

OFFLU Technical Meeting

Coordinating world-wide surveillance for influenza in swine

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Brazil update

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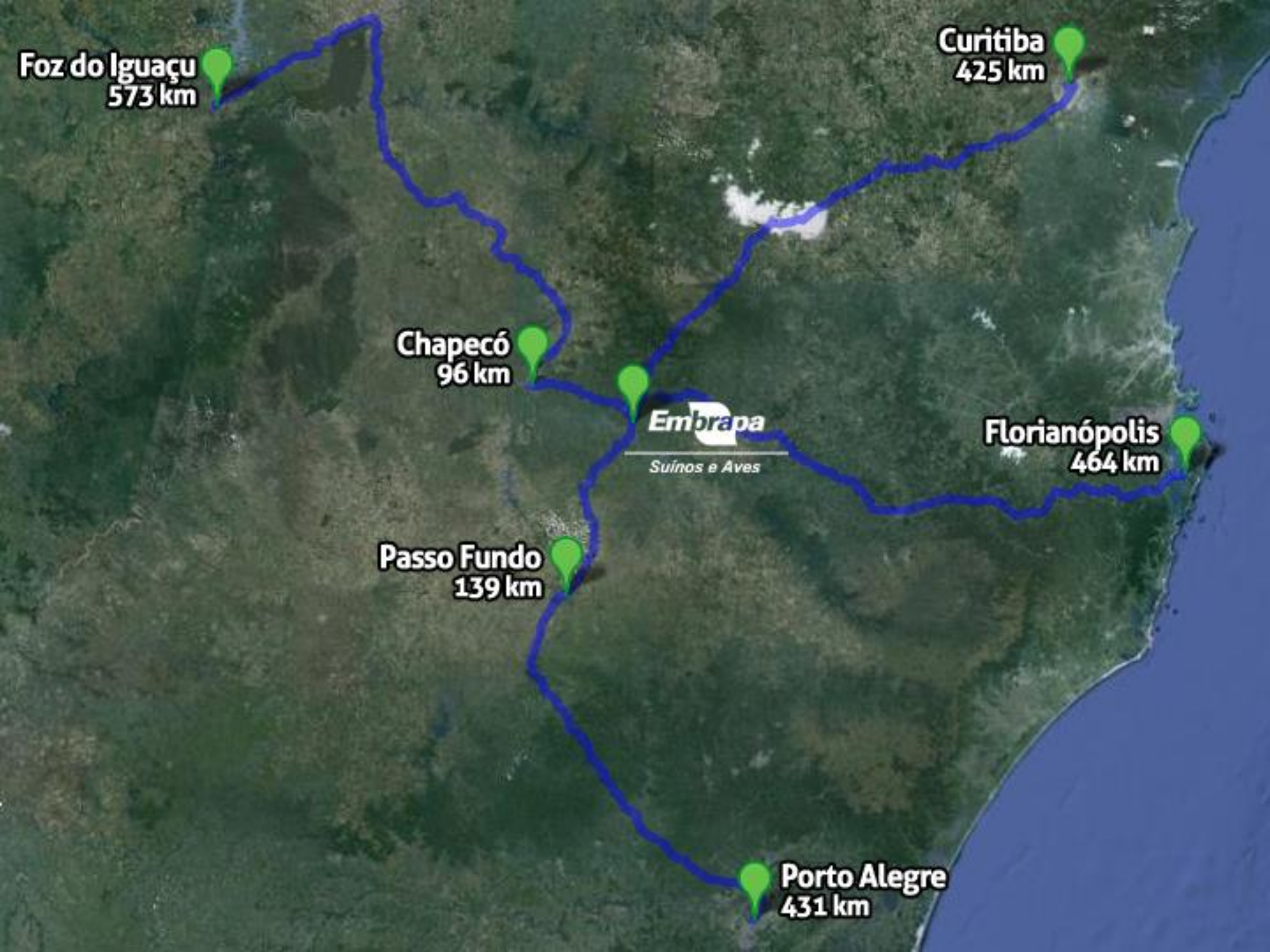


A satellite map of South America, showing the continent's green landmass against the dark blue ocean. The map includes parts of North America to the north and Africa to the east. Overlaid on the map is the Embrapa logo, which consists of the word "Embrapa" in a bold, sans-serif font, with a stylized white graphic element to its right. Below the logo is a horizontal line, followed by the text "Suínos e Aves". A yellow location pin is placed on the map, indicating a specific location in southern Brazil.

Embrapa

Suínos e Aves





Foz do Iguaçu
573 km

Curitiba
425 km

Chapecó
96 km

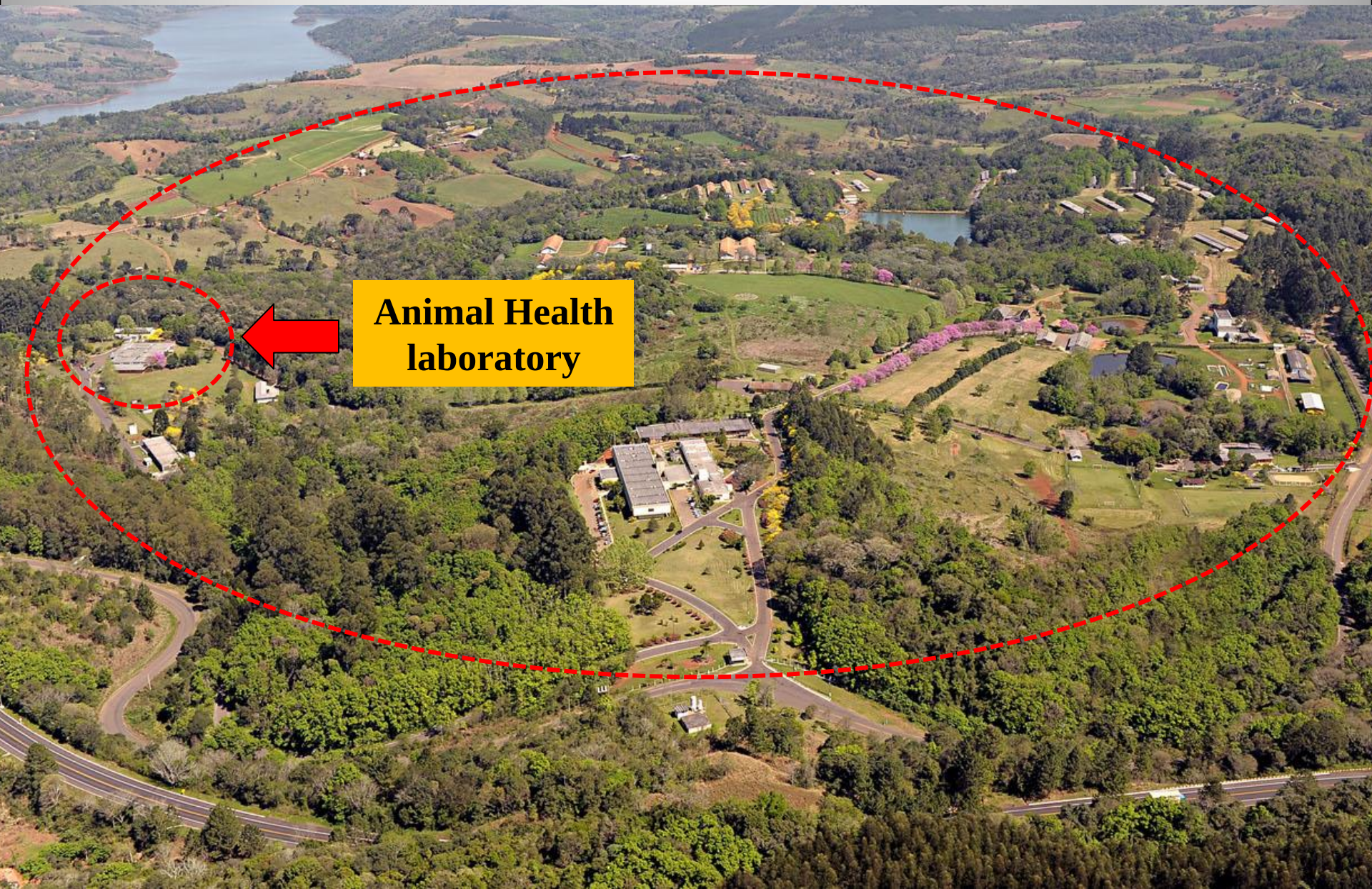
Florianópolis
464 km

Passo Fundo
139 km

Embrapa
Suínos e Aves

Porto Alegre
431 km

EMBRAPA Swine and Poultry (176 ha): 211 employees

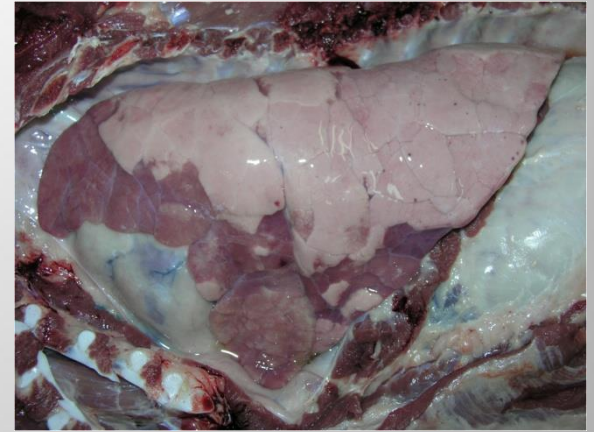
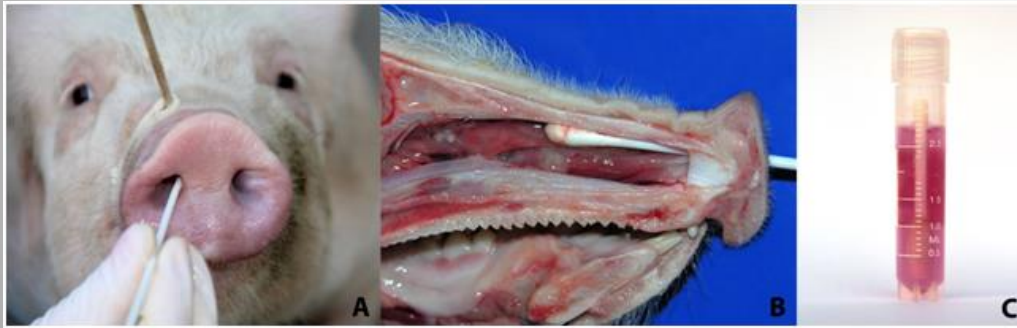


**Animal Health
laboratory**



Influenza in swine in Brazil

- » Since 2009: frequent outbreaks of H1N1pdm associated with respiratory illness (first outbreaks observed in different ages; more recent outbreaks mainly observed in growing pigs).
- » Since 2011: human-like H1N2 influenza virus detected in swine and in captive wild pigs in four Brazilian states.
- » H3N2 IAV detected in pigs in five Brazilian states.
- » H1N2 and H3N2 viruses have the internal gene segments of H1N1pdm origin.



- 1881 nasal swabs and 89 lung tissue samples were collected from swine in the southern, midwest and southeast regions of Brazil (2009-2012);
- RNA extraction, RT-qPCR (M gene of IAV and H1N1pdm);
- Virus isolation (MDCK cells or ECE);
- Genetic sequencing (ABI 3130xl and Illumina MiSeq).



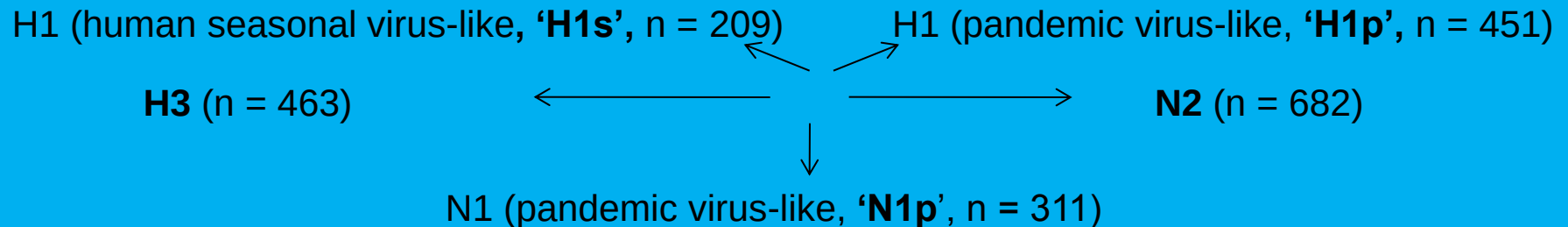
Results

Assay	Nasal swabs	Lung
RT-qPCR/ IAV	59/1881 (3.3%)	58/89 (65.2%)
Virus isolation*	14/59	27/58

*Partial sequencing (HA, NA and M gene) of 35 IAVs, eight gene segments of 11 IAVs.

Phylogenetic analysis

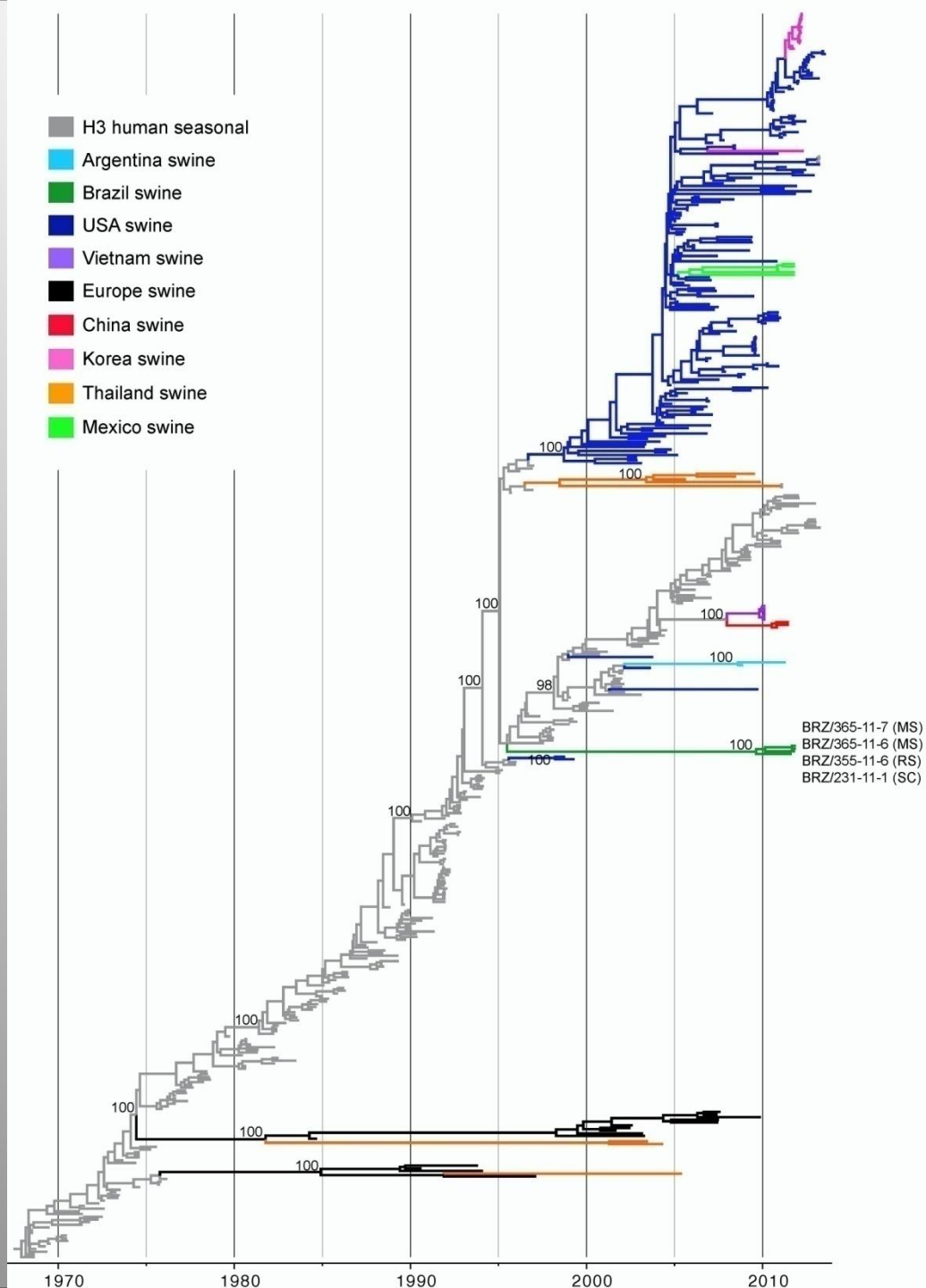
Nucleotide alignments were generated for discrete data sets:



Each data set was comprised of:

- (a) Brazilian swIAVs (16 IAVs: five H1N2, four H3N2 and seven H1N1pdm);
- (b) Related human and swine viruses, collected globally, available at NCBI's GenBank.

H3



Time-scaled Bayesian
MCC tree for the H3 gene

H1

■ H1 human seasonal (# H1N2)

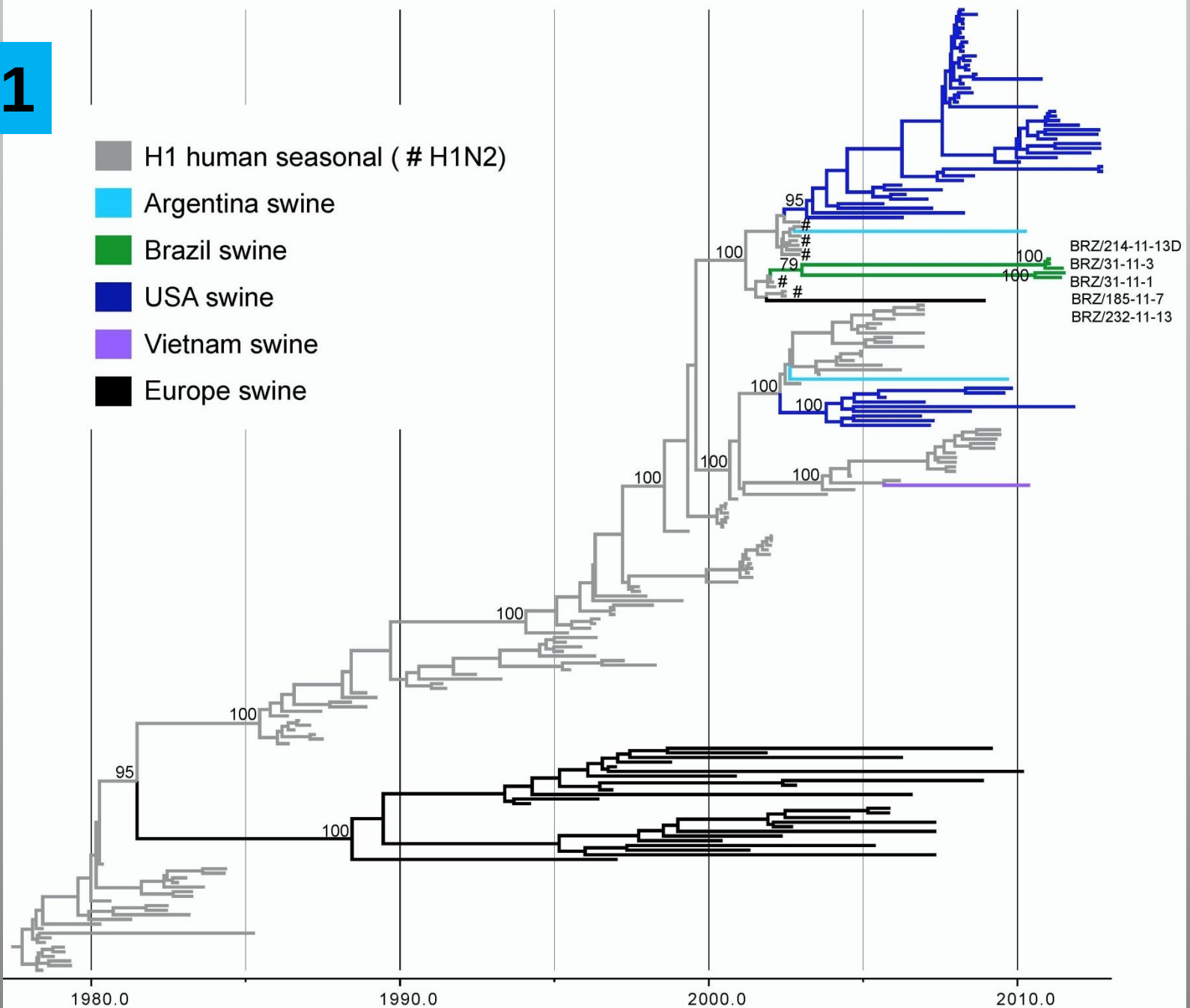
■ Argentina swine

■ Brazil swine

■ USA swine

■ Vietnam swine

■ Europe swine

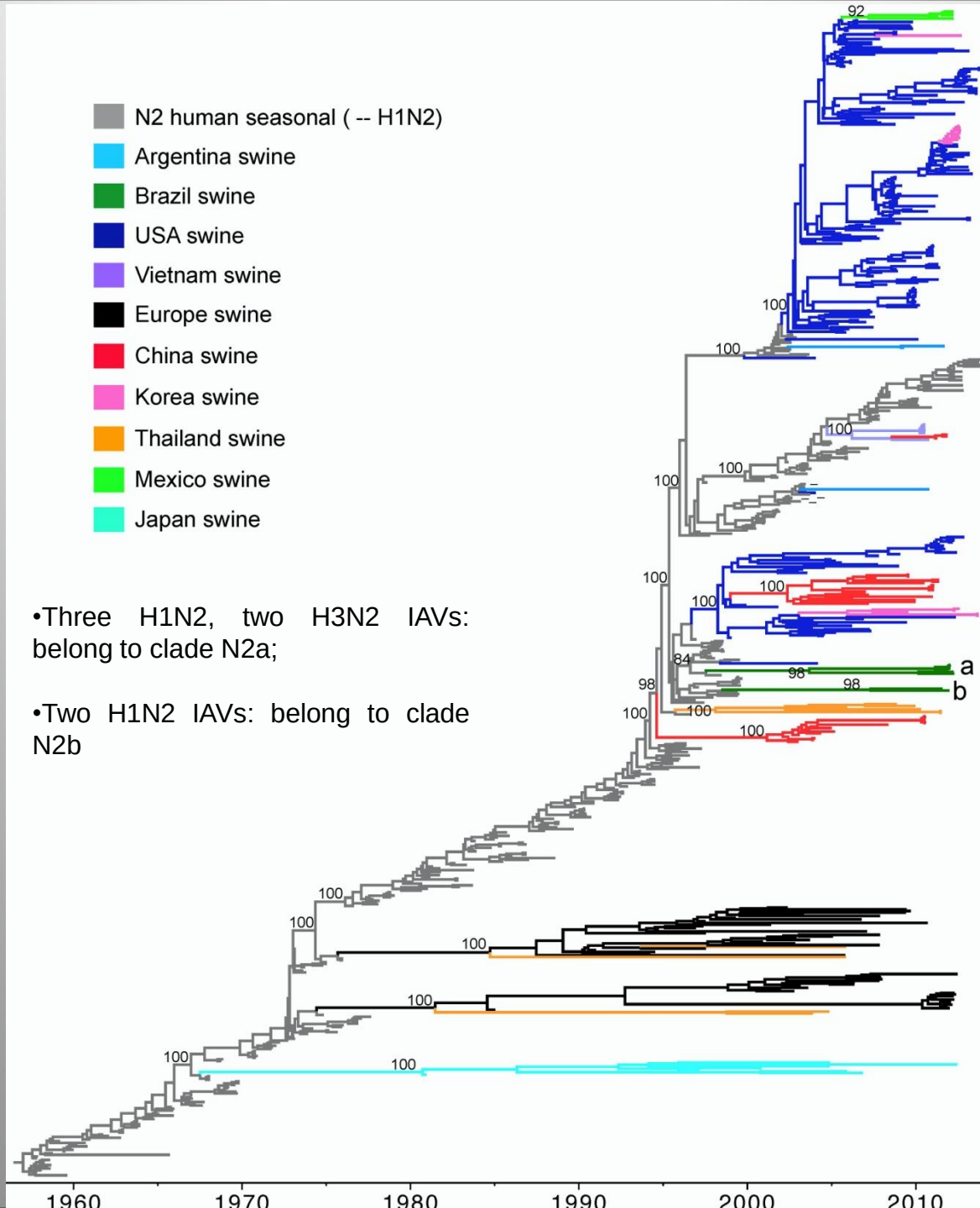


N2

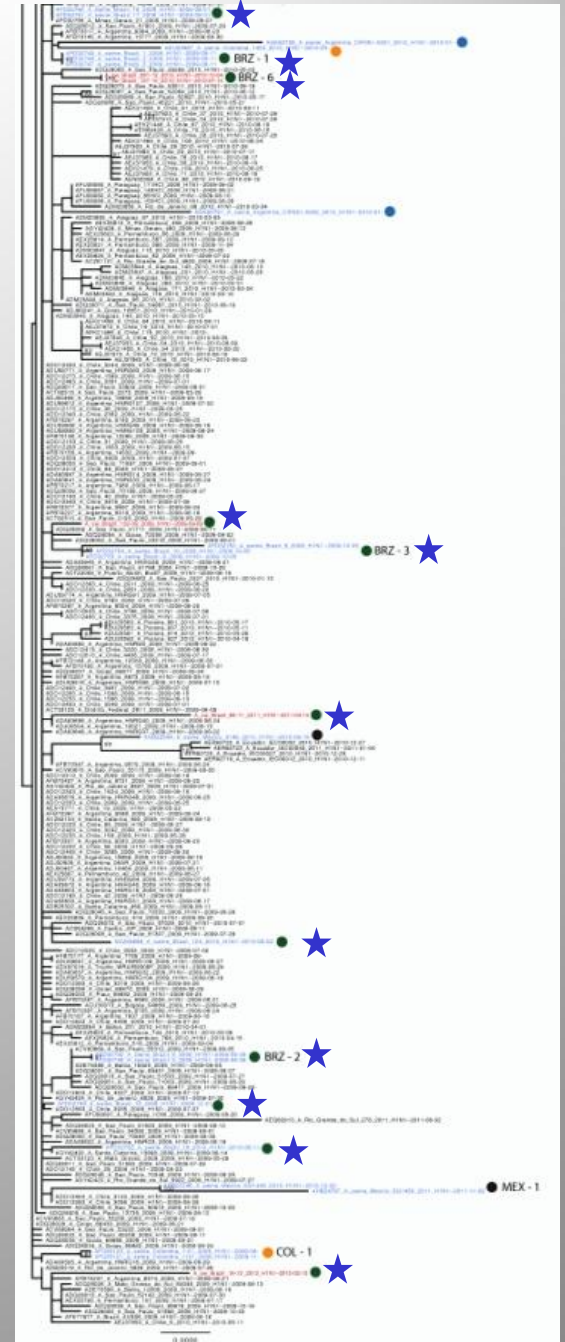
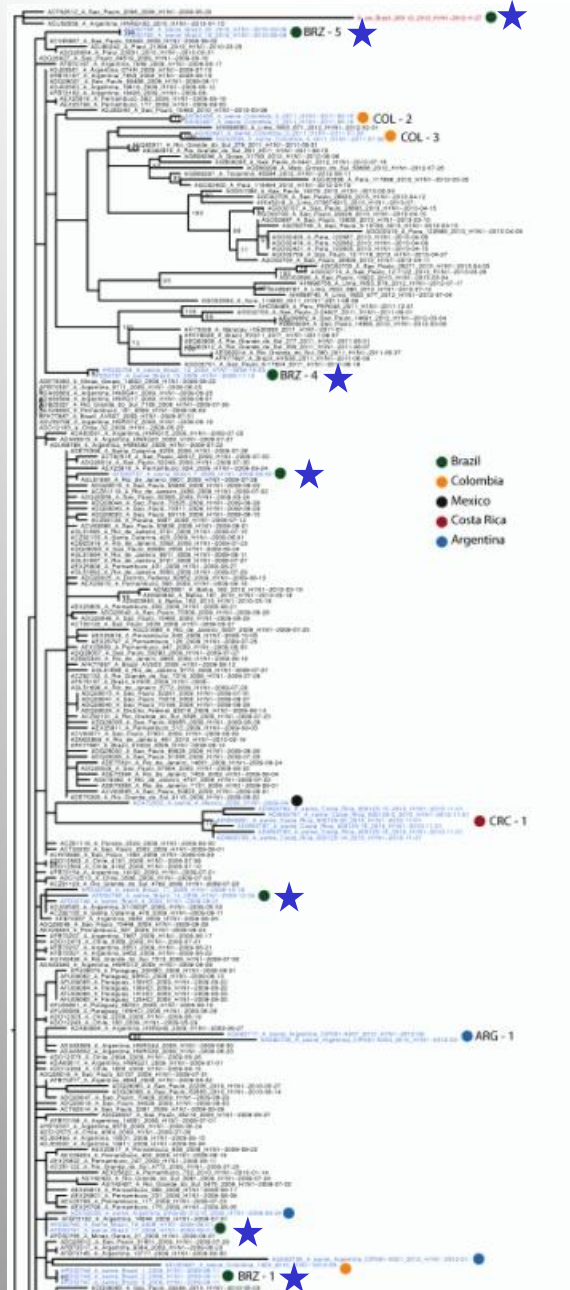
- N2 human seasonal (-- H1N2)
- Argentina swine
- Brazil swine
- USA swine
- Vietnam swine
- Europe swine
- China swine
- Korea swine
- Thailand swine
- Mexico swine
- Japan swine

• Three H1N2, two H3N2 IAVs: belong to clade N2a;

• Two H1N2 IAVs: belong to clade N2b



H1N1pdm



Virus	Subtype	HA	NA	M
A/swine/Brazil/104-09-S1/2009	H1N1	H1pdm	N1pdm	pdm
A/swine/Brazil/104-09-S7/2009	H1N1	H1pdm	N1pdm	pdm
A/swine/Brazil/104-09-S8/2009	H1N1	H1pdm	N1pdm	pdm
A/swine/Brazil/106-09/2009	H1N1	H1pdm	N1pdm	pdm
A/swine/Brazil/170h-10/2009	H1N1	H1pdm	N1pdm	pdm
A/swine/Brazil/170e-10/2009	H1N1	H1pdm	N1pdm	pdm
A/swine/Brazil/132-09/2009	H1N1	H1pdm	N1pdm	pdm
A/swine/Brazil/107-3A/2010	H1N1	H1pdm	N1pdm	pdm
A/swine/Brazil/12a10/2010	H1N1	H1pdm	N1pdm	pdm
A/swine/Brazil/136-10/2010	H1N1	H1pdm	N1pdm	pdm
A/swine/Brazil/72-11-507/2011	H1N1	H1pdm	N1pdm	pdm
A/swine/Brazil/66-11/2011	H1N1	H1pdm	N1pdm	pdm
A/swine/Brazil/95-11/2011	H1N1	H1pdm	N1pdm	pdm
A/swine/Brazil/173-11-4/2011	H1N1	H1pdm	N1pdm	pdm
A/swine/Brazil/263-12/2012	H1N1	H1pdm	N1pdm	pdm
A/swine/Brazil/18-12/2012	H1N1	H1pdm	N1pdm	pdm
A/swine/Brazil/31-11-1/2011	H1N2	H1	N2	pdm
A/swine/Brazil/31-11-3/2011	H1N2	H1	N2	pdm
A/swine/Brazil/232-11-13/2011	H1N2	H1	N2	pdm
A/wild boar/Brazil/214-11-13D/2011	H1N2	H1	N2	pdm
A/swine/Brazil/185-11-7/2011	H1N2	H1	N2	pdm
A/swine/Brazil/232-11-14/2011	H1N2	H1	N2	pdm
A/swine/Brazil/231-11-1/2011**	H3N2	H3	N2	pdm
A/swine/Brazil/365-11-6/2011	H3N2	H3	N2	pdm
A/swine/Brazil/355-11-6/2011	H3N2	H3	N2	pdm
A/swine/Brazil/365-11-7/2011	H3N2	H3	N2	pdm

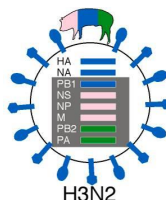
****Identified
H3N2,
H1N1pdm09
and H1N2 at
the same
farm**

Research at Embrapa– Antibody profile and Subtypes

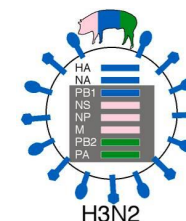
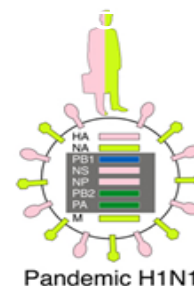
Farm (n=13)	Farrowing (n=193)	Weaning (n=253)	Growing (n=504)	Finishing (n=404)	Subtypes
A	66,7	60,0	73,3	53,3	H1N1pdm09 + H3N2
B	85,7	28,6	75,0	100,0	H1N1pdm09 + H3N2
C	93,3	60,0	91,1	73,3	H1N1pdm09 + H3N2
D	100,0	93,3	28,9	46,7	H1N1pdm09 + H1N1 + H3N2
E	93,3	46,7	34,2	96,6	H3N2
F	6,7	13,3	52,3	50,0	H3N2
G	93,3	66,7	13,3	36,7	H3N2
H	26,7	33,3	33,3	82,8	H3N2
I	0,0	23,3	80,0	81,8	H1N2 + H3N2
J	21,4	20,0	86,7	69,0	H1N1pdm09 + H3N2
K	46,7	60,0	88,6	83,3	H1N1pdm09 + H1N1 + H3N2
L	66,8	66,8	76,7	90,0	H1N1pdm09 + H3N2
M	80,0	35,7	58,6	20,0	H1N1 + H1N2 + H3N2
Avg (%)	60,0	46,7	60,9	70,0	

❖ 13 Farrow-to-finish farms (HI results):

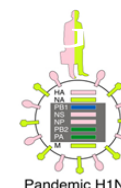
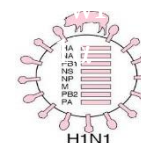
❖ Antibodies against H3N2: 4 farms



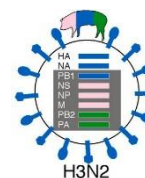
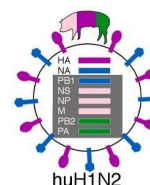
❖ Antibodies against H1N1pdm09 and H3N2: 5 farms



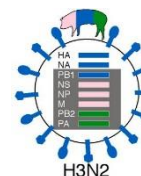
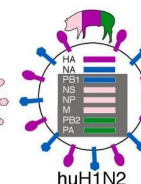
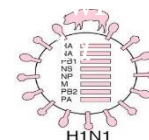
❖ Antibodies against H1N1, H1N1pdm09 and H3N2: 2 farms



❖ Antibodies against H1N2 and H3N2: 1 farm

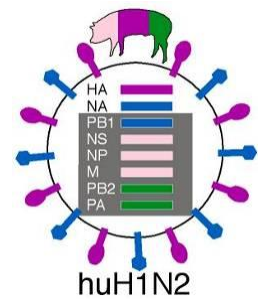
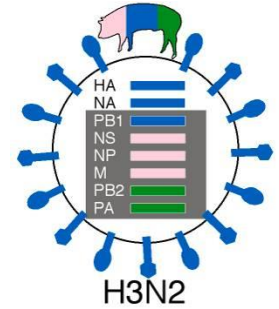
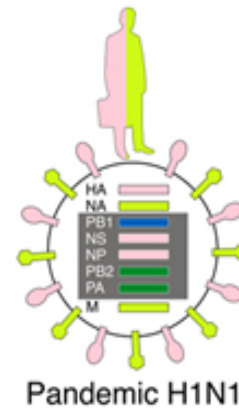
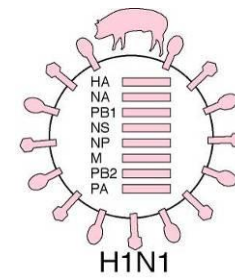
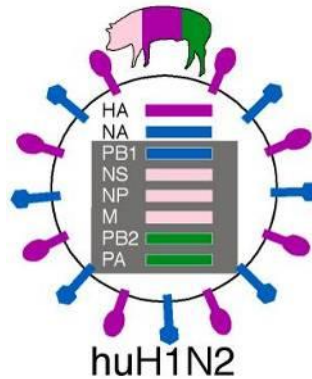
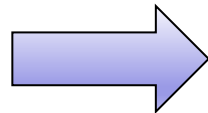
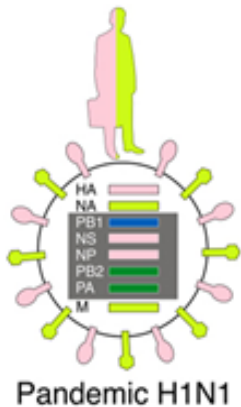
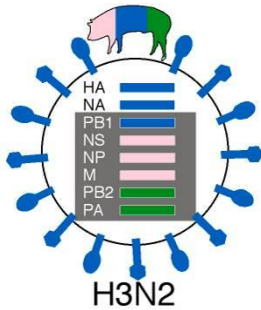
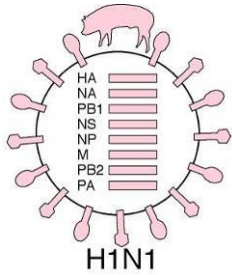


❖ Antibodies against H1N1, H1N2 and H3N2: 1 farm



Before 2010

After 2010



Conclusions

➤ **H1N1pdm, H1N2 and H3N2 IAVs are widespread** in Brazilian pig herds.

➤ We identified multiple previously uncharacterized clades of viruses that **are most closely related to human seasonal H3N2 and H1N2** viruses that circulated in the late **1990s** and early **2000s**, respectively.

➤ In contrast to the five genetically distinct HA and NA identified in Brazilian swine (H3, seasonal H1, pandemic H1, pandemic N1, and two seasonal N2 segments), the genetic diversity of the **internal gene segments was restricted to only the pandemic lineage.**

Acknowledgements



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