

A decade of swine influenza surveillance and the first report of an H1N2v case in Great Britain

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Outline



1. The Swine Influenza surveillance programme in Great Britain (GB)
2. Update on GB swIAV genetic diversity
3. H1N2 1B.1.1 viruses and the first reported H1N2v human case in GB
4. Conclusions and perspectives

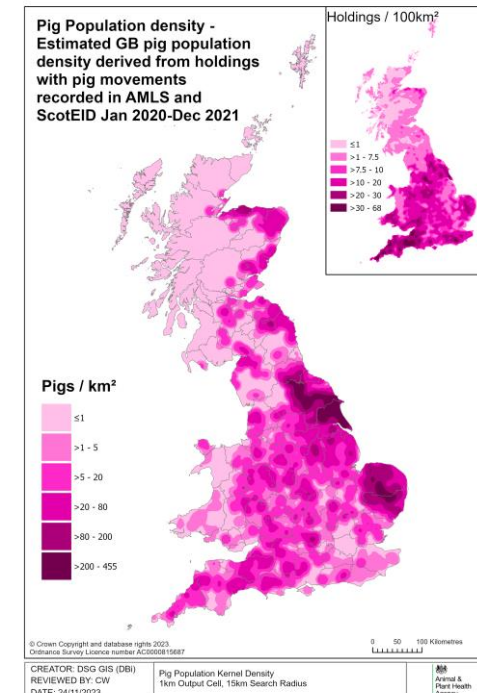
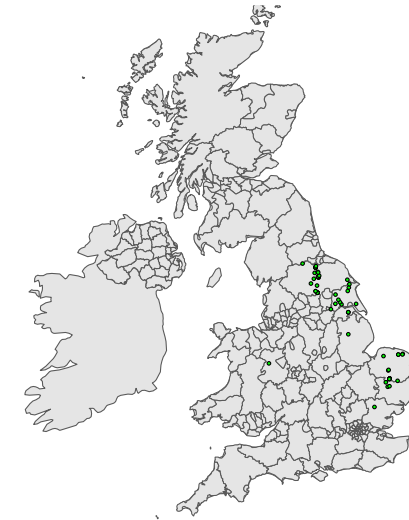
GB swine influenza surveillance

GB swine influenza surveillance allows

- sample submission based on clinical criteria
- Defra-funded molecular testing and virus isolation

On-farm surveillance allows for nasal swabs to be tested from 12 pigs in an affected epidemiological group or submission of up to 3 carcasses for pathology assessment and sampling

Swine influenza is not notifiable and not reportable and diagnostic sample submission to APHA is voluntary



GB Testing guidance:

<http://apha.defra.gov.uk/documents/surveillance/diseases/Swine%20influenza%20surveillance%20vets%20Dec2020.pdf>

APHA Diagnostic pipeline

2024 - OFFLU Swine Influenza virus Technical Meeting



Diagnostic sampling

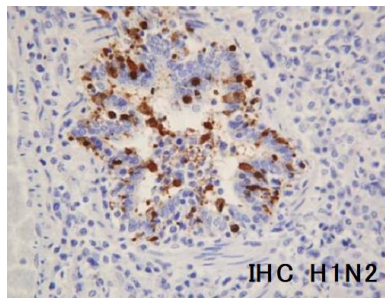


Nasal swabs from live pigs or respiratory tissues at PM



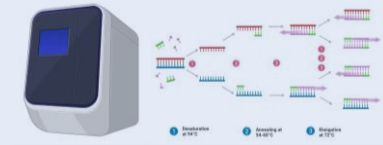
Immunohistochemistry (NP)

Tissues from suspected swine influenza cases based on lung histopathology (PCR for acute lesions only)

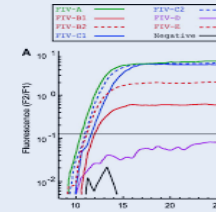


Molecular testing

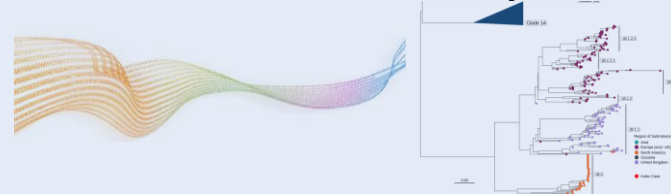
M-gene PCR



HA/NA Subtyping RRT-PCR



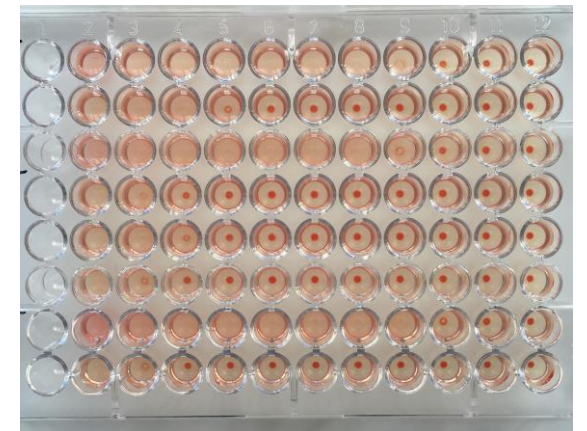
WGS and analysis



Virus isolation

Serology

Antibody detection by ELISA (influenza A) or HAIT (four strains)

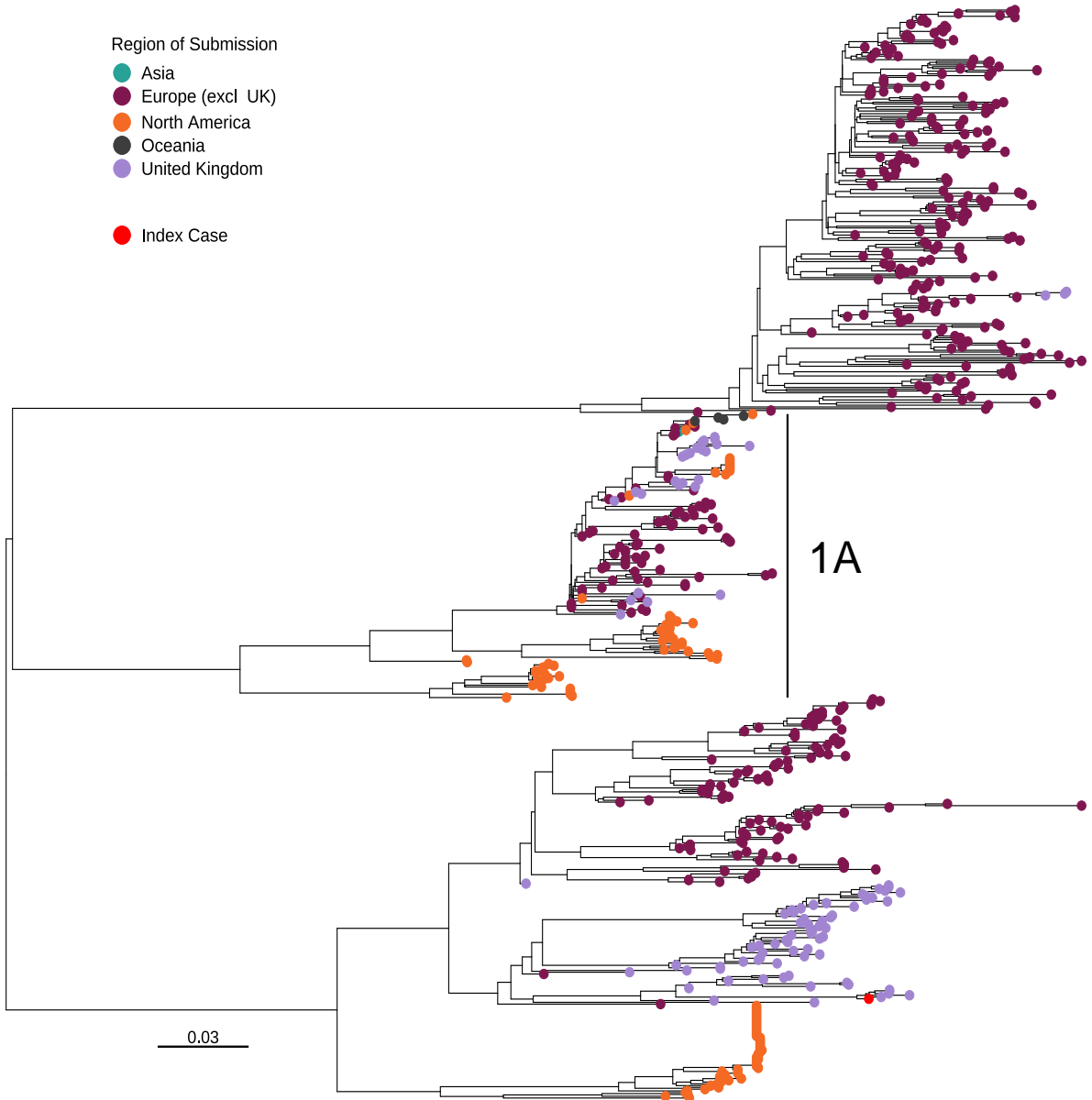


Global SwIAV H1 genetic diversity (subset 2006-2023)

Region of Submission

- Asia
- Europe (excl UK)
- North America
- Oceania
- United Kingdom

● Index Case



1C

- Three distinct clades predominate in GB
 - 1A.3.3.2 (H1pdm09)
 - 1B.1.1 (H1hu)
 - 1C.2.2 (H1av)

- Phylogenetic analysis of the HA gene suggests multiple re-introductions of human-origin 1A.3.3.2 viruses into pigs
- The H1B.1.1 lineage has only been maintained in GB. 1B.1.X viruses continue to diversify in pig populations in continental Europe
- No swine-adapted H3N2 viruses have been detected in GB since 1997

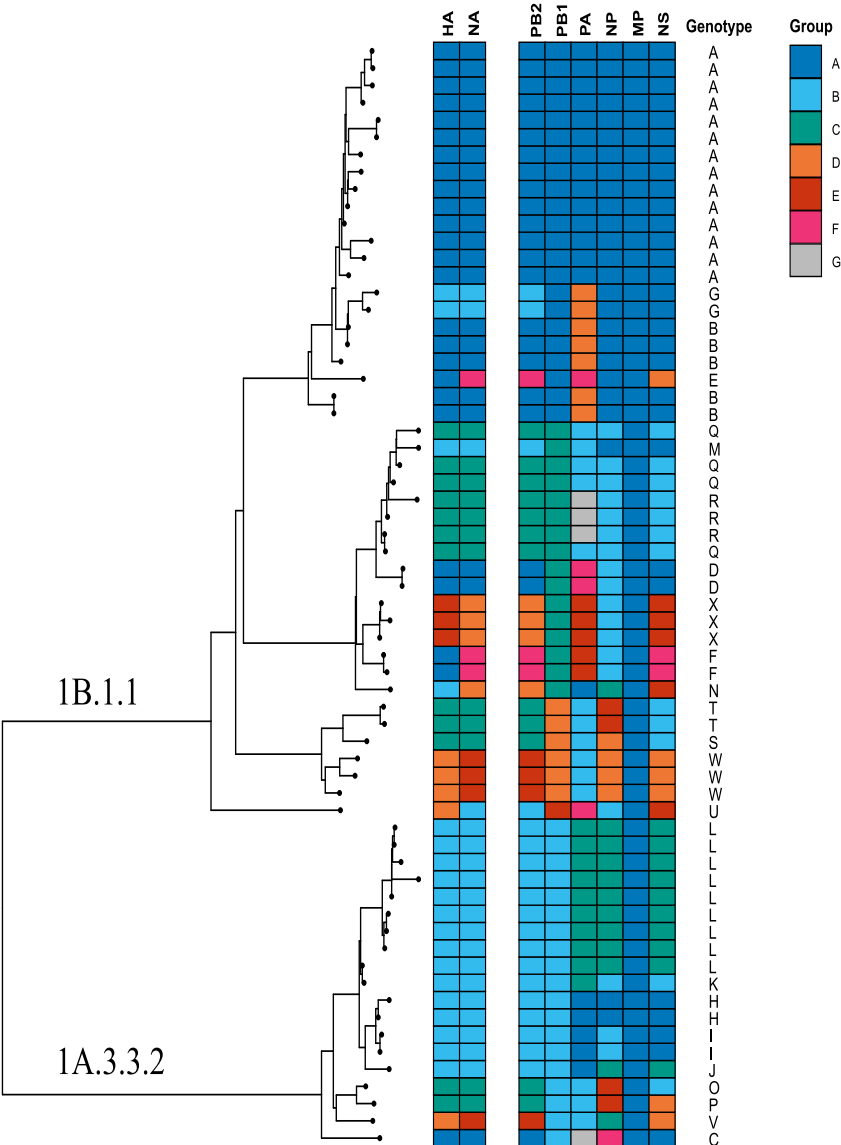
1B

1A

0.03

SwIAV H1 genetic diversity in GB

(subset 2014-2022)



- NA reassortment continues to occur but a majority of H1A+N1 and H1B+N2 viruses are detected
- Since 2012, only 1A.3.3.2 ‘internal genes’ have been detected (Octoflu)
- Genotypes were defined by sharing of a common node and monophyly within swine and greater than or equal to 75% ultrafast bootstrap support based on maximum-likelihood phylogenetic trees
- Within- and between clade average pairwise distance was calculated using MEGACC and setting between clade differences above 5% for HA and NA and above 3% for remaining genes

Subtype	HA	NA	PB2	PB1	PA	NP	MP	NS	#	%
H1N2	1B.1.1	N2s	pdm	pdm	pdm	pdm	pdm	pdm	42	65.6
H1N1	1B.1.1	pdm	pdm	pdm	pdm	pdm	pdm	pdm	03	4.7
H1N1	1A.3.3.2	pdm	pdm	pdm	pdm	pdm	pdm	pdm	13	20.3
H1N1	1A.3.3.2	EA-4	pdm	pdm	pdm	pdm	pdm	pdm	01	1.6
H1N2	1A.3.3.2	N2s	pdm	pdm	pdm	pdm	pdm	pdm	05	7.8

An H1N2v case reported in the UK

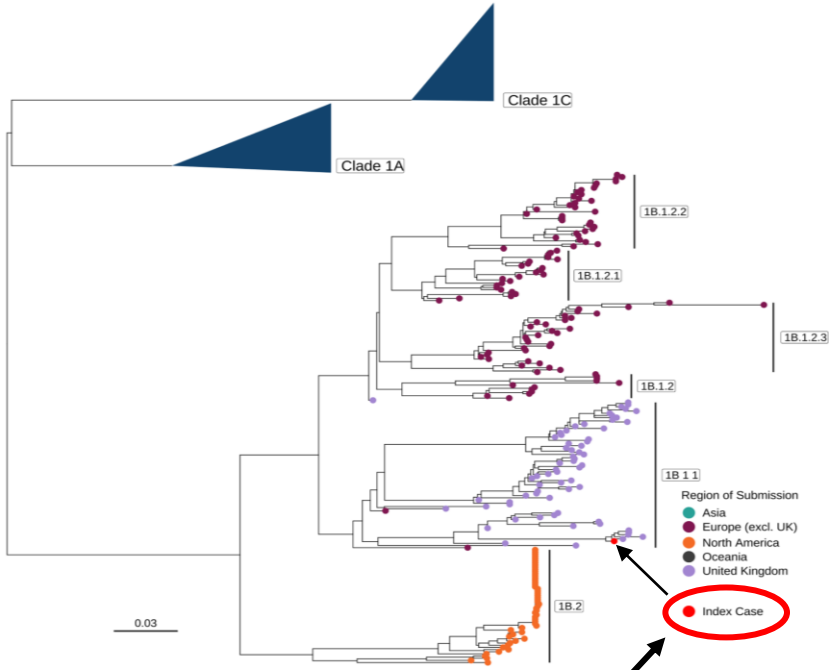


Table 8. EU Data: Hemagglutination inhibition of CVV vaccine ferret antisera against contemporary swine 1B lineage strains selected to represent clade consensus.

- >8 fold reduction
- 8 fold reduction
- 4 fold reduction

	Global Clade	US Clade	A/Michigan/383/2018 RG58A	A/Brazil/11/1978	A/Chile/1/1983
A/Michigan/383/2018 RG58A	1B.2.1	delta-2	640	160	80
A/Brazil/11/1978	seasonal		20	640	320
A/Chile/1/1983	seasonal		40	320	1280
A/swine/England/045393/2022	1B.1.1		40	80	10
A/swine/England/123045/2023	1B.1.1		20	40	10
A/swine/Belgium/Gent-117/2021	1B.1.2.1		80	640	640
A/swine/Italy/118638/2021*	1B.1.2.2		20	nt	40

- A sample confirmed as A(H1N2)v SwIAV was identified through community surveillance conducted by the UKHSA and RCGPs
- The case, a vaccinated elderly man from N. Yorkshire, did not require hospitalization and recovered from the infection
- Despite the case having no known pig contact, phylogenetic analysis identified a swIAV with an HA clustering with clade 1B.1.1 viruses and commonly associated N2 found in viruses prevalent in GB pig herds
- The internal gene cassette was derived from the 1A.3.3.2 (pdm09 lineage), similar to reassortants present in the UK since late 2009 and monitored through the Defra surveillance and research programmes (Howard et al., 2011; Everett et al., 2020)
- No A(H1N2)v isolate was obtained from the case or contacts, and APHA provided viruses characterised through IRL and OFFLU VCM activities
- A reference virus (A/swine/England/045393/2022), that was previously characterised in the Jan-Jun 2023 OFFLU report, was provided to Public Health and Academic stakeholders

Cogdale et al., 2024

[Eurosurveillance | A case of swine influenza A\(H1N2\)v in England, November 2023](https://www.eurosurveillance.org/ViewArticle.aspx?pubId=36942)

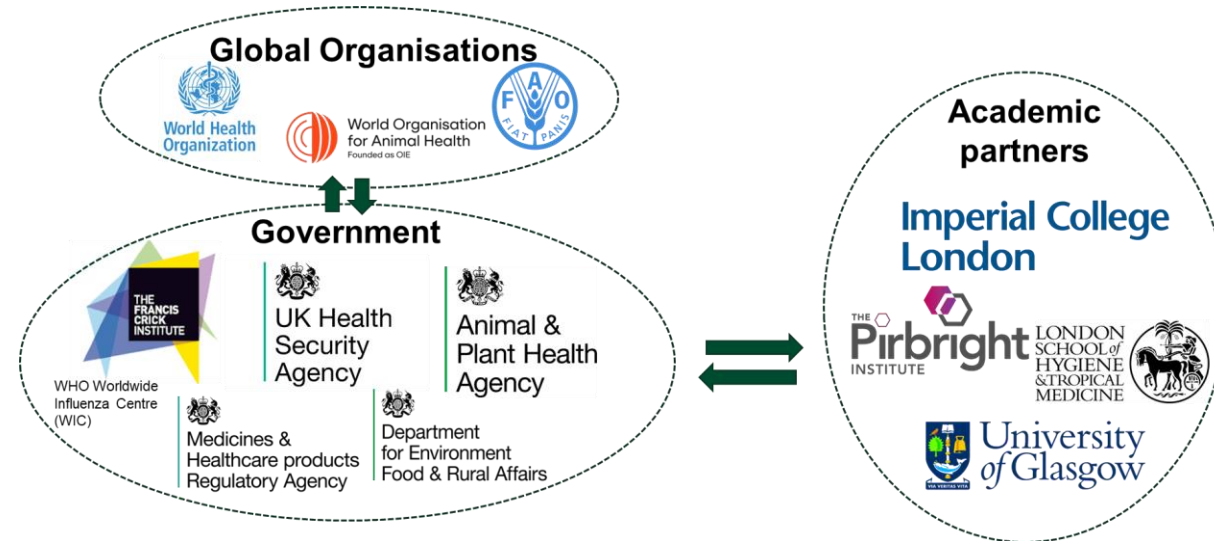
OFFLU Report Jan-Jun 2023

<https://www.offlu.org/wp-content/uploads/2023/10/OFFLU-vcm-swine-2023b.pdf>

Conclusions and future perspectives



- Clade 1B.1.1 (H1hu) and 1A.3.3.2 (H1pdm09) viruses predominate in GB, with sporadic 1C.2.2 detections
- An H1N2v case with 1B.1.1 HA has been reported in the UK
- Constant swIAV evolution in GB and globally necessitates ongoing surveillance to inform pandemic risk
- A One Health approach is needed to address spillover at the human-animal interface
- How can swine influenza control be improved in pig populations?



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Animal &
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Agency



<https://science.vla.gov.uk/fluglobalnet/>



ESFLU
European Swine
Influenza Network

<https://swineflu.eu/>



APHA

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