



SIV group technical meeting Paris, December 3rd-4th 2015

Passive surveillance of swIAVs in France

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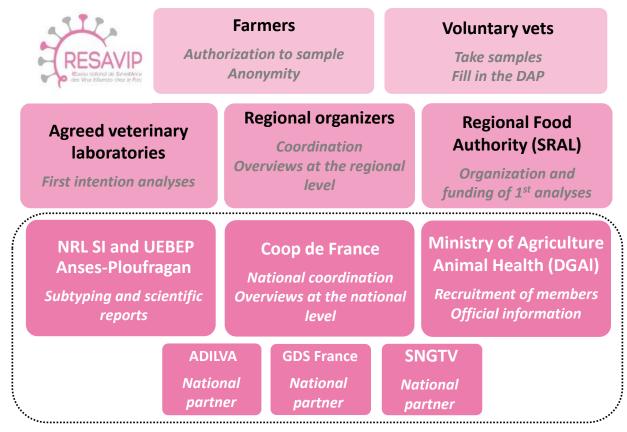
National Reference Laboratory for Swine Influenza

Ploufragan, France



Surveillance programs (1)

French National Network for swIAV surveillance



Members of « SIV Group » from the National Epidemiological Surveillance Plateform for Animal Health (Scientific and technical support)

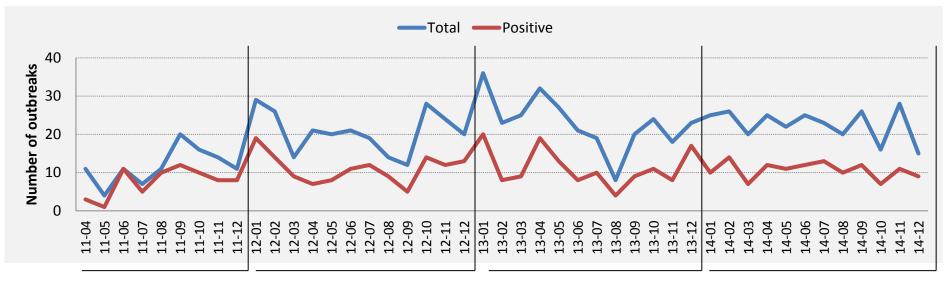
- Set up in April 2011
- Sampling kits: 3 nasal swabs + accompanying document (data sheet = DAP)
- Flu outbreaks > samples taken from pigs with body **temperature ≥40.5° C** preferentially
- 1st analyses (detection) by regional labs agreed by the Ministry
- 2nd analyses (subtyping) by NRL SI

Surveillance programs (1)

✓ French National Network for swIAV Surveillance

2011-2014: 69 voluntary veterinarians
900 farms visited in 15 out of 21 regions
465 positive herds (51,7%)





Outbreaks investigated all the year swIAVs detected each month – **no seasonality**

Pigs infected whatever the age/physiological stage Recurrent infections reported in 43% of positive herds 6/8 week old pigs frequently affected (31,2%)



Surveillance programs (2)

✓ Anses investigations in farms

- Clinical influenza-like events reported by vets, technicians, farmers
- Mainly in the Western part of France (Brittany = highest pig density area)



- Identification (ear tag)
- Nasal swabs
- Blood samples
- Clinical records

- Blood samples (same pigs)
- Clinical records

✓ Other sources of samples

- Anses cross-sectional surveys on respiratory diseases
- **Specific studies** in collaboration with **local investigators** (mainland, over-seas regions)
- Positive samples (lungs, nasal swabs) submitted by regional or private vet labs for subtyping (apart from Résavip)
- Surveillance programs conducted by medical companies (Merial, Boehringer-Ingelheim...)

✓ Other sources of data

- IDT-Biologika surveillance program (lab analyses performed by FLI, Germany)



Objectives (2)

- Anses & Résavip (farmers, vets & Ministry)
 - To describe the **nature of circulating swIAVs** (subtypes, genetic lineages)
 - To approach their distribution in the pig population
 - To **collect epidemiological data** linked to swIAV infections

>> To provide continuous monitoring of swIAVs

- To improve responsiveness and enable targeted action when necessary
- To anticipate and determine possible **measures to be applied to limit the impact of the infection**, both in terms of public health (zoonotic virus) and veterinary health
- To **ensure adequate communication**, especially in the event of a major new health episode or the emergence of new viral strains.

Anses (additional)

- To study and follow up **virus evolution**, genetically and antigenically (research, adaptation of diagnostic tools, information on vaccine adequacy, etc.)
- To further study phenotype, pathogenicity, dynamic, inter-species transmission potential of novel reassortants and/or variants



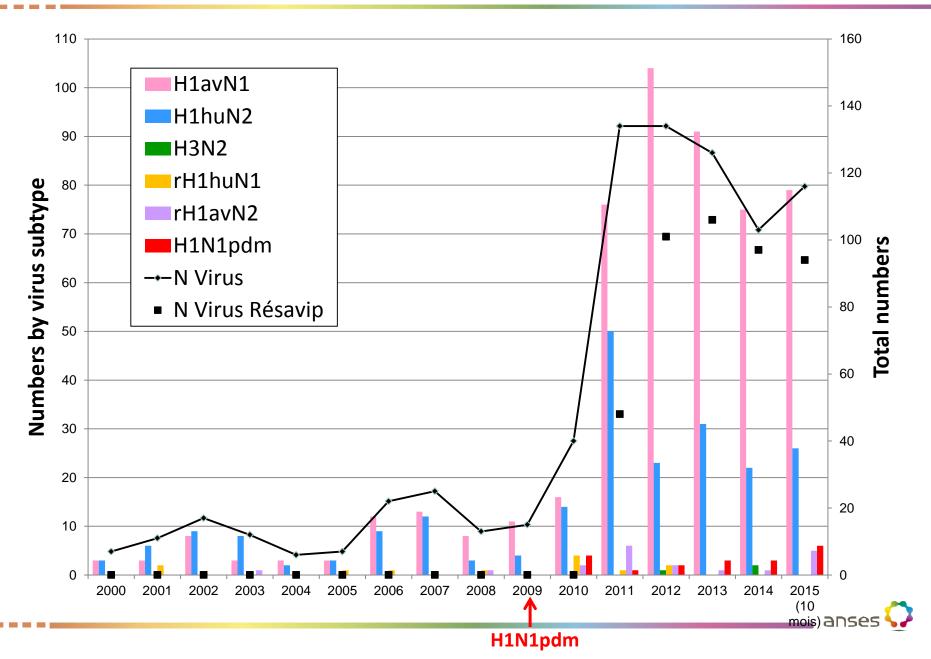
swIAV detection and identification - Methods

- Influenza A Virus detection in nasal swabs (or lung samples)
 - \triangleright M gene real-time RT-PCR (in duplex with β -actine or GAPDH gene)
 - Two commercially available kits (Biomerieux and Thermo Fisher), validated by NRL

Molecular sub-typing

- ➤ Real-time RT-PCRs specific to HA and NA genes from swIAVs enzootic in European pigs: H1_{av}N1, H3N2, H1_{hu}N2, H1N1pdm
- > In-house developed and validated (collab. FLI for some of them)
 - 5 simplex rtRT-PCRs: H1_{av}; H1_{hu}; H3; H1pdm; N1pdm
 - 1 duplex rtRT-PCR: N1+N2
- > Three commercially available kits (Biomerieux and Thermo Fisher) validated by NRL
 - 2 kits = duplex H1pdm + β-actine or GAPDH
 - 1 kit = duplex N1pdm + β -actine
- \triangleright New: in-house rtRT-PCR specific to antigenic H1_{hu} variant (H1_{huv}) detected in France
- **Virus isolation** (MDCK cells ; embryonated chicken eggs)
- **Antigenic sub-typing** (HI tests) > production of hyperimmune sera on SPF pigs
- Sequencing (HA, NA, Internal genes)

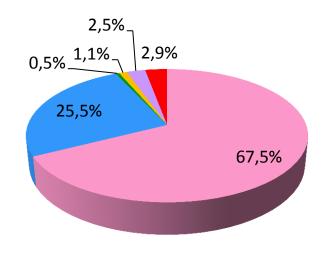
swIAVs detected in France (2000-2015)



swIAVs detected in France (2010-2015)

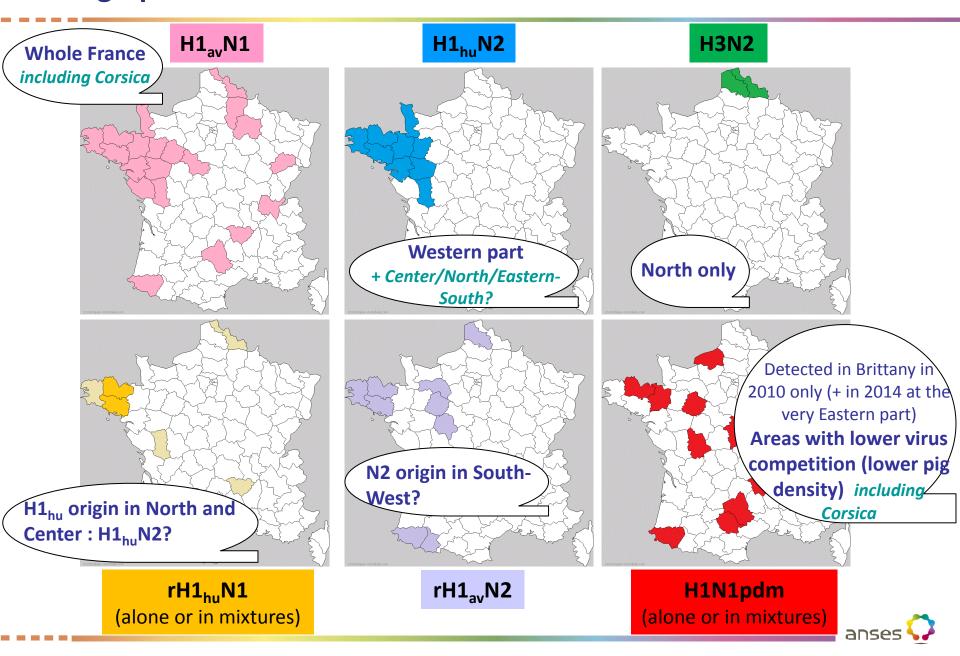
	N Virus	H1 _{av} N1	H1 _{hu} N2	H3N2	rH1 _{hu} N1	rH1 _{av} N2	H1N1pdm
2010	40	16	14	0	4	2	4
2011	134	76	50	0	1	6	1
2012	134	104	23	1	2	2	2
2013	126	91	31	0	0	1	3
2014	103	75	22	2	0	1	3
2015 (10 months)	110	75	25	0	0	4	6
Total	647	437	165	3	7	16	19

Relative frequencies





Geographical distribution of swIAVs detected in France since 2010

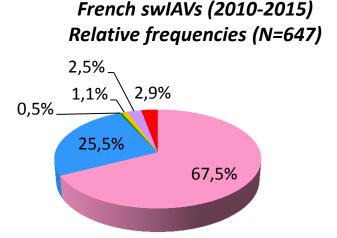


Genotypes and evolution of French swIAVs

> 7 out 23 genotypes identified at the European level (ESNIP3)

		In	External genes					
	PB2	PB1	PA	NP	M	NS	НА	NA
Α								
В								
С								
G								
Н								
J								
Р								

	European swIAVs N=270			
Lineage	Count	%		
H1 _{av} N1	85	29		
H3N2	38	13		
H1 _{hu} N2	26	9		
rH1 _{av} N2	5	2		
rH1 _{hu} N1	3	1		
H1 _{hu} N2	2	<1		
H1N1pdm	35	12		



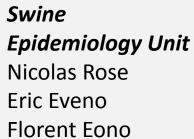
- \checkmark **H1**_{av}**N1**: slow genetic evolution; updating of reference antigens and sera every 5-6 years
- ✓ rH1_{av}N2: 2 different populations? (North-Western part versus South-Western part)
- ✓ $H1_{hu}N2$: several genetic clusters ; antigenic drift in 2012 > concomitant circulation (50/50) of 2 different viruses, $H1_{hu}N2$ and $H1_{hu}N2$ $\Delta 146-147$
- ✓ H1N1pdm: still closely related to H1N1pdm isolated in humans despite increasing number of mutations over years; de novo human to pig transmission during seasonal epidemics in humans
- ✓ H3N2: closely related to Belgian and other European H3N2 swIAVs
- ✓ To date, no reassortant with 1 or more gene(s) from H1N1pdm

Acknowledgements

Anses Ploufragan

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and coll.















Vets & farmers



























Côtes d'Armor









Frédéric Paboeuf