OFFLU virtual SIV group meeting

9 December 2020

Rachel Tell
National Veterinary Services Laboratories
Amy Vincent & Tavis Anderson
National Animal Disease Center

USDA Surveillance Summary

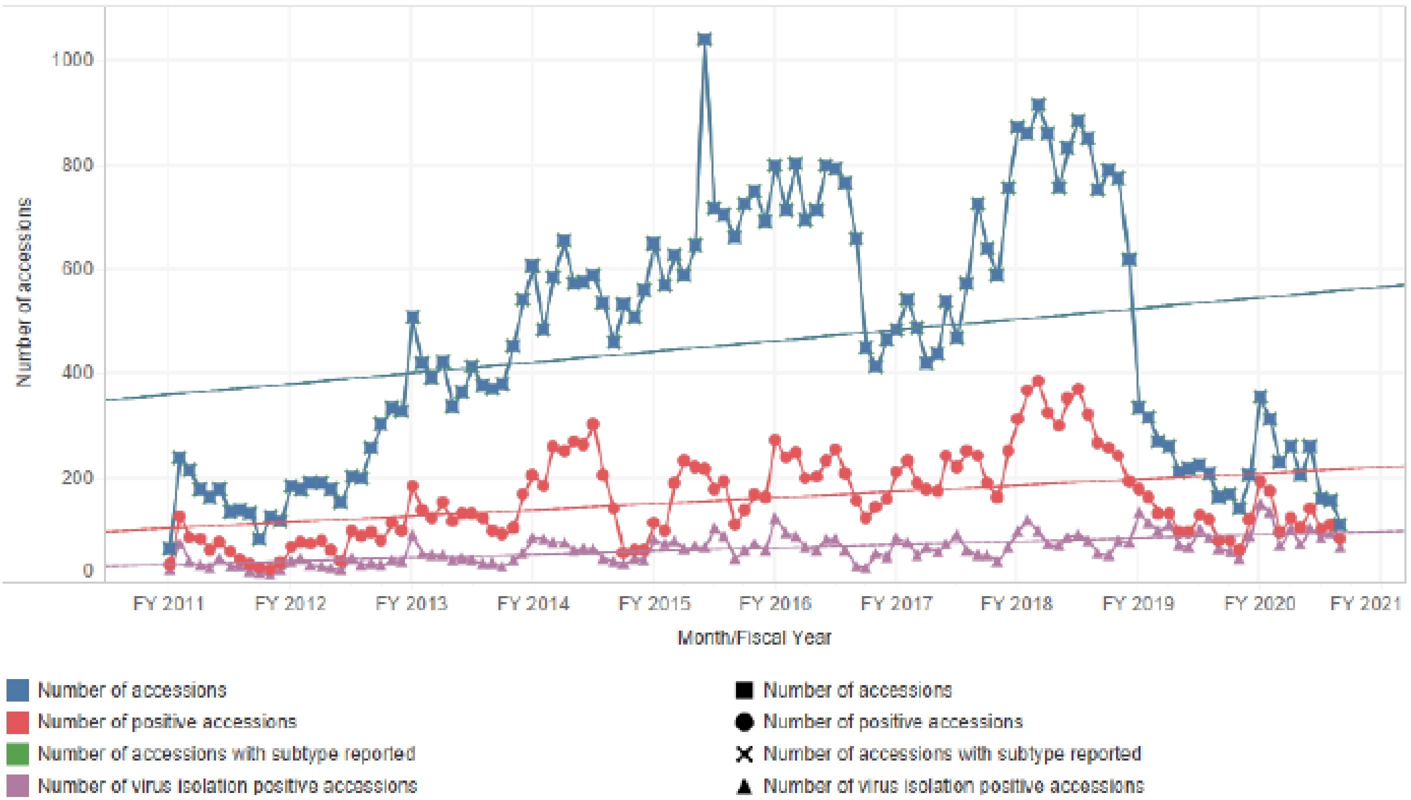


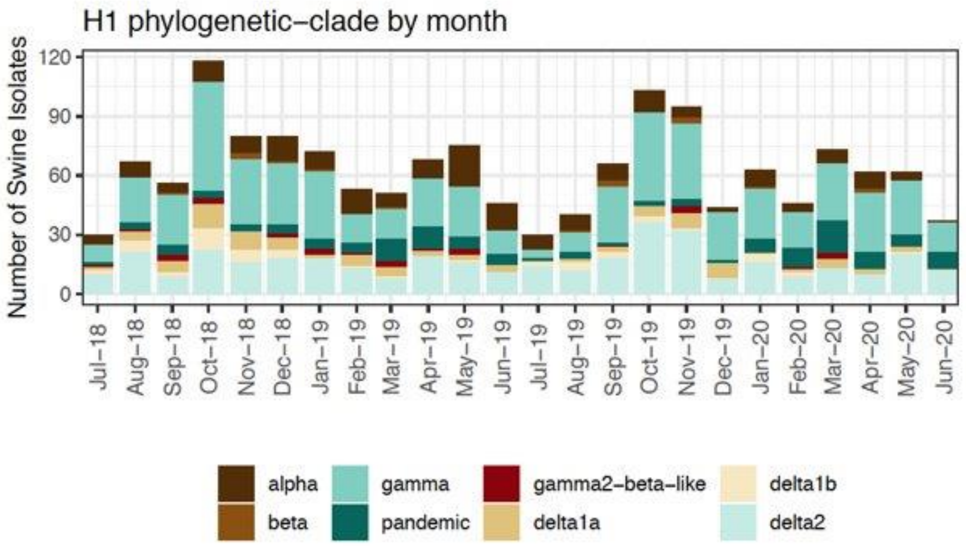
Figure 2. Accessions submitted, subtyped accessions, rRT-PCR positive accessions, and virus isolation positive accessions over time with trend lines for IAV-S, FY2011 through Q3 FY2020

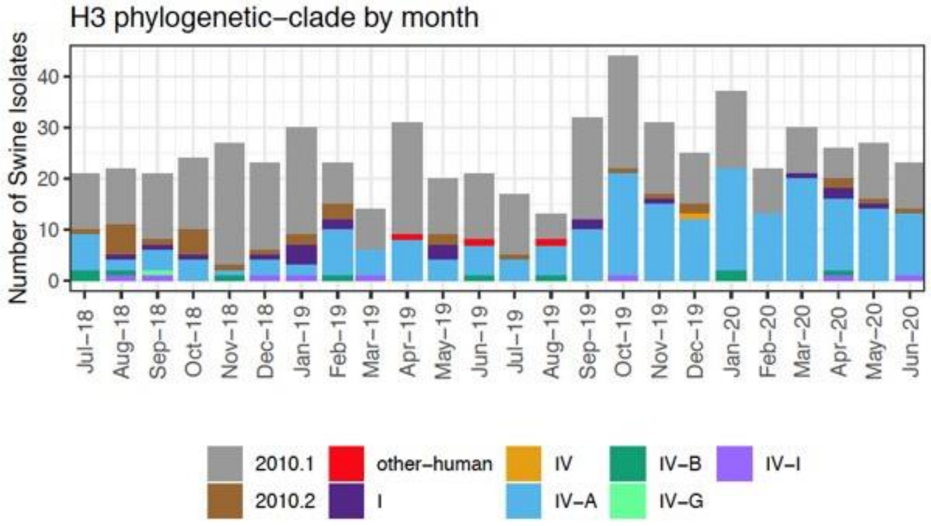
Subtyped isolates avaialbe though the repository	
H3N2	2,271
H3N1	19
H1N1	2,949
H1N2	2,742
Mixed	302
TOTAL	8,283

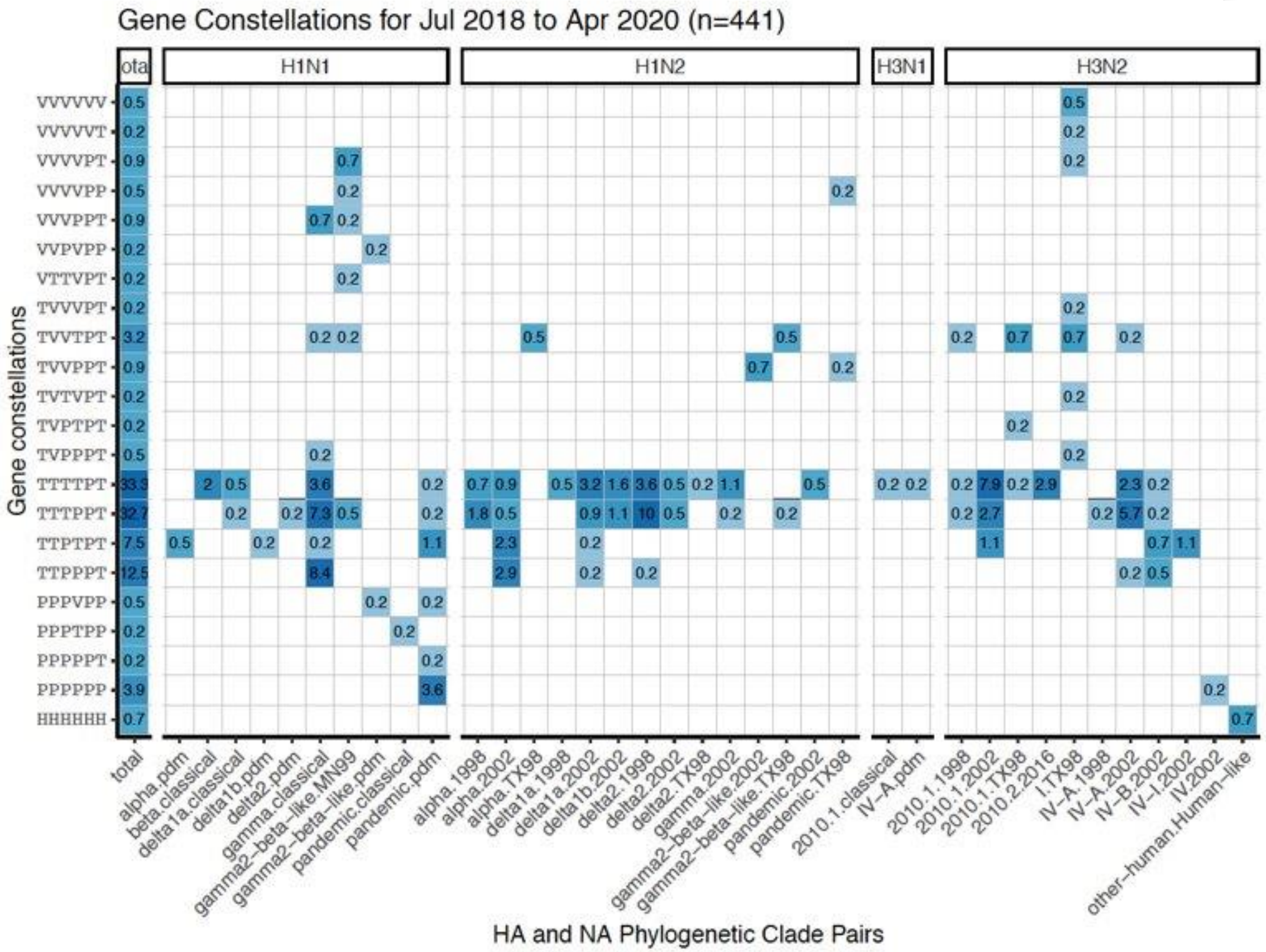
Surveillance system updates:

- Increased to 30 WGS per month
- 1700+ isolates with WGS to date

USDA Surveillance Summary







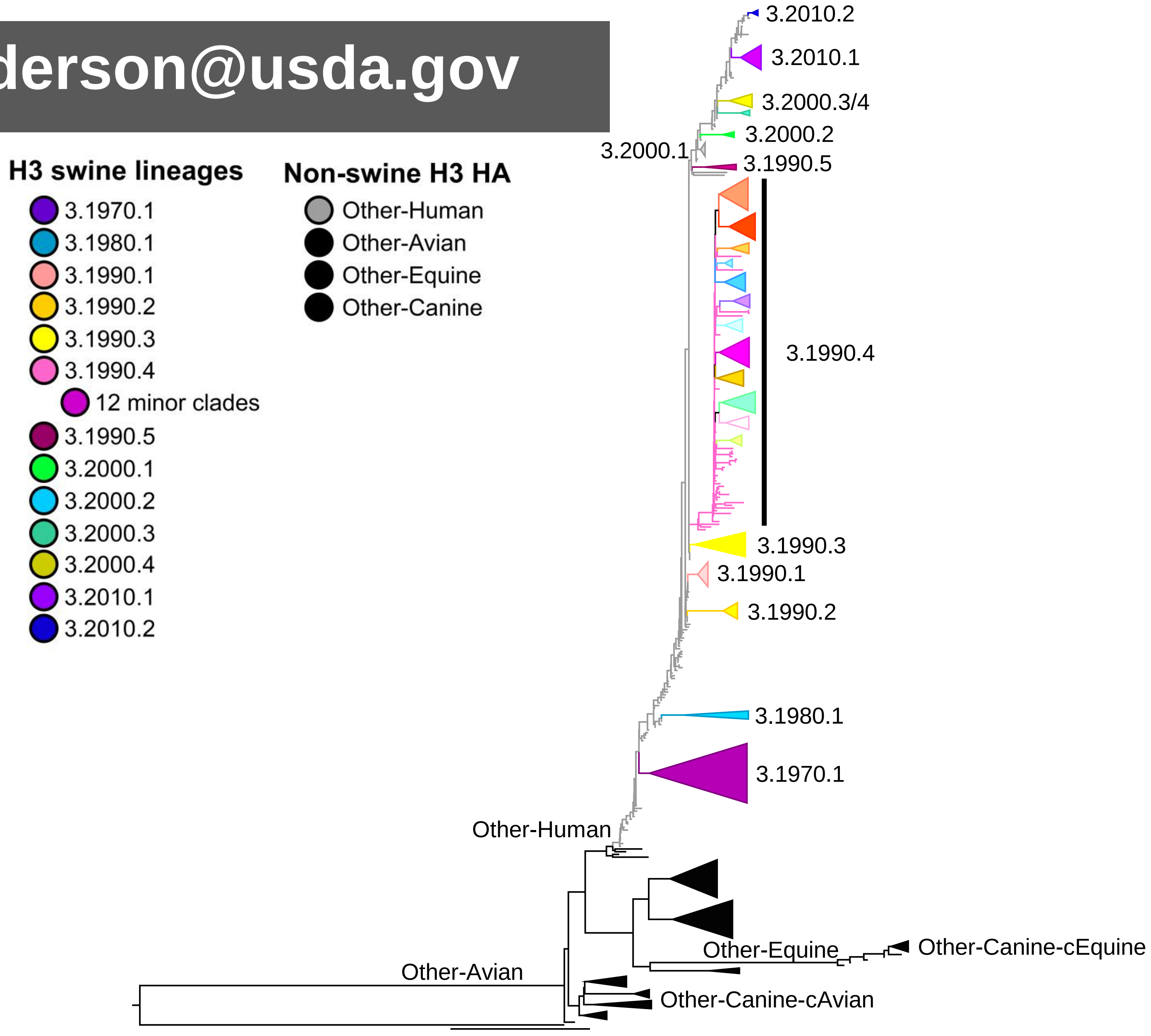
H3 nomenclature – Tavis.Anderson@usda.gov

Criteria:

- Established clades (e.g., Cluster IV => 1990.**4**)
- Statistical support (aLRT >=90; bootstrap >70)
- Average % distance (>5% between clade; <5% within clade
- >1 year of detection
- Minimum of 5 HA genes from 2010 to present
- *Antigenic divergence*

Progress:

- Classification tool is 99% accurate (all hosts)
- *Files are with IRD, developing implementation similar to the H1 tool*.
- *Manuscript March 2021*.



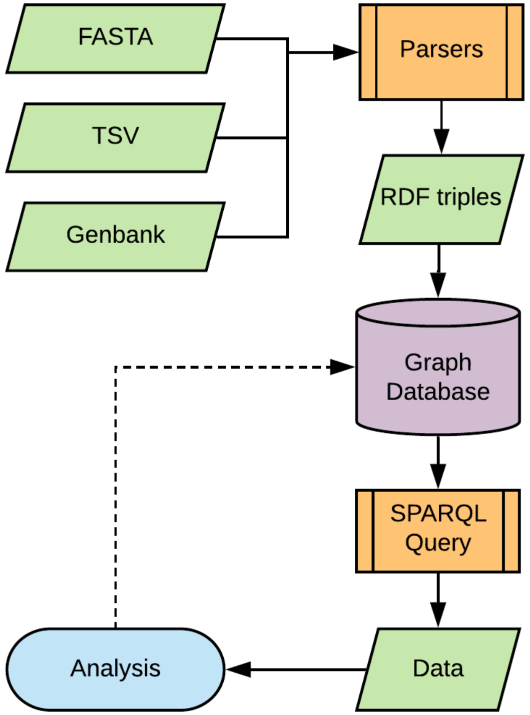
Scaffold H3 HA phylogeny used in automatic classification of unknown query sequences. Frequent non-swine spillovers result in a non-hierarchical phylogeny with low topological support for emerging clades. 377 sequences act as a scaffold and are used by the classifier algorithm and pplacer to annotate query sequences to one of the defined clades.

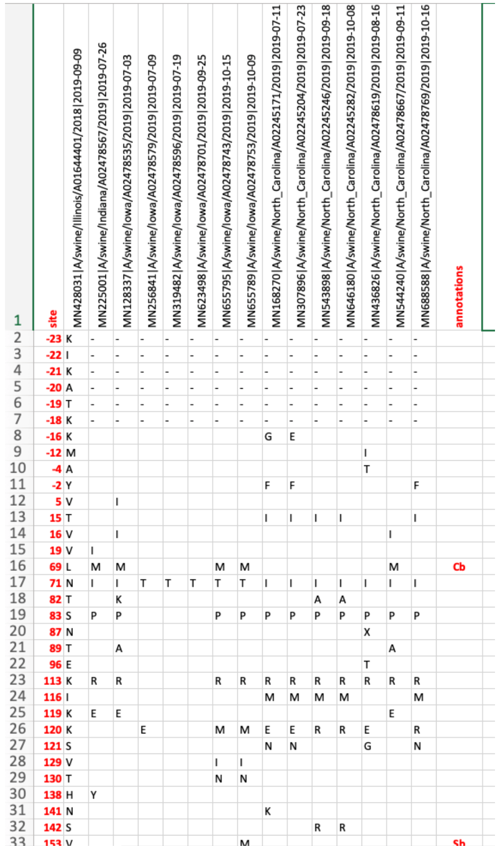
IAV tools by NADC Flu Crew

Accessed via https://flu-crew.org and https://github.com/flu-crew

octofludb

- A general-purpose graph database that links public genetic data to your lab data, relevant metadata
    - *Submit a query for: offlu-vcm tested antigens, CVVs, human vaccines, and all public data deposited to genbank in ~6 months -> output is a fasta with the definition line annotated by our query parameters (+strain name, country, etc.)*


FASTA
TSV
Genbank
Parsers
RDF triples
Graph Database
SPARQL Query
Data
Analysis



1	site	MN428031|A/swine/Illinois/A01644401/2018|2019-09-09	MN225001|A/swine/Indiana/A02478567/2019|2019-07-26	MN128337|A/swine/Iowa/A02478535/2019|2019-07-03	MN256841|A/swine/Iowa/A02478579/2019|2019-07-09	MN319482|A/swine/Iowa/A02478596/2019|2019-07-19	MN623498|A/swine/Iowa/A02478701/2019|2019-09-25	MN655795|A/swine/Iowa/A02478743/2019|2019-10-15	MN655789|A/swine/Iowa/A02478753/2019|2019-10-09	MN168270|A/swine/North_Carolina/A02245171/2019|2019-07-11	MN307896|A/swine/North_Carolina/A02245204/2019|2019-07-23	MN543898|A/swine/North_Carolina/A02245246/2019|2019-09-18	MN646180|A/swine/North_Carolina/A02245282/2019|2019-10-08	MN436826|A/swine/North_Carolina/A02478619/2019|2019-08-16	MN544240|A/swine/North_Carolina/A02478667/2019|2019-09-11	MN688588|A/swine/North_Carolina/A02478769/2019|2019-10-16	annotations
2	-23	K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
3	-22	I	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
4	-21	K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
5	-20	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
6	-19	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
7	-18	K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
8	-16	K								G	E						
9	-12	M												I			
10	-4	A												T			
11	-2	Y								F	F					F	
12	5	V		I													
13	15	T								I	I	I	I			I	
14	16	V		I											I		
15	19	V	I														
16	69	L	M	M				M	M						M		Cb
17	71	N	I	I	T	T	T	T	T	I	I	I	I	I	I	I	
18	82	T		K								A	A				
19	83	S	P	P				P	P	P	P	P	P	P	P	P	
20	87	N												X			
21	89	T		A											A		
22	96	E												T			
23	113	K	R	R				R	R	R	R	R	R	R	R	R	
24	116	I								M	M	M	M			M	
25	119	K	E	E											E		
26	120	K			E			M	M	E	E	R	R	E		R	
27	121	S								N	N			G		N	
28	129	V						I	I								
29	130	T						N	N								
30	138	H	Y														
31	141	N								K							
32	142	S										R	R				
33	153	V							M								Sh

Flutile *(H1 numbering agenda item)*

- A tool that manipulates and analyzes IAV data
- *Amino acid difference tables (swine IAV vs CVV) w/annotations (epitopes/RBS) – works for all subtypes (implements Burke et al numbering)*
- *Generates consensus sequences*
- *Generates representative alignment: for monophyletic clades, set time periods, set locations, etc. (uses sequence similarity in input alignment)*
- *Extracts HA1 for H3 and H1*