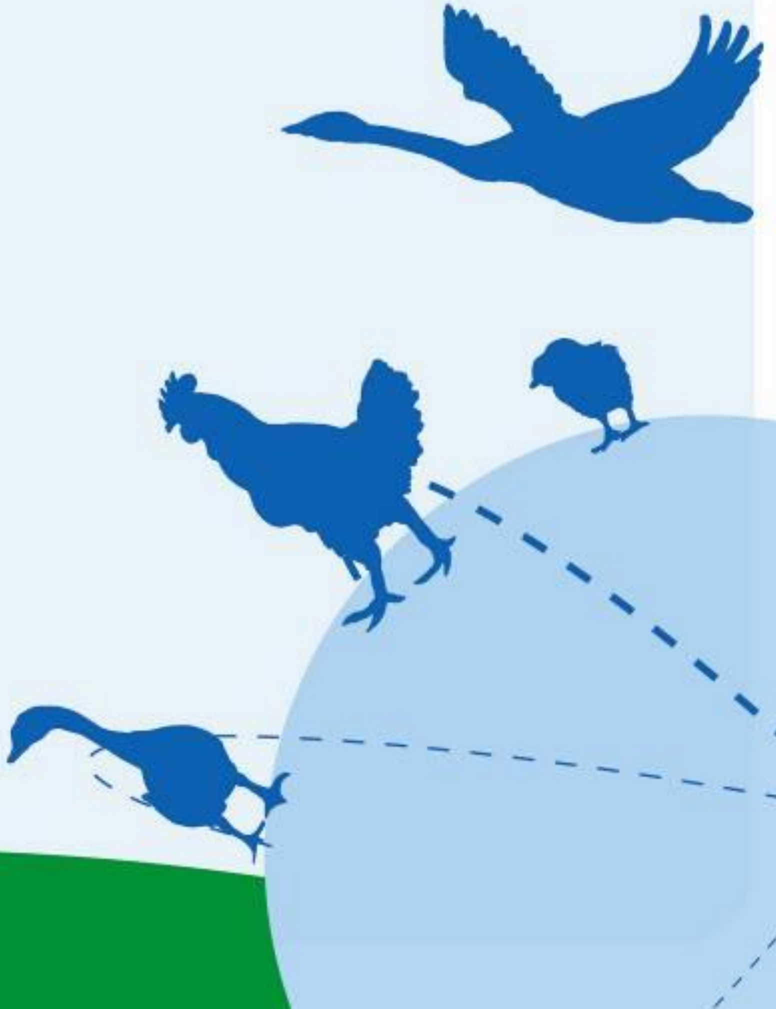
# *OFFLU virtual SIV group meeting*

## *9 December 2020*



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## Title of presentation

# Subtypes of swIAV isolated in Belgium and the Netherlands (2014 – 2020)

| Isolate subtype | Isolate lineage | Number of isolates per year | | | | | | | Total |
|---|---|---|---|---|---|---|---|---|---|
| | | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | |
| H1N1 | H1avN1av | 9 | 3 | 1 | 4 | 9 | 14 | 16 | **56** |
| | H1pdmN1av | | | | | 1 | | | **1** |
| | H1pdmN1pdm | | | | | | 1 | 7 | **8** |
| H1N2 | H1huN2 | 5 | | 1 | 1 | 8 | 9 | 8 | **32** |
| | H1avN2 | | | | 1 | | 1 | | **2** |
| | H1pdmN2 | 1 | | | | | 2 | | **3** |
| H3N2 | H3huN2 | 8 | | | 2 | 4 | 4 | 1 | **19** |
| Positive samples | | 23 | 3 | 2 | 8 | 22 | 31 | 32 | **121** |
| Total number of samples | | 51 | 11 | 3 | 24 | 58 | 53 | 59 | **259** |

# HA subtype of swIAV isolated in Belgium and the Netherlands (2014 – 2020)

| Isolate subtype | Isolate lineage | Number of isolates per year | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | **Total** |
| H1N1 | H1av | 9 | 3 | 1 | 5 | 9 | 15 | 16 | **58** |
| | H1pdm | 1 | | | | 1 | 3 | 7 | **12** |
| H1N2 | H1hu | 5 | | 1 | 1 | 8 | 9 | 8 | **32** |
| H3N2 | H3hu | 8 | | | 2 | 4 | 4 | 1 | **19** |
| Positive samples | | 23 | 3 | 2 | 8 | 22 | 31 | 32 | **121** |
| Total number of samples | | 51 | 11 | 3 | 24 | 58 | 53 | 59 | **259** |

# Genotypes of H1swIAV isolated in Belgium and the Netherlands (2014-2019)

| | | Surface genes | | Internal genes | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| **Virus isolate** | **Subtype** | **HA** | **NA** | **PB** | **PB** | **PA** | **NP** | **M** | **NS** |
| A/swine/Gent/30/2014* | H1N2 | 🟪 | 🟦 | 🟩 | 🟩 | 🟩 | 🟩 | ⬛ | 🟩 |
| A/swine/Netherlands/Gent-62/2015 | H1N1 | 🟩 | 🟩 | 🟩 | 🟩 | 🟩 | 🟩 | ⬛ | 🟩 |
| A/swine/Gent/173/2015 | H1N1 | 🟩 | 🟩 | 🟩 | 🟩 | 🟩 | 🟩 | ⬛ | 🟩 |
| A/swine/Gent/36/2016 | H1N2 | 🟪 | 🟪 | 🟩 | 🟩 | 🟩 | 🟩 | ⬛ | 🟩 |
| A/swine/Gent/150/2016 | H1N1 | 🟩 | 🟩 | 🟩 | 🟩 | 🟩 | 🟩 | ⬛ | 🟩 |
| A/swine/Gent/121/2018* | H1N1 | ⬛ | 🟩 | 🟩 | 🟩 | 🟩 | 🟩 | ⬛ | 🟩 |
| A/swine/Gent/196/2018 | H1N1 | 🟩 | 🟩 | 🟩 | 🟩 | 🟩 | 🟩 | ⬛ | 🟩 |
| A/swine/Gent/233/2018 | H1N2 | 🟪 | 🟪 | 🟩 | 🟩 | 🟩 | 🟩 | ⬛ | 🟩 |
| A/swine/Gent/241/2018 | H1N1 | 🟩 | 🟩 | 🟩 | 🟩 | 🟩 | 🟩 | ⬛ | 🟩 |
| A/swine/Gent/05/2019 | H1N1 | 🟩 | 🟩 | 🟩 | 🟩 | 🟩 | 🟩 | ⬛ | 🟩 |
| A/swine/Gent/53/2019 | H1N1 | ⬛ | ⬛ | ⬛ | ⬛ | ⬛ | ⬛ | ⬛ | ⬛ |
| A/swine/Gent/54/2019* | H1N2 | 🟩 | 🟪 | 🟩 | 🟩 | 🟩 | 🟩 | ⬛ | 🟩 |
| A/swine/Gent/114/2019 | H1N2 | 🟪 | 🟪 | 🟩 | 🟩 | 🟩 | 🟩 | ⬛ | 🟩 |
| A/swine/Gent/178/2019 | H1N2 | 🟪 | 🟪 | 🟩 | 🟩 | 🟩 | 🟩 | ⬛ | 🟩 |
| A/swine/ Netherlands/Gent-193/2019 | H1N1 | 🟩 | 🟩 | 🟩 | 🟩 | 🟩 | 🟩 | 🟩 | 🟩 |
| A/swine/Gent/203/2019 | H1N1 | 🟩 | 🟩 | 🟩 | 🟩 | 🟩 | 🟩 | ⬛ | 🟩 |
| A/swine/Gent/220/2019 | H1N2 | ⬛ | 🟪 | ⬛ | ⬛ | ⬛ | ⬛ | ⬛ | ⬛ |
| A/swine/Gent/235/2019 | H1N2 | ⬛ | 🟪 | ⬛ | ⬛ | ⬛ | ⬛ | ⬛ | ⬛ |

🟩 H1avN1 🟪 H1huN2 ⬛ H1pdm09 🟦 H3huN2 * New genotypes

OIE FAO
network of expertise on animal influenza

# Human Infection with a Eurasian Avian-like Swine Influenza A (H1N1) Virus, the Netherlands, September 2019

Parys A, Vandoorn E, King J, Graaf A, Pohlmann A, Beer M, Harder T, and Van Reeth K - EID Volume 27, Number 3, March 2021

- A swine influenza A virus (swIAV) was isolated from a farmer and his pigs
- **Antigenic characterisation** (VN): Both isolates were related to Eurasian avian-like swIAVs and pH1N1
- **Genetic characterisation** (Multiplex real-time RT-PCR and whole genome next generation sequencing): All segments were closely related to Eurasian avian-like swIAVs, HA1 clade 1C.2.2