circulating globally in humans 1977-2009*)

2 isolates with the N1 gene from 2006.

Sample 103 / 14-2 isolated in 2014 in SC, and sample 200/15 isolated in 2015 in PR.

The two samples were identified as being of subtype H1N1 in the subtyping by RT-PCR. The primer used for amplification of the HA 1 gene was designed for identification of the HA gene of human origin

Only 3 human-to-swine transmissions of H1N1 (N1) globally since 1970s

Conclusions

- H1N1pdm and human-origin H1N2 and H3N2 influenza viruses are widespread in pig herds in Brazil, where they continue to evolve.

- FLUAVs of human seasonal virus origin have been circulating in swine for more than a decade.

- These particular H3N2 and H1N2 swIAV clades appear to be specific to Brazil.

Conclusions

- A novel introduction of a human N1 in swine was detected; the most closely related human influenza virus circulated in humans between 1977 and 2009. The human-to-swine transmission probably has occurred in 2006.

- These findings show the very dynamic epidemiology of influenza virus in pigs and highlight the importance of human-to-swine transmission in the generation of influenza virus diversity in swine in Brazil.

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Embrapa

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BRAZILIAN GOVERNMENT