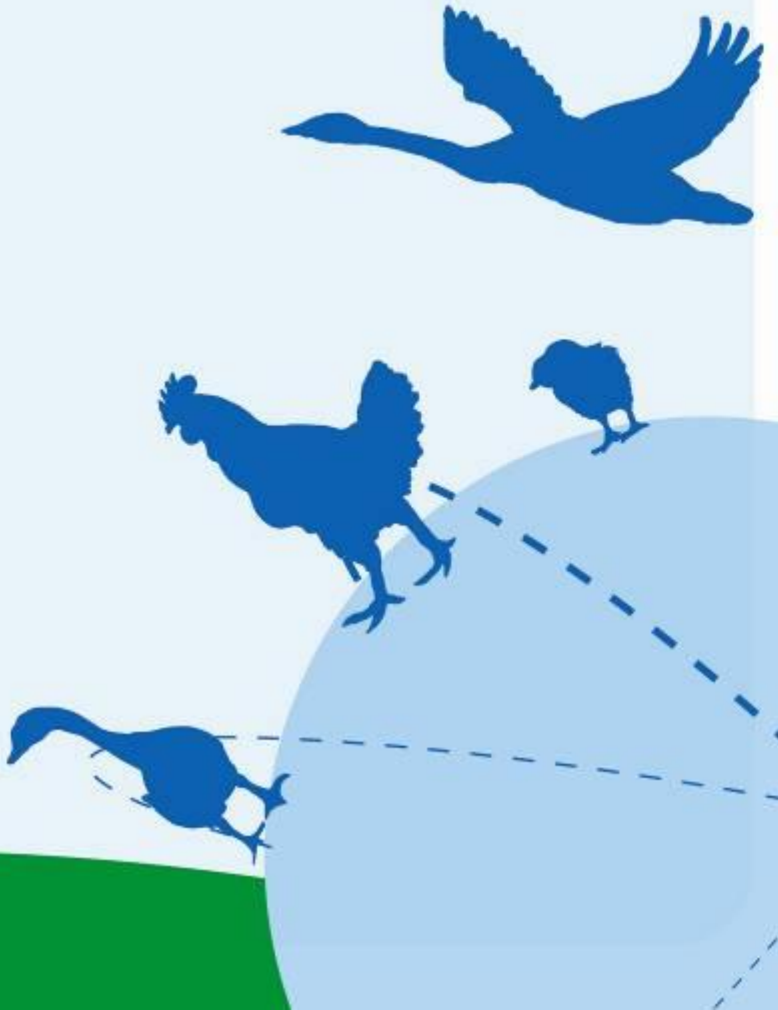
OFFLU virtual SIV group meeting

9 December 2020



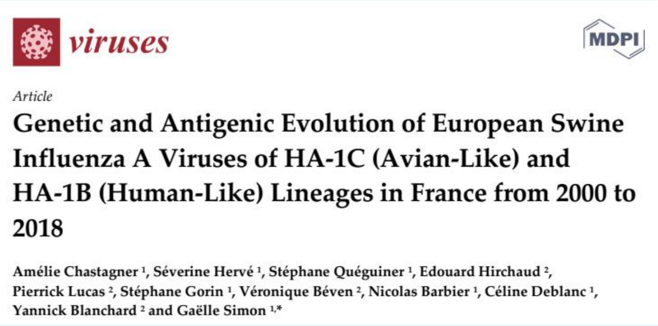
Gaëlle SIMON

Anses, France

Ongoing surveillance in Europe

2019-2020 surveillance in France

- **No H3 since 2016**
- HA-1A : 1A.3.3.2 – SeL and SwD groups
- HA-1B : **most 1997-2019 strains belong to 1B.1.2.3**
  2012: antigenic drift in $H1_{hu}\Delta146\text{-}147$ strains
  sporadic incursions of 1B.1.2.1 in 2016-2017
- HA-1C : **most 2005-2019 strains belong to 1C.2.1**
  (regional sub-groups)
  incursions of 1C.2.2 in 2013-2015 + **2019**
  incursions of 1C.2 in 2015 + 2018 + **2019**
  2020 : diffusion of 1C.2 ($H1_{av}N2$ DK-EA)

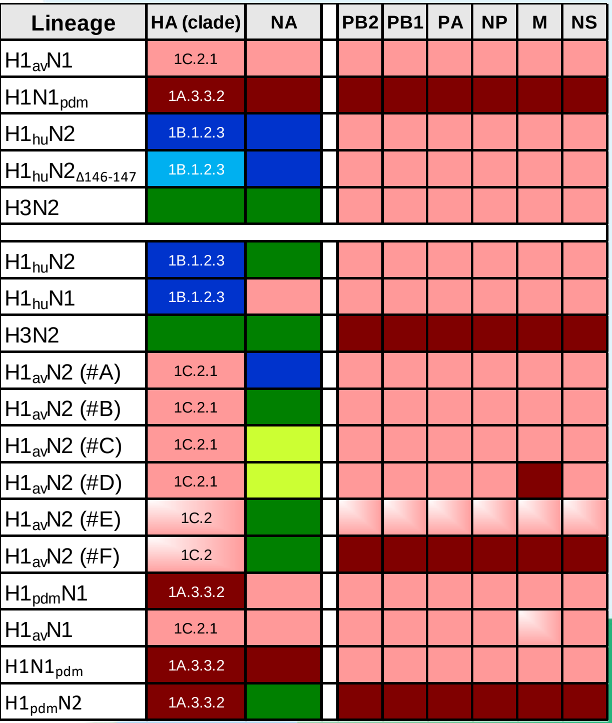


viruses MDPI

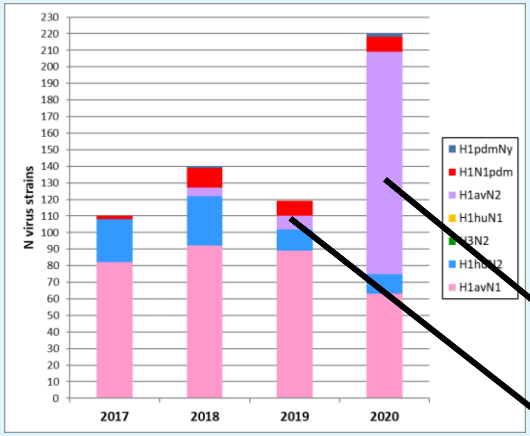
Article

Genetic and Antigenic Evolution of European Swine Influenza A Viruses of HA-1C (Avian-Like) and HA-1B (Human-Like) Lineages in France from 2000 to 2018

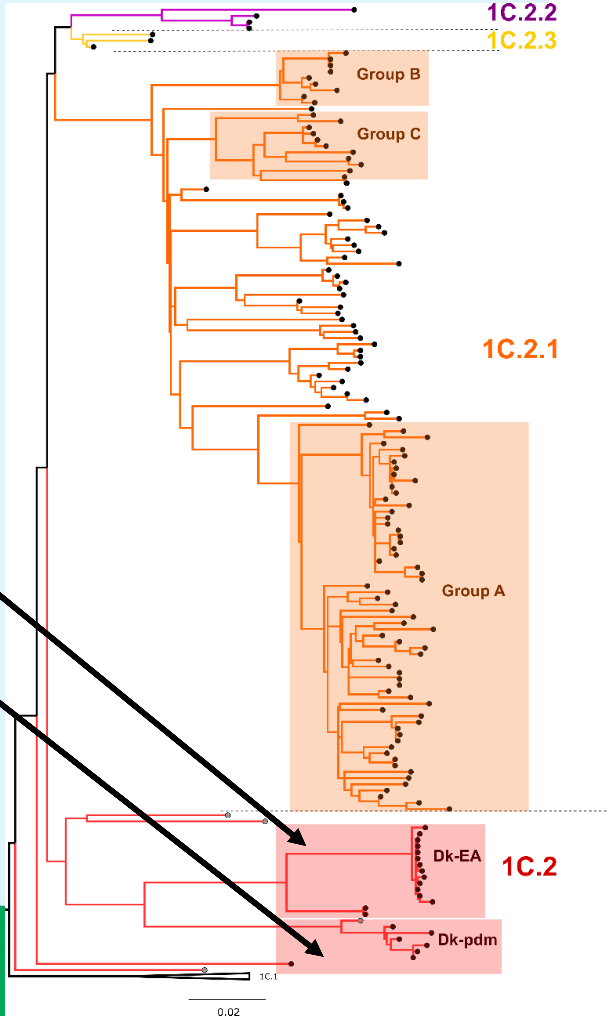
Amélie Chastagner [1], Séverine Hervé [1], Stéphane Quéguiner [1], Edouard Hirchaud [2], Pierrick Lucas [2], Stéphane Gorin [1], Véronique Béven [2], Nicolas Barbier [1], Céline Deblanc [1], Yannick Blanchard [2] and Gaëlle Simon [1,*]



Lineage	HA (clade)	NA		PB2	PB1	PA	NP	M	NS
$H1_{av}N1$	🟥 1C.2.1	🟥		🟥	🟥	🟥	🟥	🟥	🟥
$H1N1_{pdm}$	🟫 1A.3.3.2	🟫		🟫	🟫	🟫	🟫	🟫	🟫
$H1_{hu}N2$	🟦 1B.1.2.3	🟦		🟥	🟥	🟥	🟥	🟥	🟥
$H1_{hu}N2_{\Delta146\text{-}147}$	1B.1.2.3	🟦		🟥	🟥	🟥	🟥	🟥	🟥
H3N2	🟩	🟩		🟥	🟥	🟥	🟥	🟥	🟥
$H1_{hu}N2$	🟦 1B.1.2.3	🟩		🟥	🟥	🟥	🟥	🟥	🟥
$H1_{hu}N1$	🟦 1B.1.2.3	🟥		🟥	🟥	🟥	🟥	🟥	🟥
H3N2	🟩	🟩		🟫	🟫	🟫	🟫	🟫	🟫
$H1_{av}N2$ (#A)	🟥 1C.2.1	🟦		🟥	🟥	🟥	🟥	🟥	🟥
$H1_{av}N2$ (#B)	🟥 1C.2.1	🟩		🟥	🟥	🟥	🟥	🟥	🟥
$H1_{av}N2$ (#C)	🟥 1C.2.1	🟨		🟥	🟥	🟥	🟥	🟥	🟥
$H1_{av}N2$ (#D)	🟥 1C.2.1	🟨		🟥	🟥	🟥	🟥	🟫	🟥
$H1_{av}N2$ (#E)	⬜ 1C.2	🟩		⬜	⬜	⬜	⬜	⬜	⬜
$H1_{av}N2$ (#F)	⬜ 1C.2	🟩		🟫	🟫	🟫	🟫	🟫	🟫
$H1_{pdm}N1$	🟫 1A.3.3.2	🟥		🟥	🟥	🟥	🟥	🟥	🟥
$H1_{av}N1$	🟥 1C.2.1	🟥		🟥	🟥	🟥	🟥	⬜	🟥
$H1N1_{pdm}$	🟫 1A.3.3.2	🟫		🟥	🟥	🟥	🟥	🟥	🟥
$H1_{pdm}N2$	🟫 1A.3.3.2	🟩		🟫	🟫	🟫	🟫	🟫	🟫



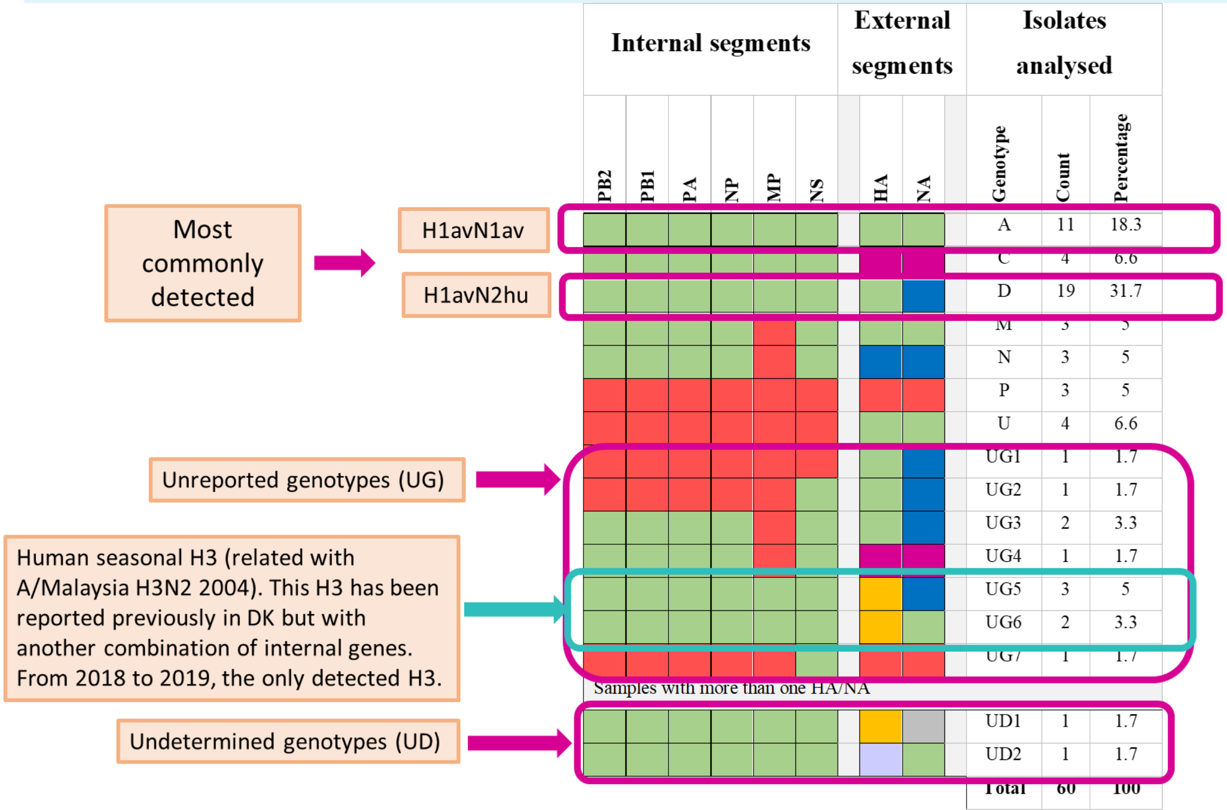
- 🟥 **EA 1C.2.1/EA**
- ⬜ **EA 1C.2/DK**
- 🟦 **Scotland/94 ($H1_{hu}N2$)**
- 🟩 **Gent/84 (H3N2)**
- 🟨 **Seasonal-like H3N2** (2003)
- 🟫 **pdm**



2017-2020 surveillance in Spain

Courtesy of G.E. Martin-Valls and E.M. Mateu de Antonio, UAB

- The number of lineages of H and N and their combinations are increasing.
- $H1_{av}N2$, undetected until 2017, is now the most prevalent lineage.
- 7 new genotypes undetected in Watson et al., 2015 are present now in Spain.
- When H1pdm and N1pdm represents only 6% of the isolates, regarding internal genes, the proportion is increased up to 30%.
- H3 Gent 84 has been replaced by **H3 Malaysia 2004**, in a different combination of internal genes if compared with the DK strain published in 2017.



Most commonly detected

H1avN1av

H1avN2hu

Unreported genotypes (UG)

Human seasonal H3 (related with A/Malaysia H3N2 2004). This H3 has been reported previously in DK but with another combination of internal genes. From 2018 to 2019, the only detected H3.

Undetermined genotypes (UD)

Internal segments						External segments		Isolates analysed		
PB2	PB1	PA	NP	MP	NS	HA	NA	Genotype	Count	Percentage
🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	A	11	18.3
🟩	🟩	🟩	🟩	🟩	🟩	🟪	🟪	C	4	6.6
🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟦	D	19	31.7
🟩	🟩	🟩	🟩	🟥	🟩	🟩	🟩	M	3	5
🟩	🟩	🟩	🟩	🟥	🟩	🟦	🟦	N	3	5
🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	P	3	5
🟥	🟥	🟥	🟥	🟥	🟥	🟩	🟩	U	4	6.6
🟥	🟥	🟥	🟥	🟥	🟥	🟩	🟦	UG1	1	1.7
🟥	🟥	🟥	🟥	🟥	🟩	🟩	🟦	UG2	1	1.7
🟩	🟩	🟩	🟩	🟥	🟩	🟩	🟦	UG3	2	3.3
🟩	🟩	🟩	🟩	🟥	🟩	🟪	🟪	UG4	1	1.7
🟩	🟩	🟩	🟩	🟩	🟩	🟧	🟦	UG5	3	5
🟩	🟩	🟩	🟩	🟩	🟩	🟧	🟩	UG6	2	3.3
🟥	🟥	🟥	🟥	🟥	🟩	🟥	🟥	UG7	1	1.7
Samples with more than one HA/NA										
🟩	🟩	🟩	🟩	🟩	🟩	🟧	▨	UD1	1	1.7
🟩	🟩	🟩	🟩	🟩	🟩	⬜	🟩	UD2	1	1.7
								Total	**60**	**100**

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ORIGINAL ARTICLE

Diversity of influenza A viruses retrieved from respiratory disease outbreaks and subclinically infected herds in Spain (2017–2019)

Silvana Sosa Portugal[1] | Martí Cortey[1] | Montserrat Tello[1] | Carlos Casanovas[2] | Susana Mesonero-Escuredo[2] | Sergio Barrabés[2] | Pilar Pineda[1] | Silke Wacheck[3] | Gerard Martín-Valls[1] | Enric Mateu[1,4]

- **H1hu :**

1B.1.2 (C)
1B.1.2.1 (C, D, UG3)

- **H1av :**

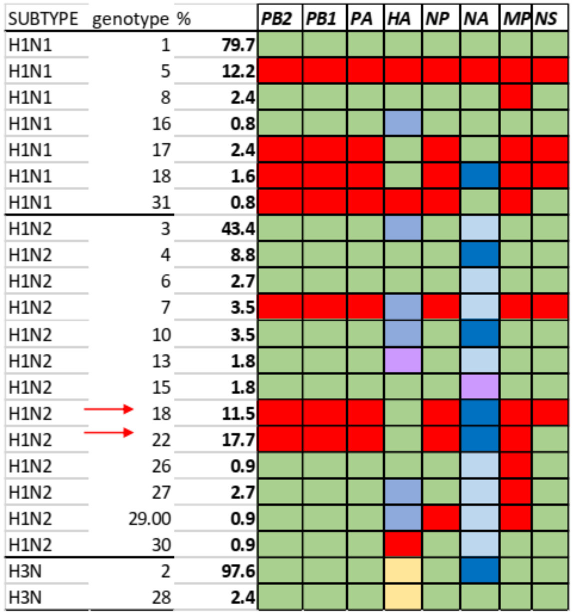
1C.2 (UG1)
1C.2.1 (A, D, M, U, UD2, UG2,UG3)
1C.2.2 (A, D, M)

2019-2020 surveillance in Italy

Courtesy of C. Chiapponi, ISZLER and A. Fusaro - M. S. Beato, IZSVE

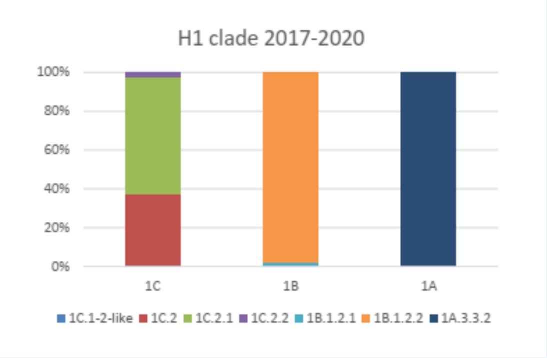
- Increasing number of genotypes - Highest diversity among H1N2 subtype
- H1 from clades A, B, C – Highest diversity among HA-1C
- Novel reassortants derived from A/sw/Italy/4675/2003-like $H1_{hu}N2$ with a **N2 derived from A/HK/2080/1997 H3N2**

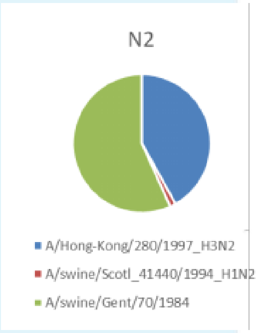
277 STRAINS



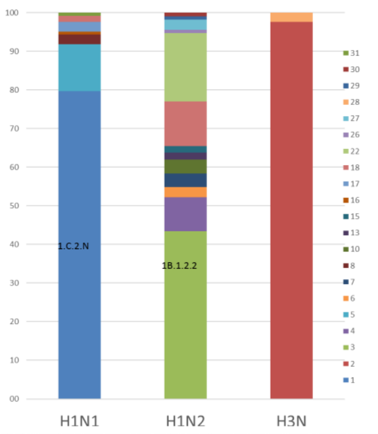
SUBTYPE	genotype	%	*PB2*	*PB1*	*PA*	*HA*	*NP*	*NA*	*MP*	*NS*
H1N1	1	**79.7**	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
H1N1	5	**12.2**	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥
H1N1	8	**2.4**	🟩	🟩	🟩	🟩	🟩	🟩	🟥	🟩
H1N1	16	**0.8**	🟩	🟩	🟩	▨	🟩	🟩	🟩	🟩
H1N1	17	**2.4**	🟥	🟥	🟥	🟩	🟥	🟩	🟥	🟥
H1N1	18	**1.6**	🟥	🟥	🟥	🟩	🟥	🟦	🟥	🟥
H1N1	31	**0.8**	🟥	🟥	🟥	🟥	🟥	🟩	🟥	🟩
H1N2	3	**43.4**	🟩	🟩	🟩	▨	🟩	▢	🟩	🟩
H1N2	4	**8.8**	🟩	🟩	🟩	🟩	🟩	🟦	🟩	🟩
H1N2	6	**2.7**	🟩	🟩	🟩	🟩	🟩	▢	🟩	🟩
H1N2	7	**3.5**	🟥	🟥	🟥	▨	🟥	▢	🟥	🟥
H1N2	10	**3.5**	🟩	🟩	🟩	▨	🟩	🟦	🟩	🟩
H1N2	13	**1.8**	🟩	🟩	🟩	🟪	🟩	▢	🟩	🟩
H1N2	15	**1.8**	🟩	🟩	🟩	🟩	🟩	🟪	🟩	🟩
H1N2	→ 18	**11.5**	🟥	🟥	🟥	🟩	🟥	🟦	🟥	🟥
H1N2	→ 22	**17.7**	🟥	🟥	🟥	🟩	🟥	🟦	🟥	🟩
H1N2	26	**0.9**	🟩	🟩	🟩	🟩	🟩	▢	🟥	🟩
H1N2	27	**2.7**	🟩	🟩	🟩	▨	🟩	▢	🟥	🟩
H1N2	29.00	**0.9**	🟩	🟩	🟩	▨	🟥	▢	🟥	🟩
H1N2	30	**0.9**	🟩	🟩	🟩	🟥	🟩	▢	🟩	🟩
H3N	2	**97.6**	🟩	🟩	🟩	🟨	🟩	🟦	🟩	🟩
H3N	28	**2.4**	🟩	🟩	🟩	🟨	🟩	🟩	🟩	🟩

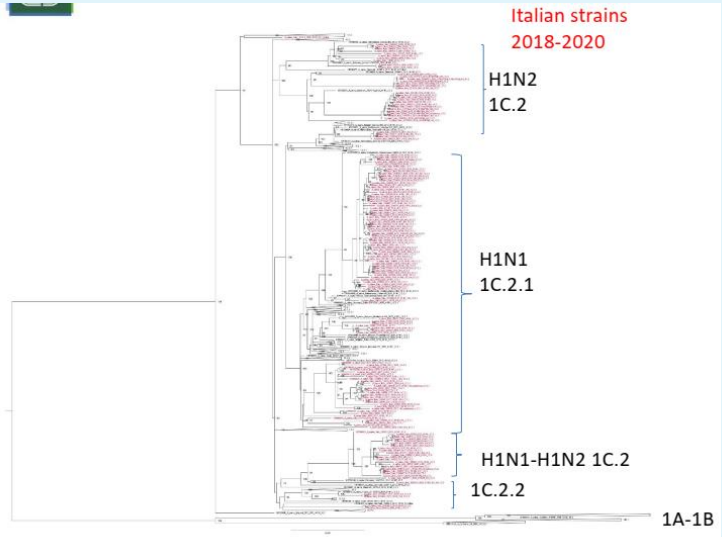
pdm	🟥
av-like	🟩
HU-LIKE-Italy-4675-2003	▨
A/swine/Scotland/410440/1994-like H1huN2	🟪
SW-H3N2-GENT-84	🟦
HU-LIKE-Hong-Kong-1997_H3N2	▢
SW-H3	🟨





H1N1: 7 GENOTYPES
H1N2: 13 GENOTYPES
H3N: 2 GENOTYPES





2018-2020 surveillance in Hungary

Courtesy of A. Dam

- 457 submissions – 18.6% positive farms from 13/19 counties
- 58 partial HA/NA subtyping: **HA-1A, 1B, 1C – No H3 strains**

				5x	H1avN1			
	11x	H1avN1		4x	H1N1 pdm09		7x	H1avN1
2018	2x	H1huN2	2019	5x	H1huN2	2020	8x	H1huN2
	1x	H1N1pdm09		1x	**rH1avN2sw**		5x	H1N1pdm09
	1x	H1avNx		1x	**rH1huN2 (seasonal H3N2)**		1x	HxN1
				1x	**rH1avN1 (internal pdm09)**			in proces
				2x	H1avNx			
				1x	H1pdm09Nx			
				1x	HxN1			

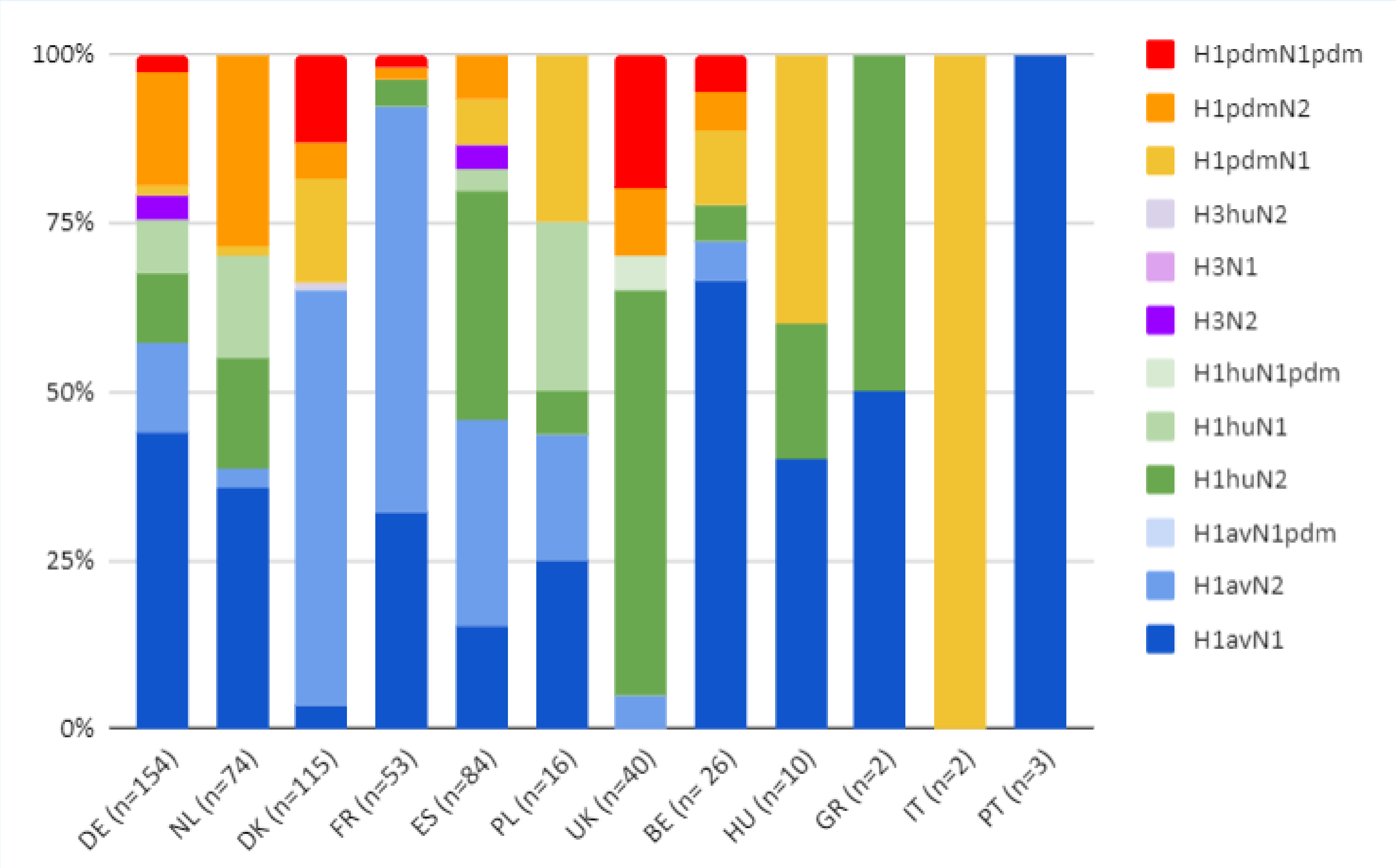
- WGS

Collection date	Samples origin	Type	Isolate, sample name	Seq name	H1 clade
2019.07.16	virus isolate CEVA	rH1avN1 (pdm09 internal genes)	D5015/8/19	HU-82	1C.2.1
2019.07.29	virus isolate CEVA	rH1avN2Gent84	D5015/10/19	HU-85	1C.2
2019.05.14	virus isolate CEVA	rH1avN2hu (seasonal H3N2 mid 90')	D5015/12/19	HU-77	1C.2
2018.04.26	tissue sample	H1avN1	SCG-1/18	HU-64	1C.2.1

Ceva Influenza Diagnostic

Courtesy of Kathrin Lillie-Jaschniski

Detected sub-types Jan-Sept 2020 (579 positive farms)



« SIV EU network »

- Driven by Ceva
- **9 public institutes from 8 EU countries**
- **Main objectives**:
  - increase sharing of surveillance data
  - diagnostic tools and flows
  - scientific forum for discussions (incl. vaccination)

- **Engage with OFFLU for established linkages?**
  - EU regional sub-group?
  - EU contribution to the WHO Vaccine Composition Meetings?
  - Take part to some OFFLU discussions?

offlu

OIE FAO

network of expertise on animal influenza