



OFFLU SWINE INFLUENZA REPORT

FEBRUARY 2020 TO SEPTEMBER 2020

SCOPE

In this document we present a summary of H1 and H3 swine influenza A virus evolution from 2018 to the present.

Swine influenza A viruses: Introduction, data sources and acknowledgements

Acknowledgements: Contributions were made from: USDA-ARS NADC: Amy Vincent, Tavis Anderson, Zebulun Arendsee, David Hufnagel, Katharine Young, Brian Kimble, Carine Kunzler-Souza; USDA-APHIS NVSL: Alicia Janas-Martindale, Mia Kim Torchetti, Rachel Tell, Karthik Shanmuganatham; APHA: Ian Brown, Steve Essen, Susan Collins, Nicola Lewis, Alexander Byrne; RVC: Nicola Lewis, Paris Patapiou. Phylogenetic and sequence analyses were performed at NADC and Royal Veterinary College (RVC). We are very grateful to the OFFLU Swine Group for their expertise and for sharing data. We acknowledge NIH-CEIRS, APHA, Istituto Zooprofilattico Sperimentale, and the USDA-APHIS IAV in Swine Surveillance Program for collection and sequencing of contemporary viruses. Antigenic data were generated by the Animal and Plant Health Agency (APHA), UK, and by the National Animal Disease Center (NADC), USDA-ARS, US. Ferret sera was kindly provided by the US-CDC.

Genetic and Antigenic Analyses - Brief Methods

Analyses were conducted by subtype and lineage or clade. Reference sequences and new data (deposited Jan 1, 2020 – June 30, 2020) were downloaded from GISAID or GenBank were aligned with MAFFT (Katoh and Standley, 2013) using default settings. Alignments for each segment were inspected manually and trimmed to the start and stop codon. Exploratory trees were run using FastTree (Price et al., 2009). Tabular comparisons between current CVVs or human seasonal vaccine strains and new swine data were generated using the NADC IAV bioinformatic toolkit (<https://github.com/flu-crew>). An HA1 consensus sequence was generated for each contemporary clade and the best matched strain was selected for testing against reference ferret antisera in hemagglutination inhibition (HI) assays. All HI assays were performed with ferret anti-sera and guinea pig red blood cells. H3N2 assays were performed with the addition of oseltamivir.

Global swine influenza A events in animals

Epidemiology

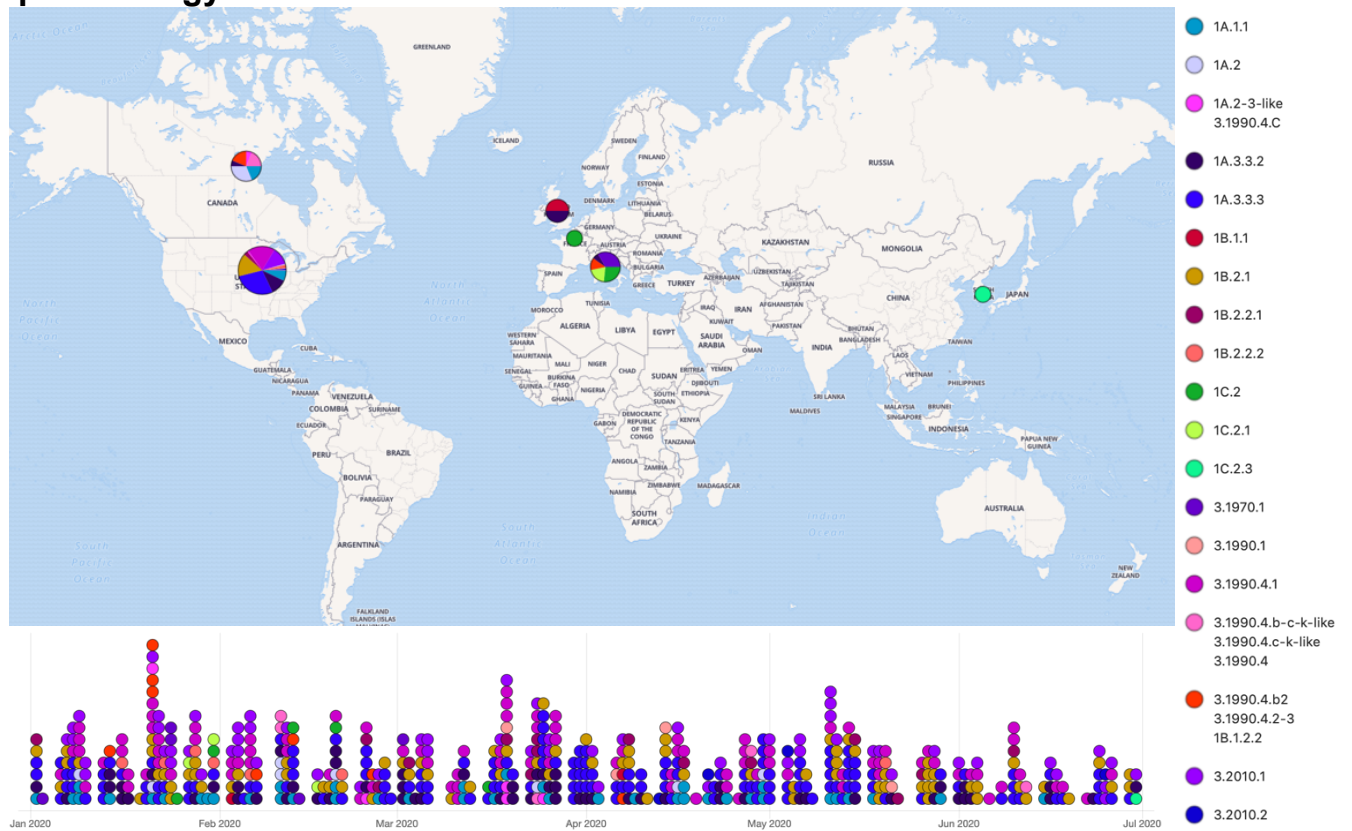
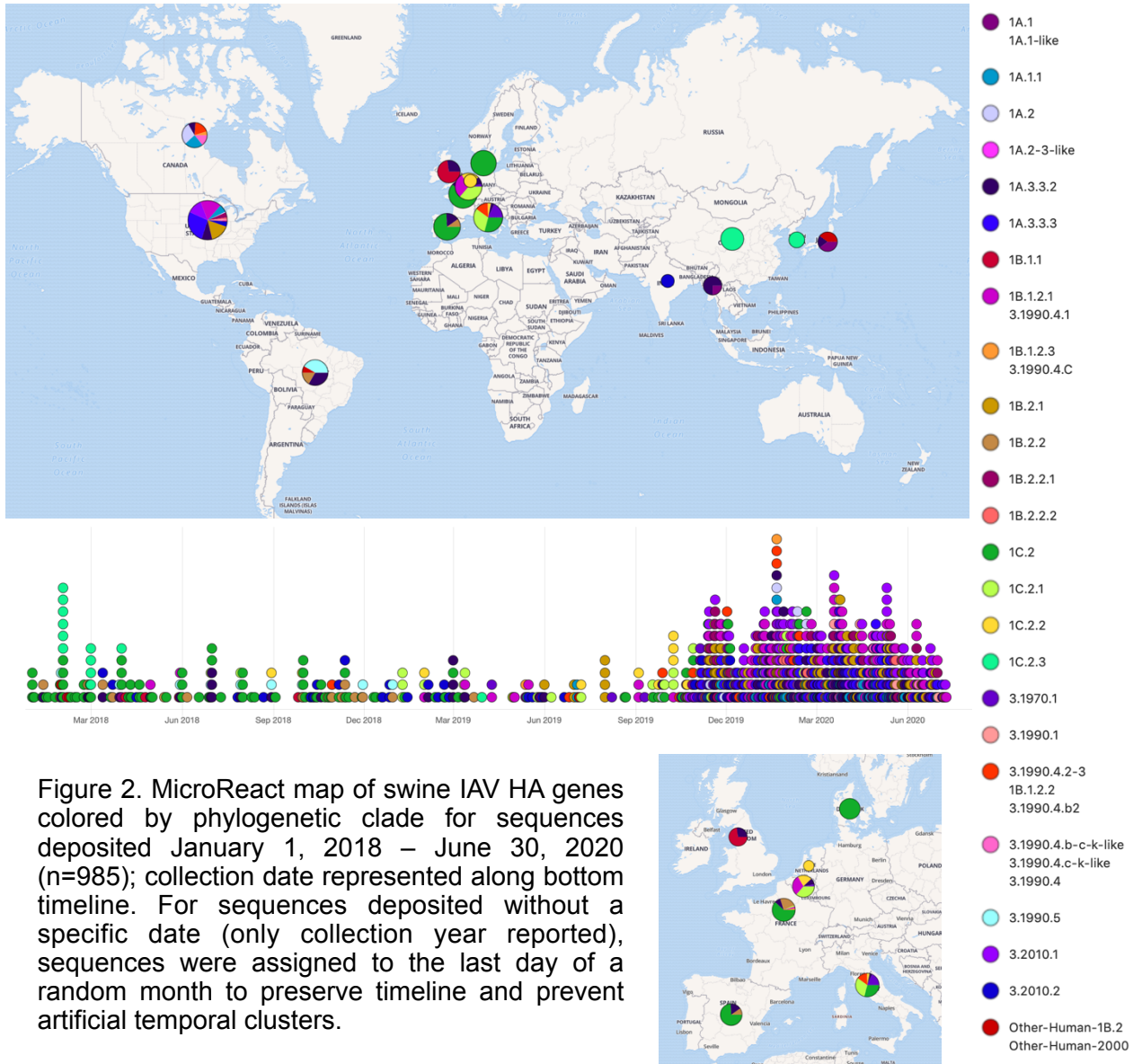


Figure 1. MicroReact map of swine IAV HA genes colored by phylogenetic clade for sequences deposited January 1, 2020 – June 30, 2020 (n=554); collection date represented along bottom timeline.



Contemporary Global H1 swine IAV: genetic diversity

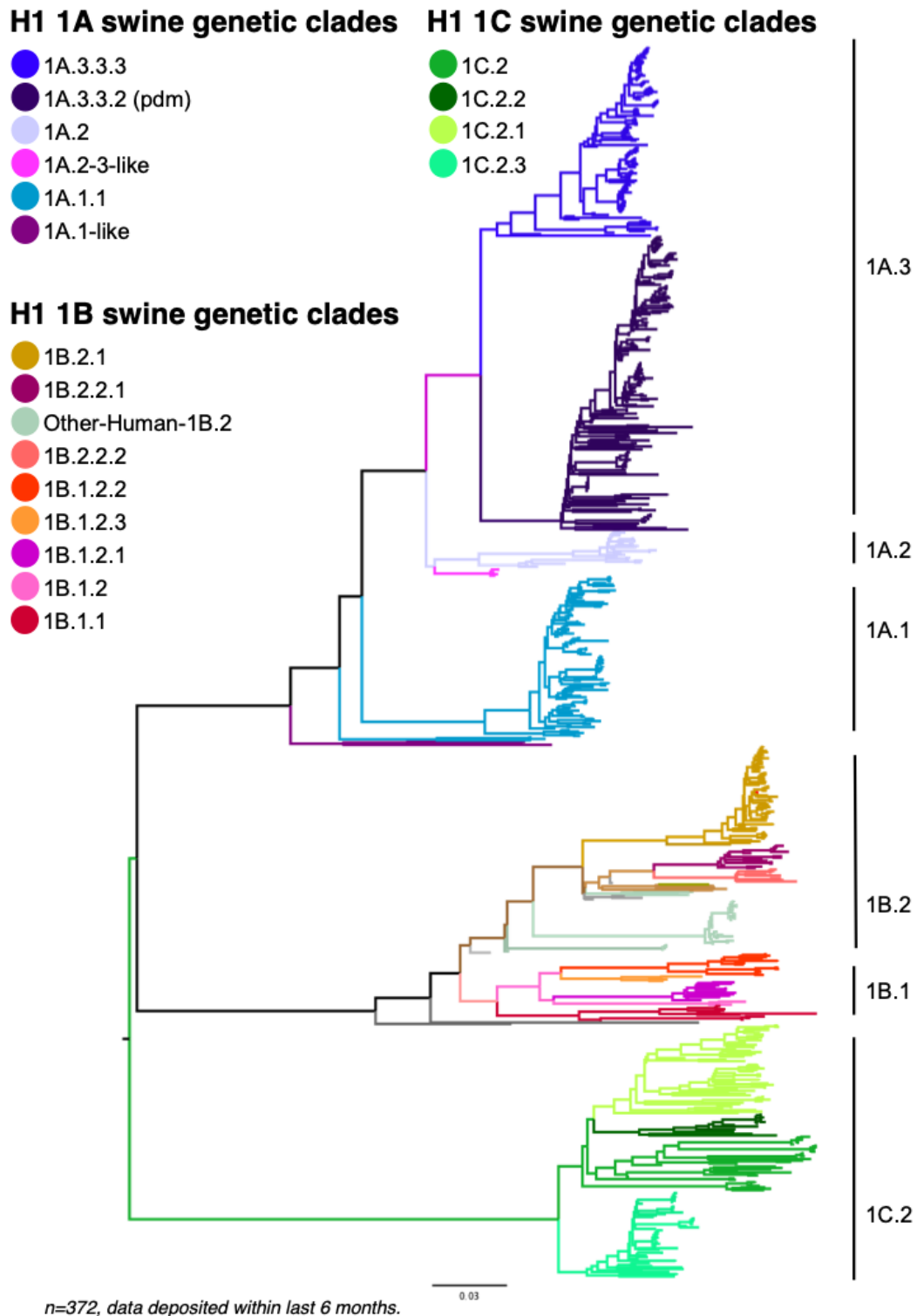
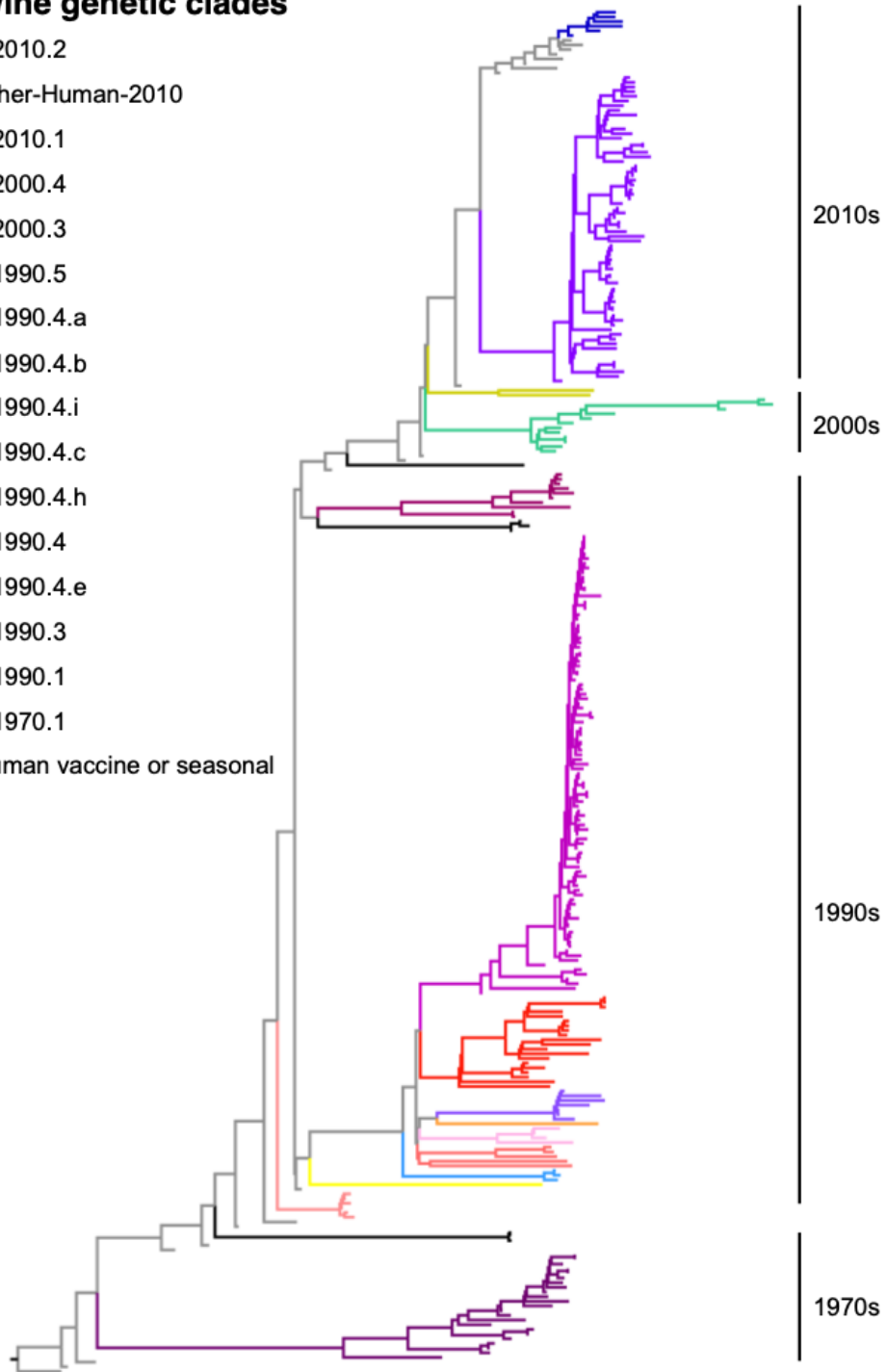


Figure 3. Global swine H1 phylogenetic tree colored by clade and annotated by global H1 lineage nomenclature. Analyses were conducted with reference sequences and new data (deposited January 1, 2020 – June 30, 2020) from Genbank or GISAID, or shared via the OFFLU swine IAV working group.

Contemporary Global H3 swine IAV: genetic diversity

H3 swine genetic clades

- 3.2010.2
- Other-Human-2010
- 3.2010.1
- 3.2000.4
- 3.2000.3
- 3.1990.5
- 3.1990.4.a
- 3.1990.4.b
- 3.1990.4.i
- 3.1990.4.c
- 3.1990.4.h
- 3.1990.4
- 3.1990.4.e
- 3.1990.3
- 3.1990.1
- 3.1970.1
- Human vaccine or seasonal



n=108, data deposited within last 6 months, and n=44 reference genes.

Figure 4. Global swine H3 phylogenetic tree colored by clade and annotated by decade of introduction from human seasonal H3. Analyses were conducted with reference sequences and new data (deposited January 1, 2020 – June 30, 2020) to Genbank or GISAID, or shared via the OFFLU swine IAV working group.

Regional geographic summary

Twenty-four genetic clades from H1 and H3 IAV in swine were detected during the reporting period (January 1, 2020 – June 30, 2020). Thirteen of these clades were within the H1 subtype, and detections were recorded from each of the lineages: 1A classical swine lineage (n=5); 1B human-seasonal lineage (n=5); and 1C Eurasian avian lineage. The remaining eleven genetic clades were within five distinct lineages that were derived from human seasonal H3 virus spillovers: these lineages are grouped by the decade of introduction into swine (1970, two from 1990, and two from 2010). In the case of the 1990.4 lineage, there has been diversification and detection of six cocirculating genetic clades.

- The H3 1990.1, 2010.1, and 2010.2 clades were restricted to the USA, and the H3 1970.1 clade was restricted to Europe. The 1990.4 lineage was detected in the USA, Canada, and South Korea.
- 1B.1 human seasonal lineage was only in Europe, and the 1B.2 human seasonal lineage was restricted to the USA. The 1A classical swine lineage viruses were detected globally. 1A.1.1 and 1A.2 in USA and Canada; 1A.3.3.3 in USA and South Korea; and the 1A.3.3.2/pdm detected in all countries that submitted sequence data during this period.
- The 1C Eurasian avian lineage was detected in Europe and China; and the clades were generally regionally restricted, i.e., 1C.2.1 and 1C.2.2 in Europe, and 1C.2.3 in China. However, for the first time, the 1C.2.3 clade was detected in South Korea, and viruses that share a common ancestor with the 1C.2.3 clade were also detected in Italy. Recent 1C sequence submissions suggest undersurveillance of the lineage: two new groups of sequences were classified generically as 1C.2 but were statistically supported genetic clades that warrant distinct names.

During this reporting period, variant cases were reported in the USA (H3, 1990.1), Netherlands (H1, 1C.2.2), and Germany (H1, 1C.2.2).

Annex 1

Geographic Distribution of swine HA phylogenetic clades by country

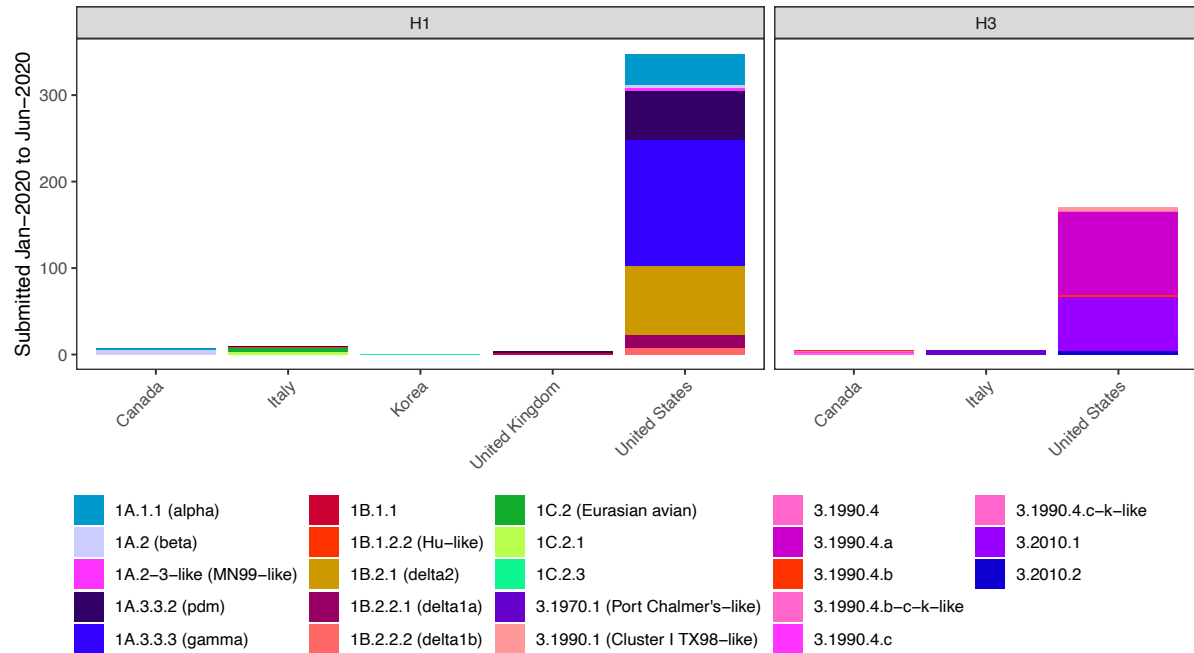


Figure A1. Summary of swine HA clades by country, colored by phylogenetic clade for sequences deposited January 1, 2020 – June 30, 2020 (n=554).

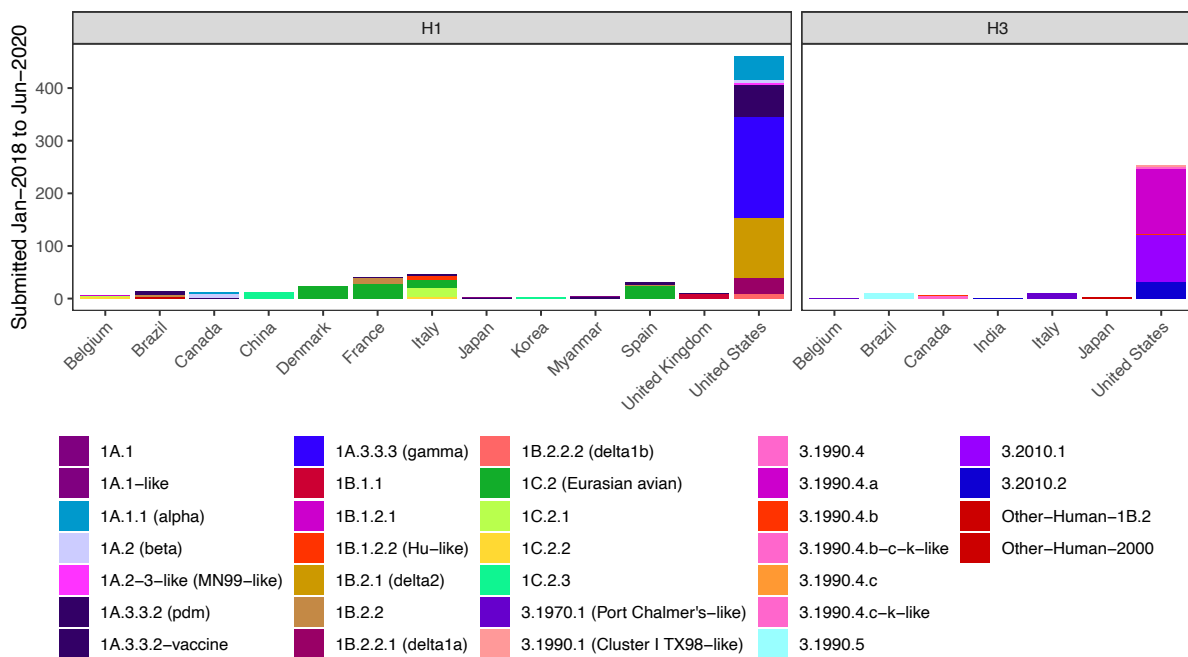


Figure A2. Summary of swine HA genes colored by phylogenetic clade for sequences deposited January 1, 2018 – June 30, 2020 (n=985).

Table A1. Summary of swine H1 clades by country and month of collection, data collected January 2018-June 2020.

Subtype	Country	Clade	Year-Month	Count
H1N1	Belgium	1A.3.3.2	2019-03	1
H1N1	Belgium	1C.2.1	2018-06	1
H1N1	Belgium	1C.2.1	2018-07	1
H1N1	Belgium	1C.2.1	2019-01	4
H1N1	Belgium	1C.2.1	2019-03	1
H1N1	Belgium	1C.2.1	2019-04	1
H1N1	Belgium	1C.2.1	2019-05	1
H1N1	Belgium	1C.2.1	2019-10	2
H1N1	Belgium	1C.2.1	2019-11	1
H1N1	Belgium	1C.2.2	2018-08	1
H1N1	Belgium	1C.2.2	2018-09	1
H1N1	Belgium	1C.2.2	2019-01	1
H1N1	Belgium	1C.2.2	2019-09	1
H1N1	Belgium	1C.2.2	2019-10	3
H1N2	Belgium	1A.3.3.2	2019-10	1
H1N2	Belgium	1A.3.3.2	2019-11	1
H1N2	Belgium	1B.1.2.1	2018-04	1
H1N2	Belgium	1B.1.2.1	2018-05	1
H1N2	Belgium	1B.1.2.1	2019-01	1
H1N2	Belgium	1B.1.2.1	2019-03	1
H1N2	Belgium	1B.1.2.1	2019-04	1
H1N2	Belgium	1B.1.2.1	2019-05	2
H1N2	Belgium	1B.1.2.1	2019-09	2
H1N2	Belgium	1B.1.2.1	2019-10	1
H1N1	Brazil	1A.3.3.2	2018-01	1
H1N1	Brazil	1A.3.3.2	2018-03	2
H1N1	Brazil	1A.3.3.2	2018-04	1
H1N1	Brazil	1A.3.3.2	2018-05	1
H1N1	Brazil	1A.3.3.2	2018-06	1
H1N1	Brazil	1A.3.3.2	2018-07	1
H1N1	Brazil	1A.3.3.2	2018-08	1
H1N2	Brazil	1B.2.2	2018-09	1
H1N2	Brazil	1B.2.2	2018-10	1
H1N2	Brazil	1B.2.2	2018-11	1
H1N2	Brazil	1B.2.2	2018-12	1
H1N2	Brazil	Other-Human-1B.2	2018-01	1
H1N2	Brazil	Other-Human-1B.2	2018-02	1
H1N1	Canada	1A.2	2019-09	1
H1N1	Canada	1A.2	2020-01	1
H1N1	Canada	1A.2	2020-02	3
H1N1	Canada	1A.2	2020-03	1
H1N1	Canada	1A.3.3.2	2019-09	1
H1N2	Canada	1A.1.1	2019-07	2
H1N2	Canada	1A.1.1	2020-02	2
H1N1	China	1C.2.3	2018-02	6
H1N1	China	1C.2.3	2018-03	4
H1N1	China	1C.2.3	2018-04	1
H1N1	China	1C.2.3	2019-05	1
H1N2	Denmark	1C.2	2018-01	3

H1N2	Denmark	1C.2	2018-02	4
H1N2	Denmark	1C.2	2018-03	1
H1N2	Denmark	1C.2	2018-04	3
H1N2	Denmark	1C.2	2018-05	1
H1N2	Denmark	1C.2	2018-06	3
H1N2	Denmark	1C.2	2018-07	2
H1N2	Denmark	1C.2	2018-08	3
H1N2	Denmark	1C.2	2018-10	3
H1N1	France	1A.3.3.2	2018-01	1
H1N1	France	1A.3.3.2	2018-02	1
H1N1	France	1A.3.3.2	2018-03	1
H1N1	France	1A.3.3.2	2019-03	1
H1N1	France	1B.2.2	2018-11	1
H1N1	France	1C.2	2018-01	6
H1N1	France	1C.2	2018-02	1
H1N1	France	1C.2	2018-04	1
H1N1	France	1C.2	2018-05	2
H1N1	France	1C.2	2018-06	2
H1N1	France	1C.2	2018-07	1
H1N1	France	1C.2	2018-08	2
H1N1	France	1C.2	2018-09	1
H1N1	France	1C.2	2018-10	4
H1N1	France	1C.2	2018-11	4
H1N1	France	1C.2	2018-12	1
H1N1	France	1C.2.1	2019-03	1
H1N2	France	1B.1.2.1	2019-05	1
H1N2	France	1B.1.2.3	2019-05	1
H1N2	France	1B.2.2	2018-01	2
H1N2	France	1B.2.2	2018-02	1
H1N2	France	1B.2.2	2018-03	2
H1N2	France	1B.2.2	2018-05	1
H1N2	France	1B.2.2	2018-06	1
H1N2	France	1B.2.2	2018-10	2
H1N2	France	1B.2.2	2018-11	1
H1N2	France	1C.2	2018-10	1
H1N2	France	1C.2	2018-12	1
H1N2	France	1C.2	2019-08	1
H1N2	France	1C.2	2020-02	1
H1N1	Italy	1A.3.3.2	2019-10	1
H1N1	Italy	1A.3.3.2	2020-03	1
H1N1	Italy	1C.2	2019-09	2
H1N1	Italy	1C.2	2019-10	1
H1N1	Italy	1C.2	2019-12	1
H1N1	Italy	1C.2	2020-02	1
H1N1	Italy	1C.2.1	2019-06	1
H1N1	Italy	1C.2.1	2019-07	1
H1N1	Italy	1C.2.1	2019-09	4
H1N1	Italy	1C.2.1	2019-10	3
H1N1	Italy	1C.2.1	2019-11	1
H1N1	Italy	1C.2.1	2019-12	3
H1N1	Italy	1C.2.1	2020-01	2
H1N1	Italy	1C.2.1	2020-02	1
H1N1	Italy	1C.2.2	2019-10	1
H1N2	Italy	1B.1.2.2	2018-10	1
H1N2	Italy	1B.1.2.2	2019-06	1
H1N2	Italy	1B.1.2.2	2019-10	2
H1N2	Italy	1B.1.2.2	2019-12	2
H1N2	Italy	1B.1.2.2	2020-02	2
H1N2	Italy	1C.2	2019-01	1
H1N2	Italy	1C.2	2019-02	1
H1N2	Italy	1C.2	2019-08	1

H1N2	Italy	1C.2	2019-09	1
H1N2	Italy	1C.2	2019-10	2
H1N2	Italy	1C.2	2019-11	1
H1N2	Italy	1C.2	2019-12	1
H1N2	Italy	1C.2	2020-01	2
H1N2	Italy	1C.2	2020-03	1
H1N2	Italy	1C.2.1	2019-11	1
H1N2	Italy	1C.2.2	2019-07	1
H1N1	Japan	1A.3.3.2	2019-05	1
H1N2	Japan	1A.1-like	2019-05	2
H1N2	Korea	1C.2.3	2019-03	1
H1N2	Korea	1C.2.3	2020-04	1
H1N1	Myanmar	1A.1	2018-04	1
H1N1	Myanmar	1A.3.3.2	2018-07	3
H1N1	Spain	1A.3.3.2	2018-02	1
H1N1	Spain	1A.3.3.2	2018-10	1
H1N1	Spain	1A.3.3.2	2019-02	1
H1N1	Spain	1A.3.3.2	2019-03	2
H1N1	Spain	1C.2	2018-02	3
H1N1	Spain	1C.2	2018-04	3
H1N1	Spain	1C.2	2018-12	1
H1N1	Spain	1C.2	2019-03	1
H1N2	Spain	1B.2.2	2018-11	2
H1N2	Spain	1B.2.2	2019-03	1
H1N2	Spain	1C.2	2018-01	1
H1N2	Spain	1C.2	2018-02	2
H1N2	Spain	1C.2	2018-03	1
H1N2	Spain	1C.2	2018-04	3
H1N2	Spain	1C.2	2018-06	1
H1N2	Spain	1C.2	2018-10	3
H1N2	Spain	1C.2	2018-11	1
H1N2	Spain	1C.2	2019-02	1
H1N2	Spain	1C.2	2019-03	2
H1N1	the Netherlands	1C.2.2	2019-09	1
H1N1	United Kingdom	1A.3.3.2	2018-02	1
H1N1	United Kingdom	1A.3.3.2	2020-01	2
H1N1	United Kingdom	1B.1.1	2019-11	1
H1N1	United Kingdom	1B.1.1	2020-04	1
H1N2	United Kingdom	1B.1.1	2018-02	1
H1N2	United Kingdom	1B.1.1	2018-04	2
H1N2	United Kingdom	1B.1.1	2018-05	1
H1N2	United Kingdom	1B.1.1	2018-09	1
H1N2	United Kingdom	1B.1.1	2020-02	1
H1N1	United States	1A.2	2019-11	2
H1N1	United States	1A.2	2020-01	1
H1N1	United States	1A.2	2020-04	2
H1N1	United States	1A.2-3-like	2020-03	3
H1N1	United States	1A.3.3.2	2019-06	1
H1N1	United States	1A.3.3.2	2019-11	3
H1N1	United States	1A.3.3.2	2019-12	1
H1N1	United States	1A.3.3.2	2020-01	7
H1N1	United States	1A.3.3.2	2020-02	11
H1N1	United States	1A.3.3.2	2020-03	15
H1N1	United States	1A.3.3.2	2020-04	7
H1N1	United States	1A.3.3.2	2020-05	4

H1N1	United States	1A.3.3.2	2020-06	6
H1N1	United States	1A.3.3.2	2020-07	1
H1N1	United States	1A.3.3.3	2019-10	3
H1N1	United States	1A.3.3.3	2019-11	18
H1N1	United States	1A.3.3.3	2019-12	24
H1N1	United States	1A.3.3.3	2020-01	25
H1N1	United States	1A.3.3.3	2020-02	17
H1N1	United States	1A.3.3.3	2020-03	28
H1N1	United States	1A.3.3.3	2020-04	30
H1N1	United States	1A.3.3.3	2020-05	28
H1N1	United States	1A.3.3.3	2020-06	15
H1N1	United States	1A.3.3.3	2020-07	2
H1N1	United States	1B.2.1	2020-03	1
H1N1	United States	1B.2.2.1	2020-03	2
H1N2	United States	1A.1.1	2019-11	5
H1N2	United States	1A.1.1	2019-12	3
H1N2	United States	1A.1.1	2020-01	9
H1N2	United States	1A.1.1	2020-02	5
H1N2	United States	1A.1.1	2020-03	7
H1N2	United States	1A.1.1	2020-04	10
H1N2	United States	1A.1.1	2020-05	5
H1N2	United States	1A.1.1	2020-06	1
H1N2	United States	1A.1.1	2020-07	1
H1N2	United States	1A.2-3-like	2020-02	1
H1N2	United States	1A.3.3.2	2020-03	1
H1N2	United States	1A.3.3.2	2020-04	1
H1N2	United States	1A.3.3.2	2020-05	2
H1N2	United States	1A.3.3.2	2020-06	2
H1N2	United States	1A.3.3.3	2020-02	1
H1N2	United States	1A.3.3.3	2020-03	1
H1N2	United States	1B.2.1	2019-05	1
H1N2	United States	1B.2.1	2019-06	1
H1N2	United States	1B.2.1	2019-07	2
H1N2	United States	1B.2.1	2019-08	4
H1N2	United States	1B.2.1	2019-10	1
H1N2	United States	1B.2.1	2019-11	17
H1N2	United States	1B.2.1	2019-12	7
H1N2	United States	1B.2.1	2020-01	16
H1N2	United States	1B.2.1	2020-02	9
H1N2	United States	1B.2.1	2020-03	12
H1N2	United States	1B.2.1	2020-04	10
H1N2	United States	1B.2.1	2020-05	20
H1N2	United States	1B.2.1	2020-06	12
H1N2	United States	1B.2.1	2020-07	1
H1N2	United States	1B.2.2.1	2019-11	6
H1N2	United States	1B.2.2.1	2019-12	8
H1N2	United States	1B.2.2.1	2020-01	1
H1N2	United States	1B.2.2.1	2020-02	2
H1N2	United States	1B.2.2.1	2020-03	3
H1N2	United States	1B.2.2.1	2020-04	3
H1N2	United States	1B.2.2.1	2020-05	3
H1N2	United States	1B.2.2.1	2020-06	1
H1N2	United States	1B.2.2.1	2020-07	1
H1N2	United States	1B.2.2.2	2019-12	1
H1N2	United States	1B.2.2.2	2020-01	4
H1N2	United States	1B.2.2.2	2020-02	2
H1N2	United States	1B.2.2.2	2020-05	1

Table A2 Summary of swine H3 clades by country and month of collection.

Subtype	Country	Clade	Year-Month	Count
H3N2	Belgium	3.1970.1	2019-04	1
H3N2	Brazil	3.1990.5	2018-01	1
H3N2	Brazil	3.1990.5	2018-02	1
H3N2	Brazil	3.1990.5	2018-03	1
H3N2	Brazil	3.1990.5	2018-05	1
H3N2	Brazil	3.1990.5	2018-06	1
H3N2	Brazil	3.1990.5	2018-07	1
H3N2	Brazil	3.1990.5	2018-08	1
H3N2	Brazil	3.1990.5	2018-09	1
H3N2	Brazil	3.1990.5	2018-11	1
H3N2	Brazil	3.1990.5	2018-12	1
H3N2	Canada	3.1990.4.b-c-k-like	2020-03	1
H3N2	Canada	3.1990.4.b2	2019-09	1
H3N2	Canada	3.1990.4.b2	2020-02	1
H3N2	Canada	3.1990.4.c	2020-01	1
H3N2	Canada	3.1990.4.c-k-like	2020-02	2
H3N2	India	3.2010.2	2018-03	1
H3N2	Italy	3.1970.1	2019-08	1
H3N2	Italy	3.1970.1	2019-09	1
H3N2	Italy	3.1970.1	2019-11	3
H3N2	Italy	3.1970.1	2020-01	3
H3N2	Italy	3.1970.1	2020-02	1
H3N2	Italy	3.1970.1	2020-03	1
H3N2	Japan	Other-Human-2000	2018-02	1
H3N2	Japan	Other-Human-2000	2019-07	1
H3N1	United States	3.1990.4.1	2020-02	1
H3N1	United States	3.2010.1	2020-01	1
H3N2	United States	3.1990.1	2020-03	1
H3N2	United States	3.1990.1	2020-04	2
H3N2	United States	3.1990.1	2020-05	1
H3N2	United States	3.1990.1	2020-07	1
H3N2	United States	3.1990.4	2019-12	1
H3N2	United States	3.1990.4	2020-04	1
H3N2	United States	3.1990.4	2020-06	1
H3N2	United States	3.1990.4.1	2019-10	3
H3N2	United States	3.1990.4.1	2019-11	10
H3N2	United States	3.1990.4.1	2019-12	12
H3N2	United States	3.1990.4.1	2020-01	21
H3N2	United States	3.1990.4.1	2020-02	12
H3N2	United States	3.1990.4.1	2020-03	20
H3N2	United States	3.1990.4.1	2020-04	15
H3N2	United States	3.1990.4.1	2020-05	14
H3N2	United States	3.1990.4.1	2020-06	12
H3N2	United States	3.1990.4.1	2020-07	3
H3N2	United States	3.1990.4.2-3	2020-01	2
H3N2	United States	3.1990.4.2-3	2020-04	1
H3N2	United States	3.2010.1	2019-10	4
H3N2	United States	3.2010.1	2019-11	12
H3N2	United States	3.2010.1	2019-12	9
H3N2	United States	3.2010.1	2020-01	14

H3N2	United States	3.2010.1	2020-02	11
H3N2	United States	3.2010.1	2020-03	9
H3N2	United States	3.2010.1	2020-04	6
H3N2	United States	3.2010.1	2020-05	12
H3N2	United States	3.2010.1	2020-06	9
H3N2	United States	3.2010.1	2020-07	2
H3N2	United States	3.2010.2	2018-03	1
H3N2	United States	3.2010.2	2018-04	1
H3N2	United States	3.2010.2	2018-07	1
H3N2	United States	3.2010.2	2018-08	1
H3N2	United States	3.2010.2	2018-10	4
H3N2	United States	3.2010.2	2018-11	2
H3N2	United States	3.2010.2	2018-12	3
H3N2	United States	3.2010.2	2019-01	1
H3N2	United States	3.2010.2	2019-02	5
H3N2	United States	3.2010.2	2019-05	3
H3N2	United States	3.2010.2	2019-06	1
H3N2	United States	3.2010.2	2019-10	1
H3N2	United States	3.2010.2	2019-11	1
H3N2	United States	3.2010.2	2019-12	2
H3N2	United States	3.2010.2	2020-04	2
H3N2	United States	3.2010.2	2020-05	1
H3N2	United States	3.2010.2	2020-06	1