

Swine influenza update – Australia

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OFFLU SWINE INFLUENZA EXPERTS TECHNICAL MEETING
28 – 29 April 2026
WOAH Headquarters, Paris



Brief background

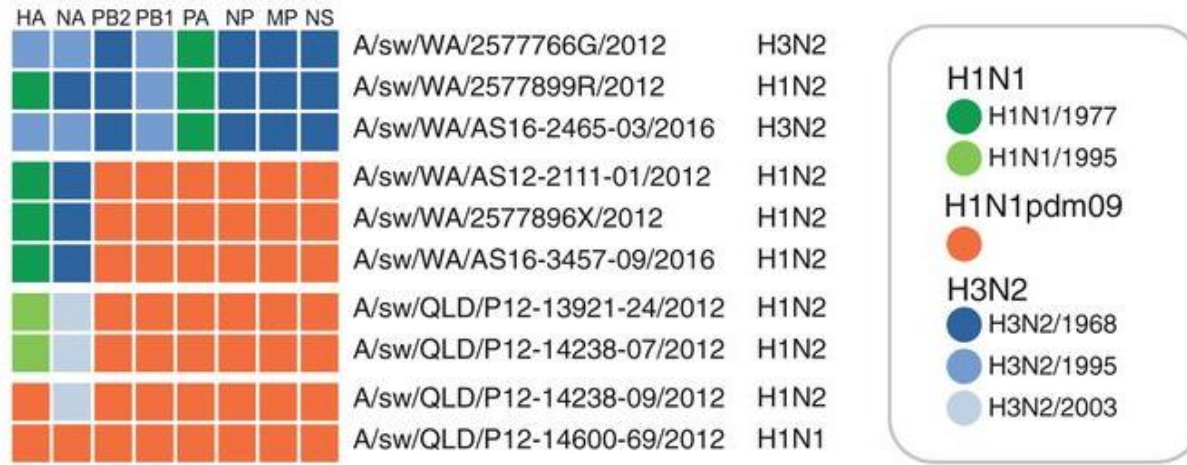
- Detection of influenza A in pigs is reportable in some Australian states¹
- The first confirmed IAV detection in Australian pigs occurred in 2009, following introduction of the H1N1pdm09 virus in humans
- In July-August 2012 (and 2016), unique H1N2 and H3N2 IAV reassortants were separately detected in commercial pigs in Western Australia and Queensland, consisting of genes derived from past human pandemic and seasonal IAV lineages
- These showed that some IAV gene lineages have been maintained in Australian pig populations for at least 50 years
- These IAVs continue to evolve in isolation in Australia, separate from other global swIAV populations
- Swine influenza surveillance in commercial/production pigs in Australia remains passive, with positive laboratory detections often opportunistic (there is a systematic knowledge gap)

Reference:

¹Animal Health Australia (2018). Response policy brief: Influenza A viruses in swine (Version 4.0). Australian Veterinary Emergency Plan (AUSVETPLAN), Edition 4, National Biosecurity Committee, Canberra, ACT



Snapshot of swine influenza virus diversity in Australia: 2012-2016



- H1N1, H1N2 and H3N2 subtypes have been detected, including various reassortant genotypes of:
- Other-human derived H1 clade “1B.3” viruses
- Other-human derived H1 clade “1B.2” viruses
- H1N1pdm09-origin clade 1A.3.3.2 viruses
- Clade 1990-like H3N2, and older and more recent Other-human H3N2 lineage clusters



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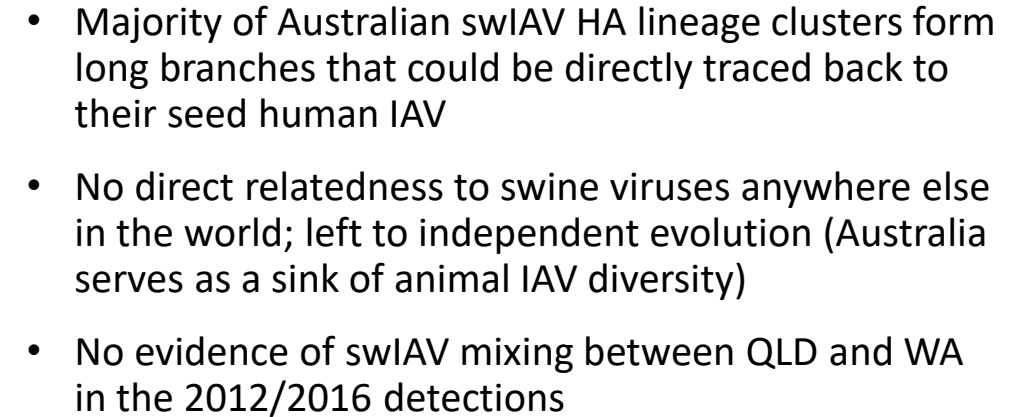
GENETIC DIVERSITY AND EVOLUTION

Divergent Human-Origin Influenza Viruses Detected in Australian Swine Populations

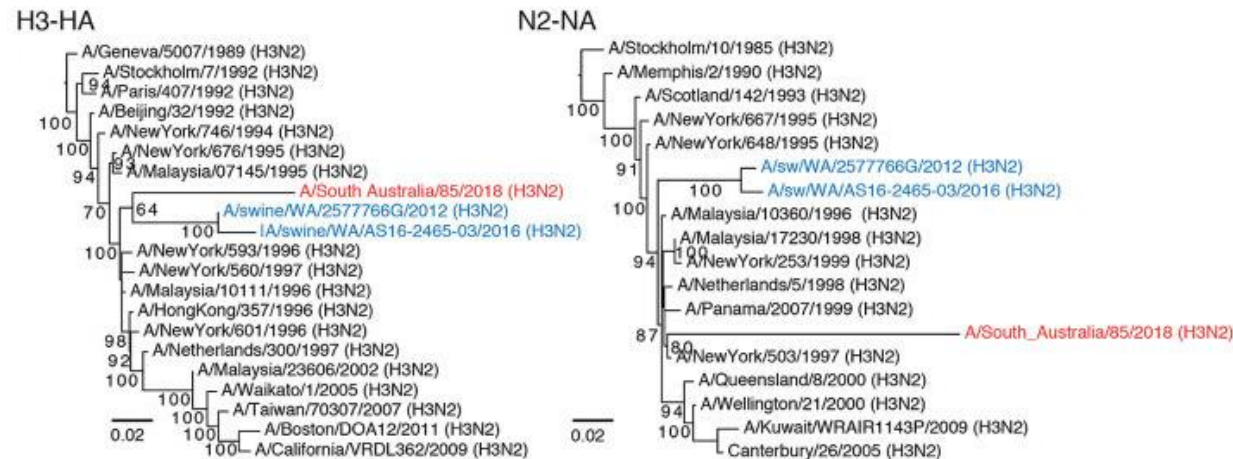


Reference: Wong FYK, Donato C, Deng Y-M, Teng D, et. al. 2018. Divergent human-origin influenza viruses detected in Australian swine populations. J. Virol 92:e00316-18.
<https://doi.org/10.1128/JVI.00316-18>





Variant H3N2v human cases in Australia: 2018 & 2021



- In September 2018, a case of human infection with a swine influenza virus was detected through routine human influenza virus surveillance by the WHO-CCRI Melbourne¹
- Patient was an adolescent female in South Australia who was unvaccinated in 2018, and had contact with animals at an agricultural show before onset of illness

A/South Australia/85/2018 (H3N2v) genome:

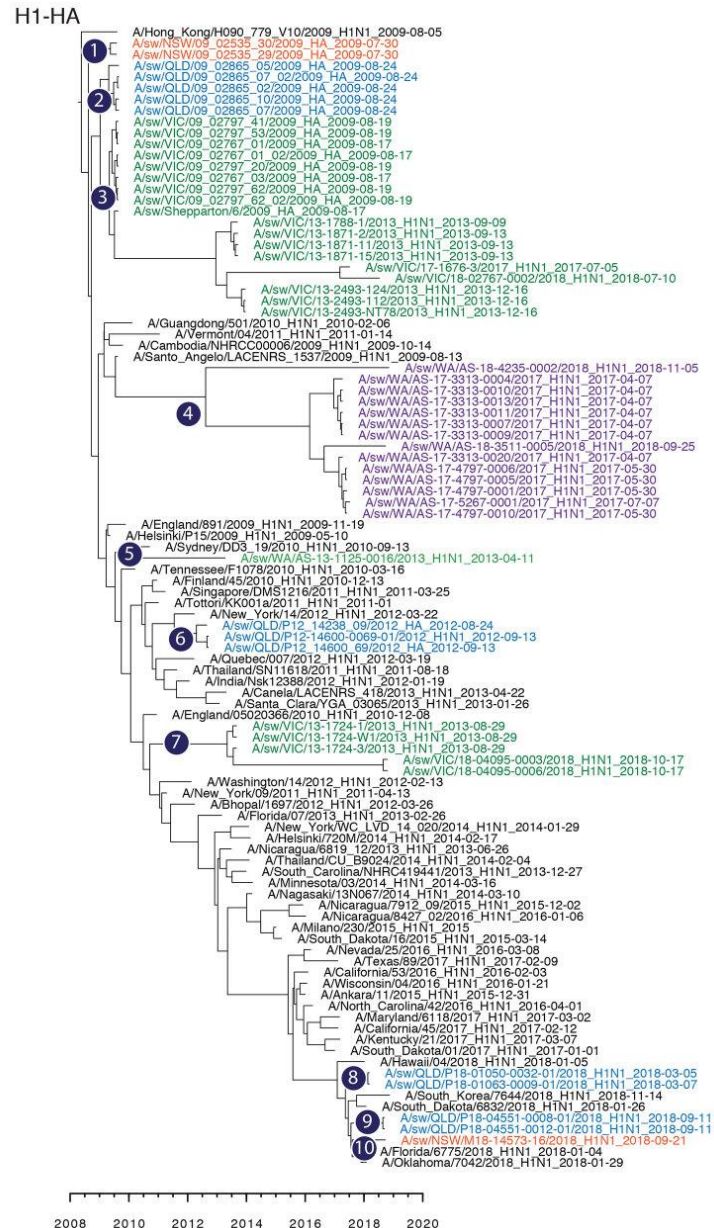
- HA and NA independently derived from clade 1990-like H3N2 viruses; most closely related to clade 1990-like H3-HA in WA pigs in 2012/2016
- Internal genes are clade 1A.3.3.2 H1 lineage, with 5 of 6 genes closest to a H1N1 virus detected in swine in VIC in that year (2018)
- In January 2021, a 10-yo male child in South Australia presenting with respiratory and gastrointestinal symptoms was also confirmed to be infected with a genetically related A(H3N2)v virus²
- There remains no IAV surveillance data from pigs in South Australia



References:

¹Deng Y, Wong F, Spirason N, Kaye M, Beazley R, Grau ML, et al. Locally Acquired Human Infection with Swine-Origin Influenza A(H3N2) Variant Virus, Australia, 2018. Emerg Infect Dis. 2020;26(1):143-147. <https://doi.org/10.3201/eid2601.191144>

²WHO Human-Animal Interface web page http://www.who.int/influenza/human_animal_interface/en/



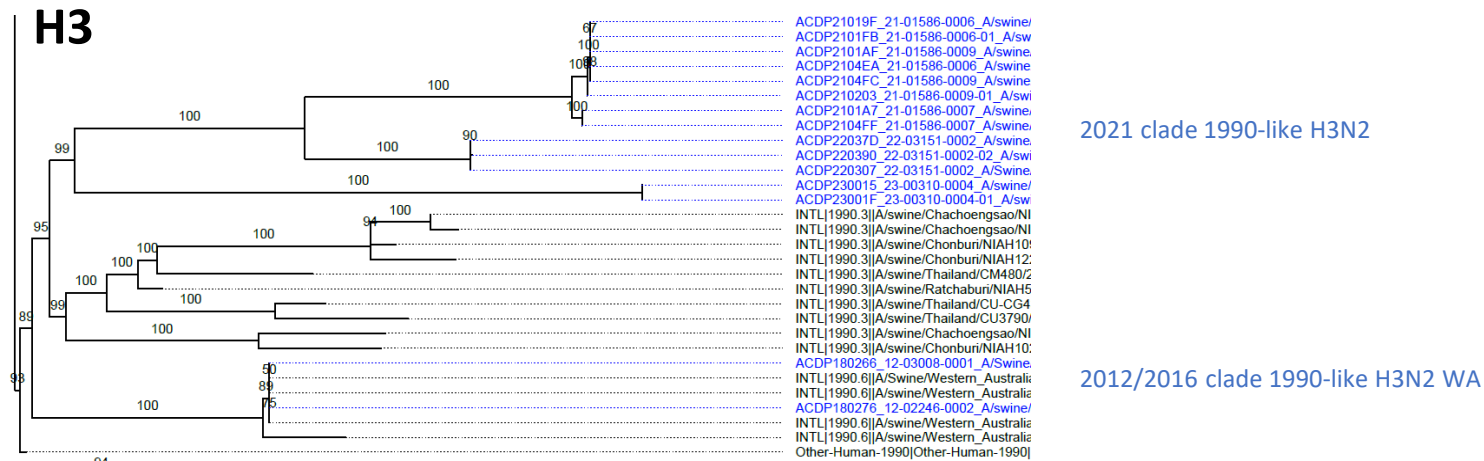
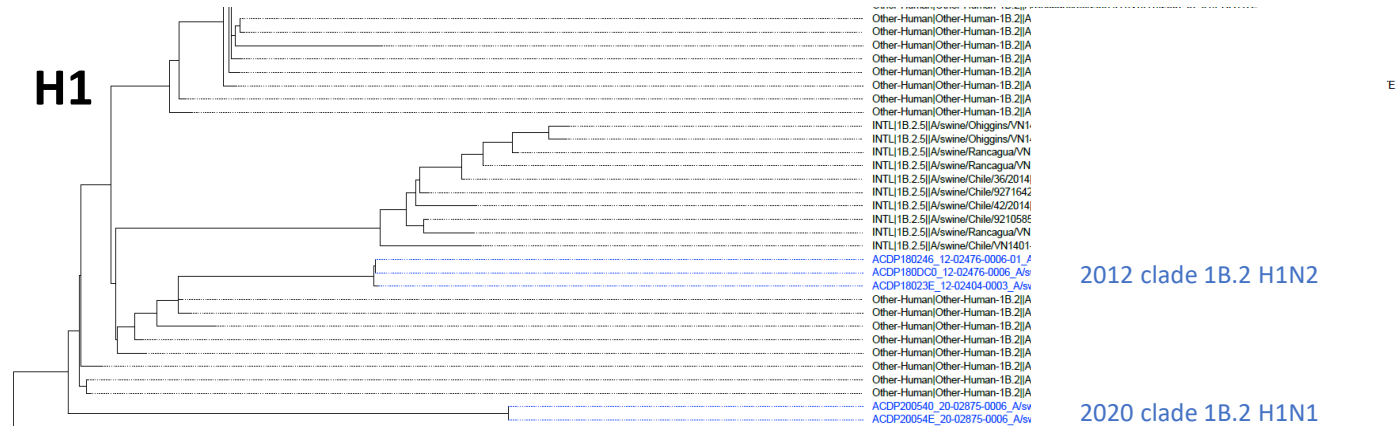
Widespread clade A1.3.3.2 H1N1 circulation in separated swine populations following independent spillovers from human seasonal H1N1



Reference:

¹Deng Y, Wong F, Spirason N, Kaye M, Beazley R, Grau ML, et al. Locally Acquired Human Infection with Swine-Origin Influenza A(H3N2) Variant Virus, Australia, 2018. *Emerg Infect Dis.* 2020;26(1):143-147. <https://doi.org/10.3201/eid2601.191144>

Continued co-circulation of independent clade 1B.x H1N2, H1N1 and other-human 1990-like H3N2 reassortants detected sporadically in different states



Closing Note

AN UPDATE OF INFLUENZA A IN AUSTRALIAN COMMERCIAL PIGGERIES

Current study by CSIRO-ACDP with swine producers in Australian east coast

- Serology testing of 420 serum samples collected in October 2025 from healthy fit-to-load market progeny (22-24 weeks) or culled sows
- Utilized serum samples from abattoir collections in 2025 collected from seven farms in southeastern Australia
- IAV seropositivity was detected in samples from healthy fit-to-load market progeny, with culled sows sampled within the same production flows also seropositive

Thank you

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