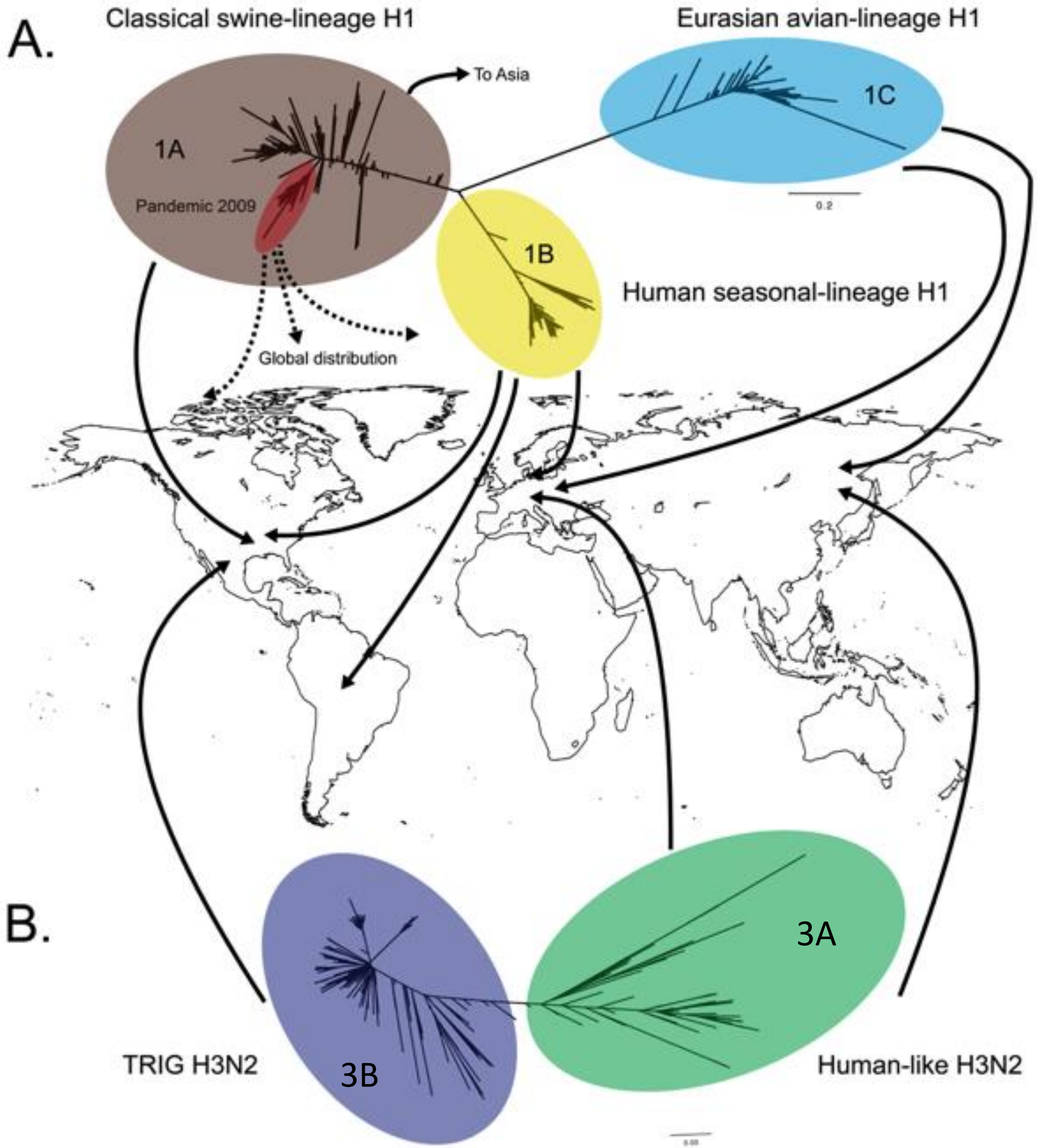
Clade Nomenclature Activity

Group members: Amy, Nicola, Richard, Ian, Todd

Support for this program is provided by: Tavis



Vincent et al 2014, adapted from Zell, *et. al*. 2013 CTMI, etc.

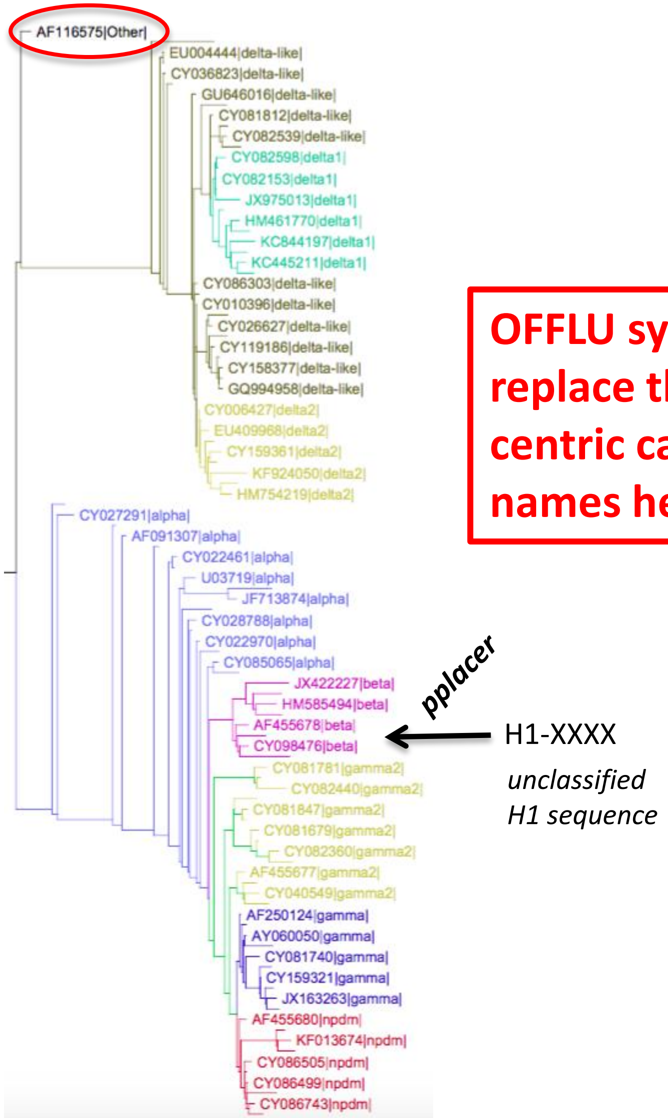
Justification for a global swine clade nomenclature system

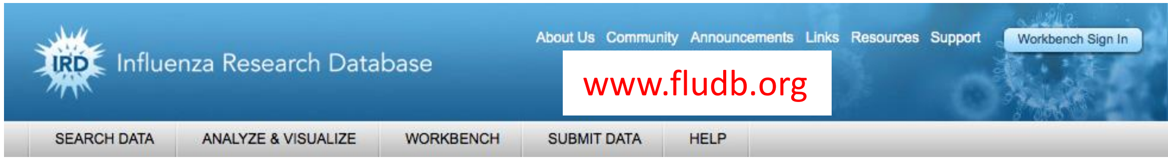
- Common terminology for all regions to use
- Non-incriminating (ie, gets away from reporting a “North American” virus in South America, etc.)
- Provides a system to describe swine IAV in relationship to common human ancestors
- Provides a common nomenclature for automated clade tools on IRD
    - Beta tool for US swine H1 already in use
    - H3 in the pipeline

Swine H1 clade classification in IRD

C. Macken (IRD/Auckland) and T. Anderson (USDA)

Reference classification tree

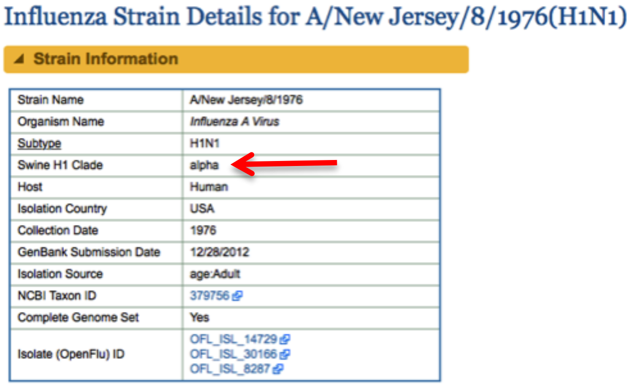




www.fludb.org

Strain Detail Page

Pre-computed annotations for ***all H1 viruses in all hosts***



Influenza Strain Details for A/New Jersey/8/1976(H1N1)

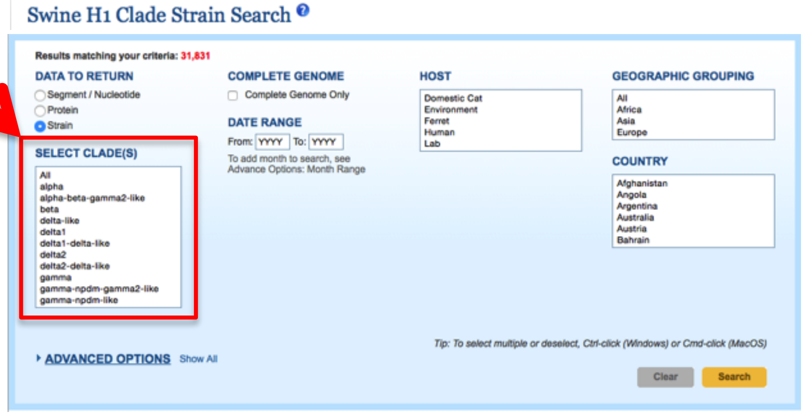
Strain Information

Strain Name	A/New Jersey/8/1976
Organism Name	*Influenza A Virus*
Subtype	H1N1
Swine H1 Clade	alpha
Host	Human
Isolation Country	USA
Collection Date	1976
GenBank Submission Date	12/28/2012
Isolation Source	age:Adult
NCBI Taxon ID	379756
Complete Genome Set	Yes
Isolate (OpenFlu) ID	OFL_ISL_14729 OFL_ISL_30166 OFL_ISL_8287

OFFLU system will replace the US-centric categorical names here

Search Data Menu

Clade-specific strain/segment /protein search



Swine H1 Clade Strain Search

Results matching your criteria: 31,831

DATA TO RETURN

○ Segment / Nucleotide
○ Protein
● Strain

COMPLETE GENOME

☐ Complete Genome Only

DATE RANGE

From: YYYY To: YYYY

To add month to search, see Advance Options: Month Range

HOST

Domestic Cat
Environment
Ferret
Human
Lab

GEOGRAPHIC GROUPING

All
Africa
Asia
Europe

SELECT CLADE(S)

All
alpha
alpha-beta-gamma2-like
beta
delta-like
delta1
delta1-delta-like
delta2
delta2-delta-like
gamma
gamma-npdm-gamma2-like
gamma-npdm-like

COUNTRY

Afghanistan
Angola
Argentina
Australia
Austria
Bahrain

Tip: To select multiple or deselect, Ctrl-click (Windows) or Cmd-click (MacOS)

Analyze Tool Menu

Clade assignment of user sequences

Swine H1 Clade Classification Tool

ANALYSIS NAME

INPUT SEQUENCES

○ Upload a file containing my sequences in FASTA format.
○ Paste sequences in FASTA format.
○ Analyze my custom sequences and associated metadata with IRD/ViPR sequences.
Upload your sequence file to the workbench.

Draft Criteria

Basic Criteria:

- Common phylogenetic node
- In well-sampled geographic areas, >70 bootstrap value
- >93-95% within clade nucleotide identity (95% for H1 and 93% for H3)
- >7% between clade divergence (most are >10%)
- Minimum number of isolates (>10)
- Minimum time period (>1 year)
- Antigenic support based on HI cross-reactivity recommended
- *Considering isolates from 5 most recent years (2010-15)*

Emerging or transitional sequence criteria:

- Unique interspecies spillover without minimum number or minimum time period:
  - >70 bootstrap support
  - long branch lengths from nearest common swine ancestor
  - supported by homologous HI sero-surveillance
- Clusters with poor bootstrap for internal node, but high bootstrap for contemporaneous node (>2010) in under-surveilled areas:
  - continued detection >1 year
  - branch length is 3 times longer than the standard error of branch lengths in the phylogeny
  - HA sequence quality and length confirmed
  - minimum of 10 independent isolates