OFFLU Swine Influenza Virus group meeting
27 – 28 March 2017
FAO Headquarters, Rome, Italy

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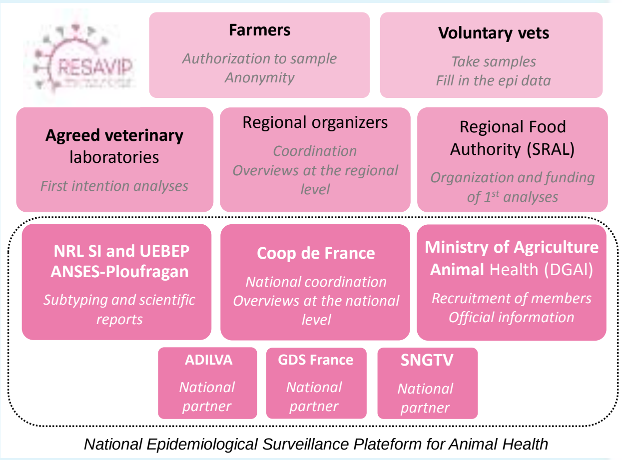
France

Surveillance in France

updated data since 12/2015

Passive surveillance in France

- ✓ **Résavip**: French National Network for swIAV surveillance
- ✓ **ANSES investigations** in farms
- ✓ **Local studies** with regional investigators
- ✓ Surveillance programs conducted by medical companies



Farmers
Authorization to sample
Anonymity

Voluntary vets
Take samples
Fill in the epi data

Agreed veterinary laboratories
First intention analyses

Regional organizers
Coordination
Overviews at the regional level

Regional Food Authority (SRAL)
Organization and funding of 1st analyses

NRL SI and UEBEP ANSES-Ploufragan
Subtyping and scientific reports

Coop de France
National coordination
Overviews at the national level

Ministry of Agriculture Animal Health (DGAl)
Recruitment of members
Official information

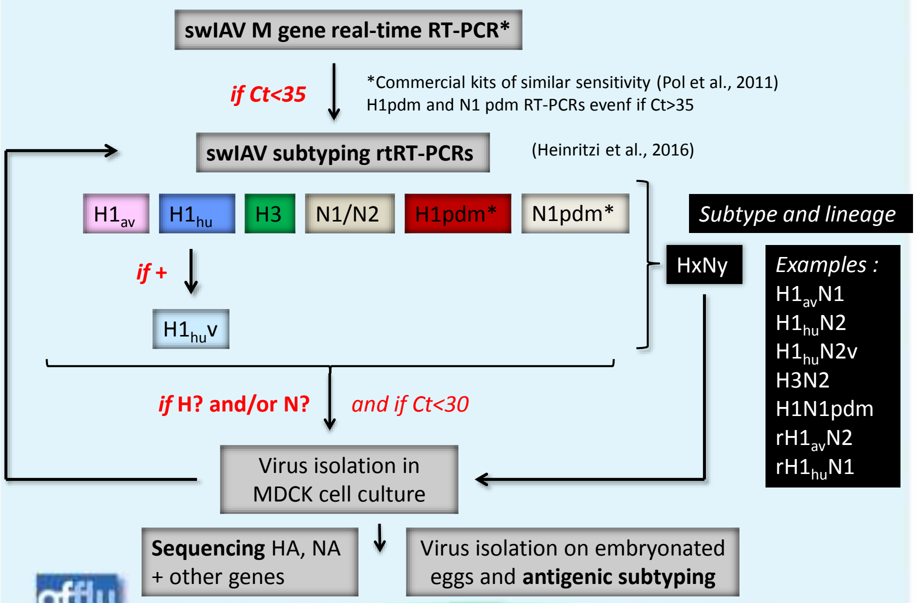
ADILVA
National partner

GDS France
National partner

SNGTV
National partner

National Epidemiological Surveillance Plateform for Animal Health

Analytical workflow



swIAV M gene real-time RT-PCR*

if Ct<35

*Commercial kits of similar sensitivity (Pol et al., 2011)
H1pdm and N1 pdm RT-PCRs evenf if Ct>35

swIAV subtyping rtRT-PCRs

(Heinritzi et al., 2016)

$H1_{av}$ | $H1_{hu}$ | H3 | N1/N2 | H1pdm* | N1pdm*

if +

$H1_{hu}v$

HxNy

Subtype and lineage

Examples :
$H1_{av}N1$
$H1_{hu}N2$
$H1_{hu}N2v$
H3N2
H1N1pdm
$rH1_{av}N2$
$rH1_{hu}N1$

if **H? and/or N?** *and if Ct<30*

Virus isolation in MDCK cell culture

Sequencing HA, NA + other genes

Virus isolation on embryonated eggs and **antigenic subtyping**

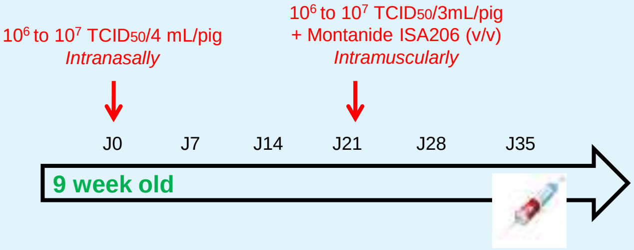
Sequencing

- Since 2016: ≈ **10 virus strains selected every 3 months** (based on subtype, geographical area, associated flu severity, epidemiological context…) → 30 to 40 strains per year
- **Propagation in MDCK cells**
- **Whole genome sequencing**
  - NGS platform
  - Ion Torrent™ Life Technologies

- Partial sequencing
  - Sanger sequencing
- **Phylogenetic analyses**

Antigenic subtyping

- Reference strains selected and propagated on eggs
- Production of **hyperimmune sera in SPF pigs**



10^6 to 10^7 $TCID_{50}$/4 mL/pig
Intranasally

10^6 to 10^7 $TCID_{50}$/3mL/pig
+ Montanide ISA206 (v/v)
Intramuscularly

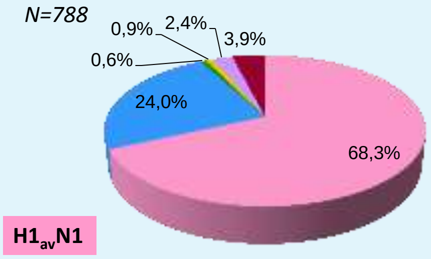
- A large panel of antisera - mostly directed against strains from European lineages
- **9 HI sera used for routine analyses on virus strains isolated in France**
- ≈ **10 isolates selected every 3 months for antigenic subtyping** (same strains as for sequencing)

swIAVs identified in France (2010-2016)

- M gene positive cases > ≈ 50% of investigated acute respiratory syndromes
- HxNy subtyped viruses (molecularly) > ≈ 75-80% of positive cases
- HA and/or NA mixtures

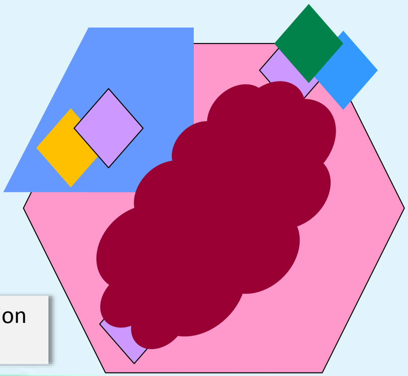
	N Virus	$H1_{av}N1$	$H1_{hu}N2$	H3N2	$rH1_{hu}N1$	$rH1_{av}N2$	H1N1pdm
2010	40	16	14	0	4	2	4
2011	134	76	50	0	1	6	1
2012	134	104	23	1	2	2	2
2013	126	91	31	0	0	1	3
2014	103	75	22	2	0	1	3
2015	146	101	32	1	0	5	8
2016	105	75	17	1	0	2	10
Total	**788**	**538**	**189**	**5**	**7**	**19**	**31**

swIAVs identified in France (2010-2016)



$H1_{av}N1$
$H1_{hu}N2$
H3N2
$rH1_{hu}N1$
$rH1_{av}N2$
H1N1pdm

Relative frequencies over time
↗ $H1_{av}N1$ and ↘ $H1_{hu}N2$
↗ H1N1pdm
↗ H3N2
→ $rH1_{av}N2$, ↘ $rH1_{hu}N1$
No H1pdmNy or HxN1pdm reassortant



Geographical distribution (2017)

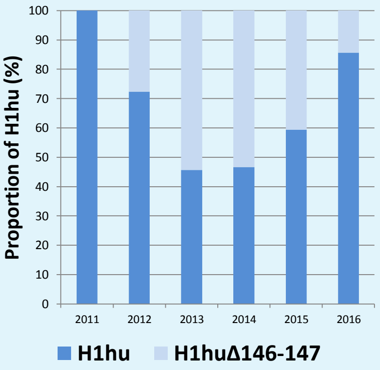
$H1_{hu}N2_{\Delta 146\text{-}147}$ variant

$H1_{hu}N2$
↓
$H1_{hu}N2_{\Delta 146\text{-}147}$

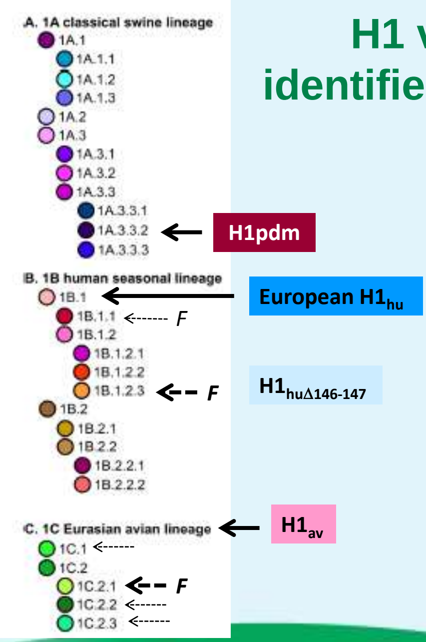
- First detection in 2012
- 2-amino acid deletion + 1 mutation in RBS + other mutations in antigenic sites

➢ ***Antigenic drift***

- Development of a specific rtRT-PCR for rapid identification (subtyping)
- 2 $H1_{hu}N2$ sub-populations in co-circulation during 5 years at least
- Disappearance ?



H1 viruses identified in France



H1pdm

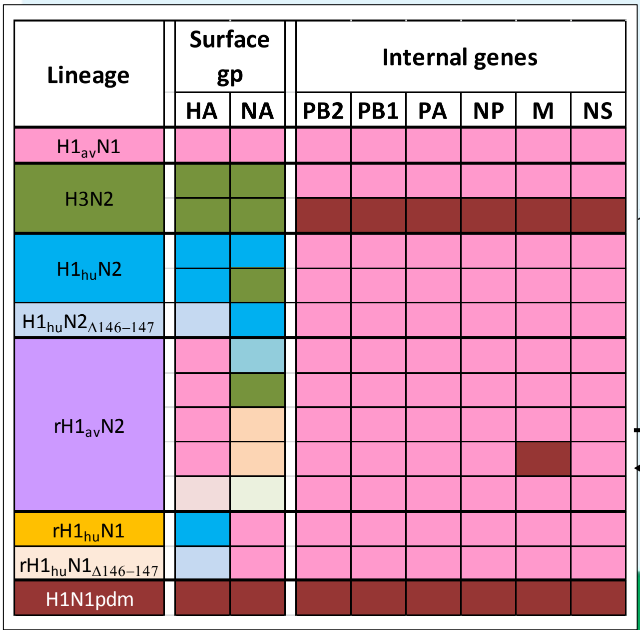
European $H1_{hu}$

$H1_{hu\Delta 146\text{-}147}$

$H1_{av}$

Anderson et al., 2016

French swIAV genotypes (2010-2016)



Lineage	Surface gp		Internal genes					
	HA	NA	PB2	PB1	PA	NP	M	NS
$H1_{av}N1$	🟪	🟪	🟪	🟪	🟪	🟪	🟪	🟪
H3N2	🟩	🟩	🟪	🟪	🟪	🟪	🟪	🟪
	🟩	🟩	🟥	🟥	🟥	🟥	🟥	🟥
$H1_{hu}N2$	🟦	🟦	🟪	🟪	🟪	🟪	🟪	🟪
	🟦	🟩	🟪	🟪	🟪	🟪	🟪	🟪
$H1_{hu}N2_{\Delta 146-147}$	🔷	🟦	🟪	🟪	🟪	🟪	🟪	🟪
$rH1_{av}N2$	🟪	🔹	🟪	🟪	🟪	🟪	🟪	🟪
	🟪	🟩	🟪	🟪	🟪	🟪	🟪	🟪
	🟪	🟧	🟪	🟪	🟪	🟪	🟪	🟪
	🟪	🟧	🟪	🟪	🟪	🟪	🟥	🟪
	▫	◻	🟪	🟪	🟪	🟪	🟪	🟪
$rH1_{hu}N1$	🟦	🟪	🟪	🟪	🟪	🟪	🟪	🟪
$rH1_{hu}N1_{\Delta 146-147}$	🔷	🟪	🟪	🟪	🟪	🟪	🟪	🟪
H1N1pdm	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥

- ✓ 3 subtypes
- ✓ 8 lineages
- ✓ 14 genotypes

$H1_{av}N2$ reassortants:
5 different genotypes

> In Belgium in 2013 (ESNIP3)

2016-2017 : first detections of reassortants with internal genes from H1N1pdm

NA from human seasonal H3N2 (≈ 2003)
+ Mpdm

- *Increased zoonotic potential ?*

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ESNIP3

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FLI

RESAVIP

CoVetLab
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Local labs

MERIAL

IDT

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