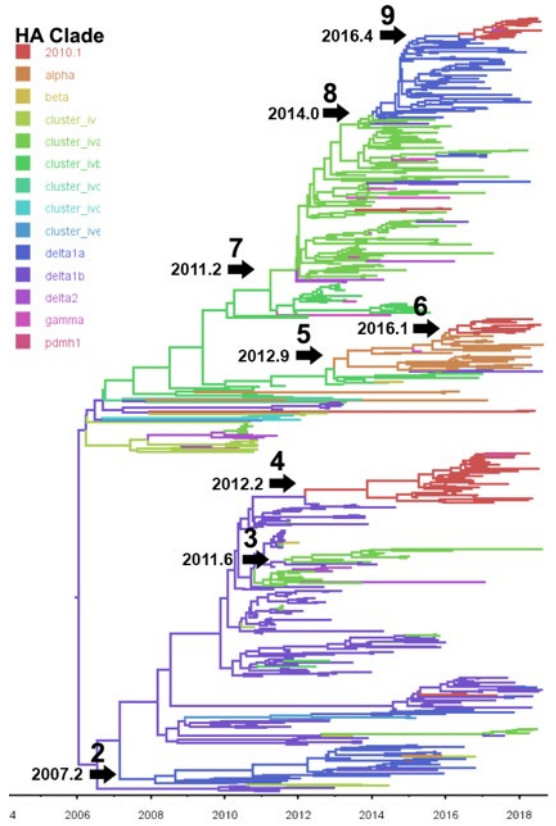
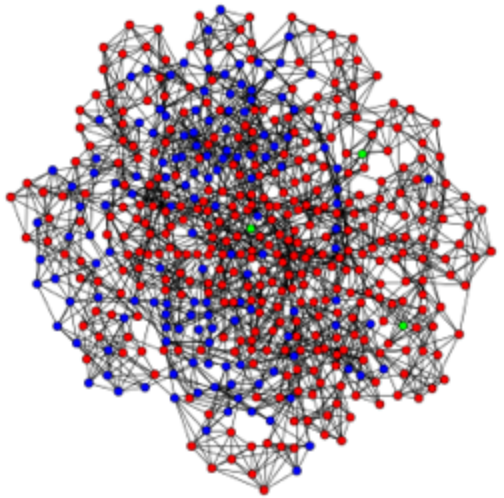
Emergence and interstate spread of HPAI A(H5N1) in dairy cattle

Tavis Anderson
Virus and Prion Research Unit
National Animal Disease Center
Agricultural Research Service
United States Department of Agriculture





Reports of nonspecific illness in February 2024

- Reduced feed intake and rumination
- Abrupt drop in milk production
- ~10-15% ill dairy cattle, minimal mortality
- … in March 2024, cats fed raw colostrum and milk resulted in neurologic signs (and some mortality)

NEWS

Eyes are focused on an illness affecting milk output in dairy cows in the Texas panhandle

Lee Mielke Farmers' Advance

Published 11:40 a.m. ET March 25, 2024 | **Updated 4:02 p.m. ET March 25, 2024**

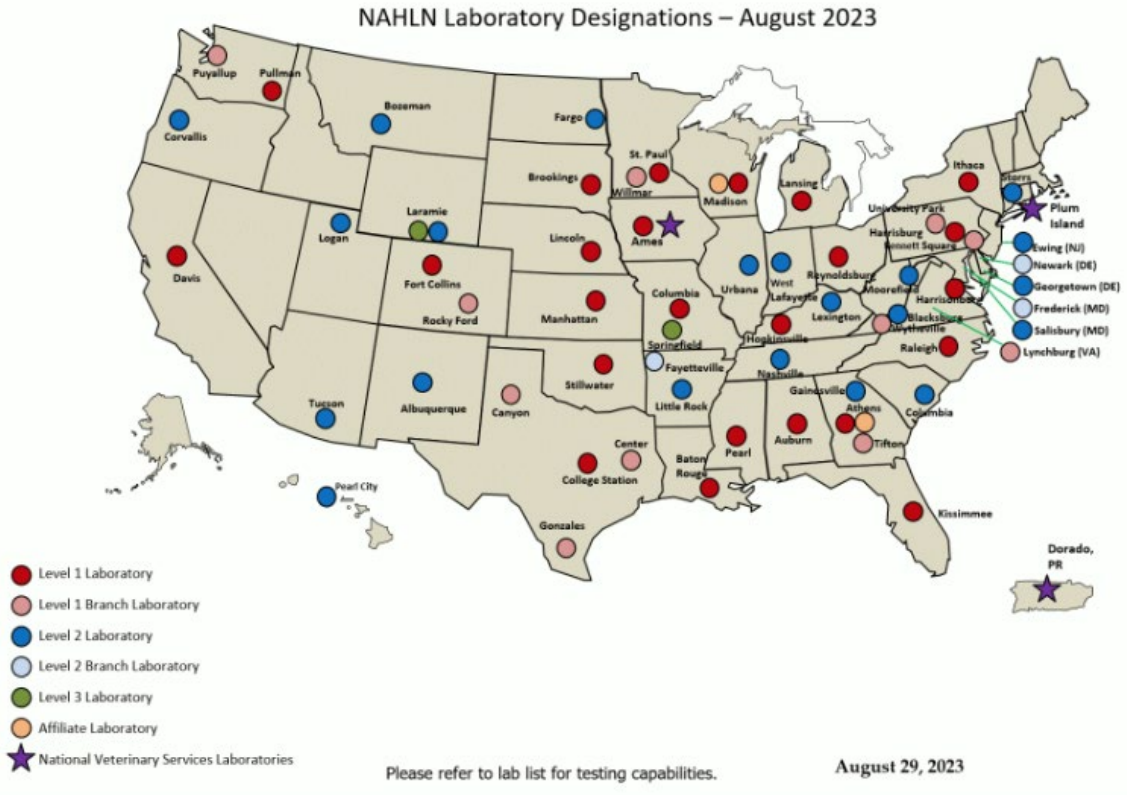
U.S. milk production remained below a year ago in February, the eighth consecutive month to do so, thanks to lower cow numbers and output per cow.

Photo: Baker et al. (in review) bioRxiv

Burrough et al. (2024) EID

National Animal Health Surveillance System

- USDA-APHIS-Veterinary Services
- National Preparedness and Incident Coordination
- HPAI Emergency Response
  - Intramural epidemiology
  - Intramural computational
  - … diagnostics, surveillance, etc.
- https://www.aphis.usda.gov/livestock-poultry-disease



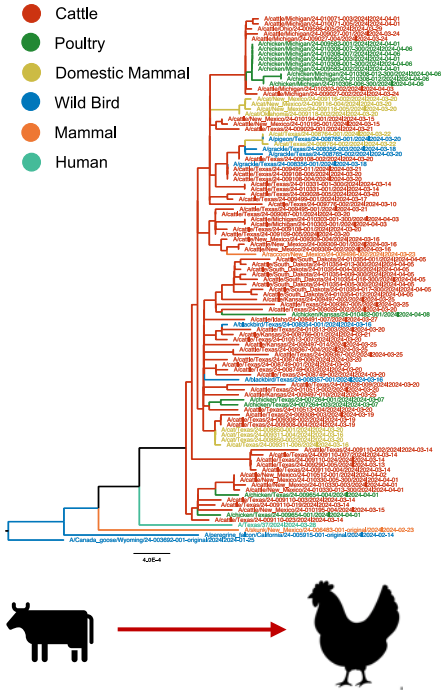
Samples submitted through NAHLN were confirmed as HPAI H5N1 on March 25, 2024

What was it? Where did it come from?
When did this happen?

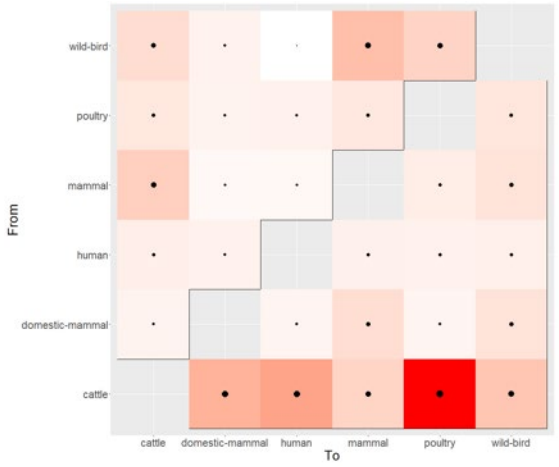
General approaches used to detect transmission

Individual gene trees

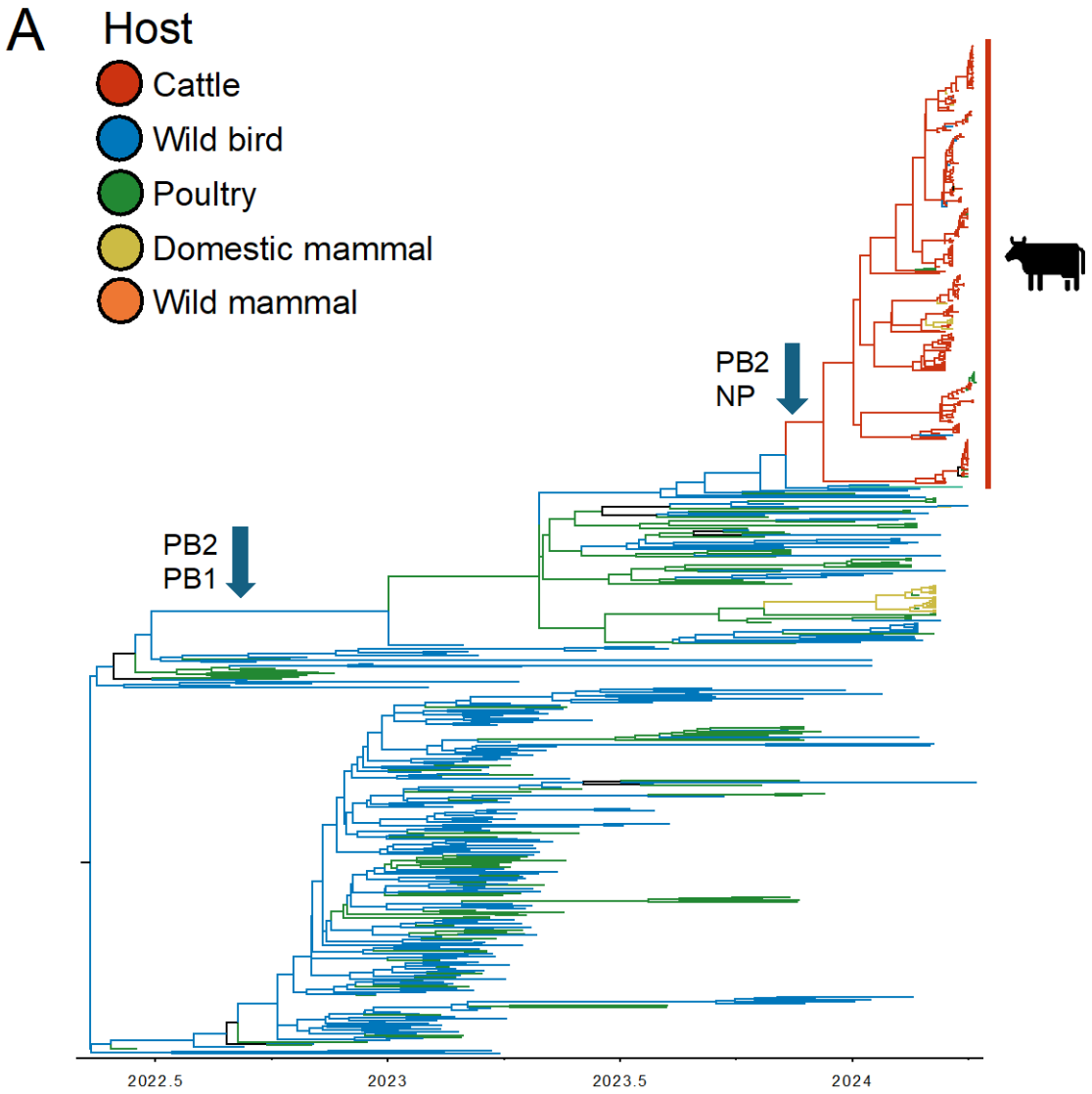
Genome trees

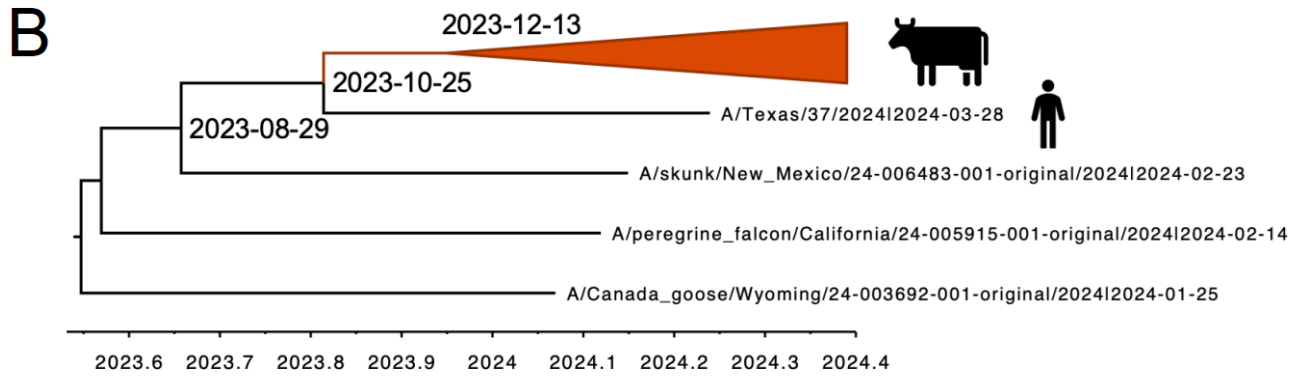


Ancestral state reconstruction



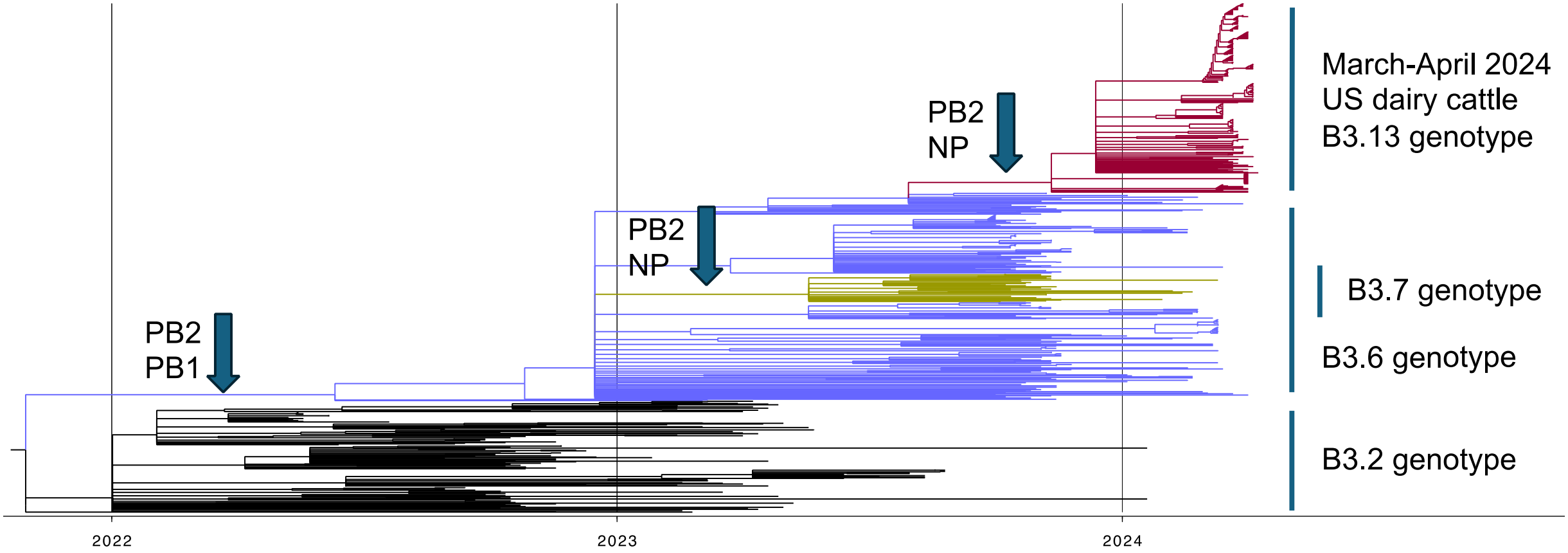
Single spillover in late 2023





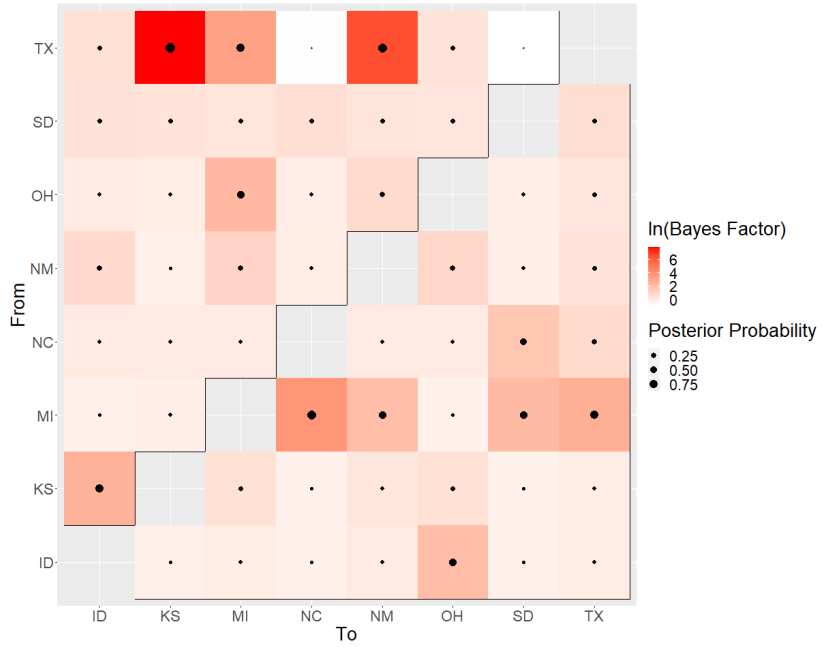
Nguyen et al. bioRxiv (in review)

Reassortment in wild birds preceded spillover



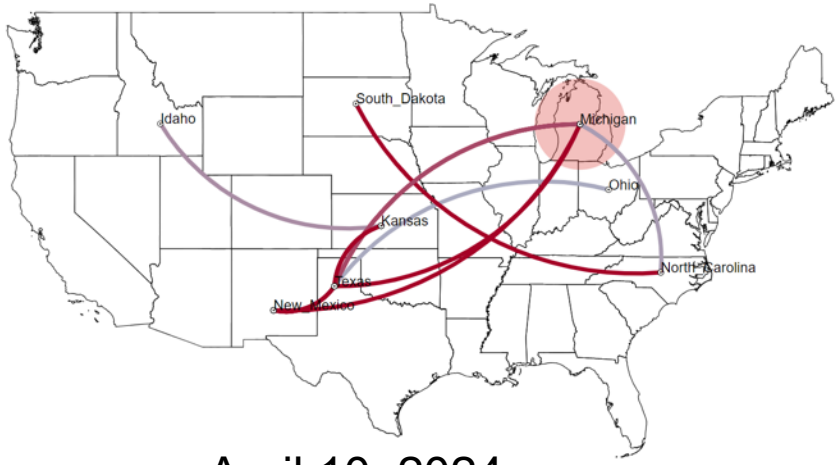
TreeSort: https://github.com/flu-crew/TreeSort

Dairy cattle movement drove initial dissemination



March 13, 2024

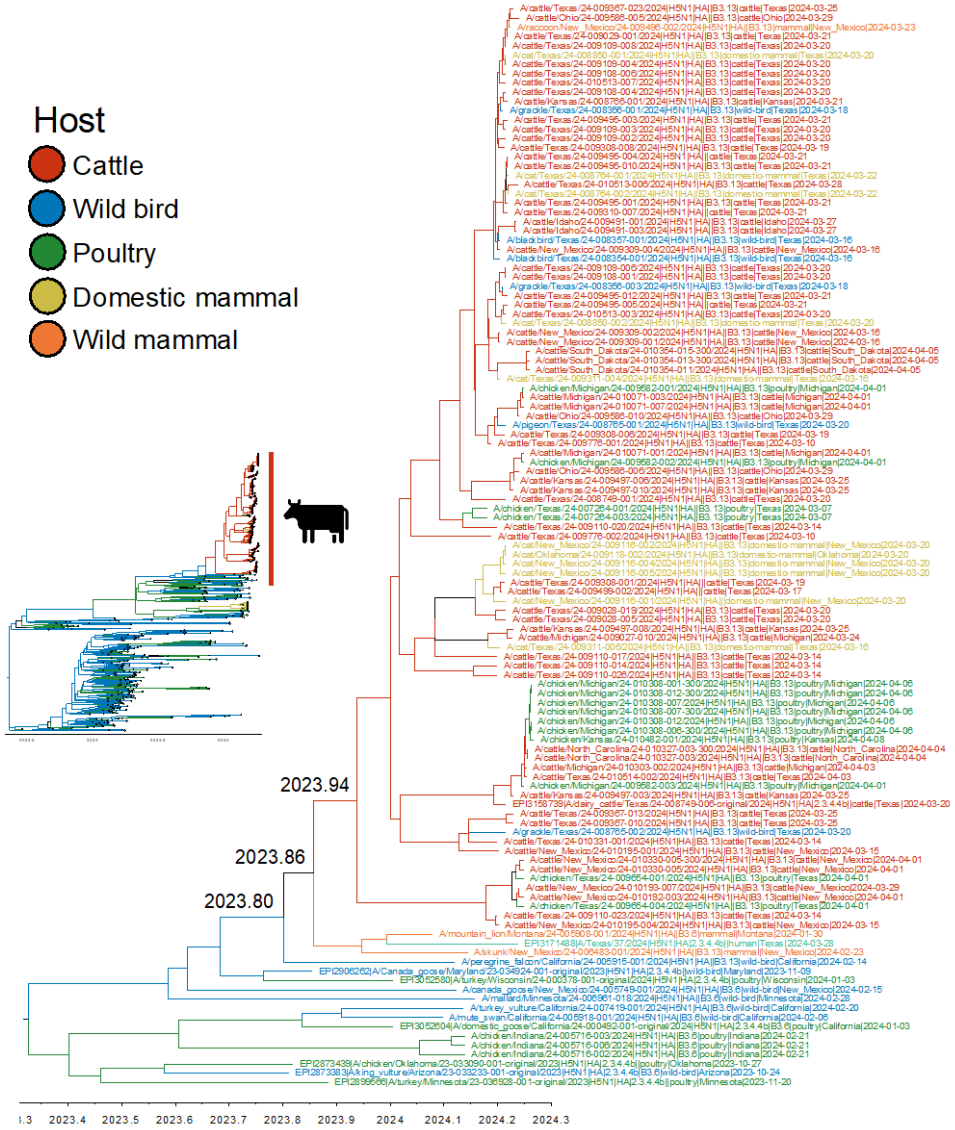
March 27, 2024



April 10, 2024

What is happening now it’s in dairy cattle?

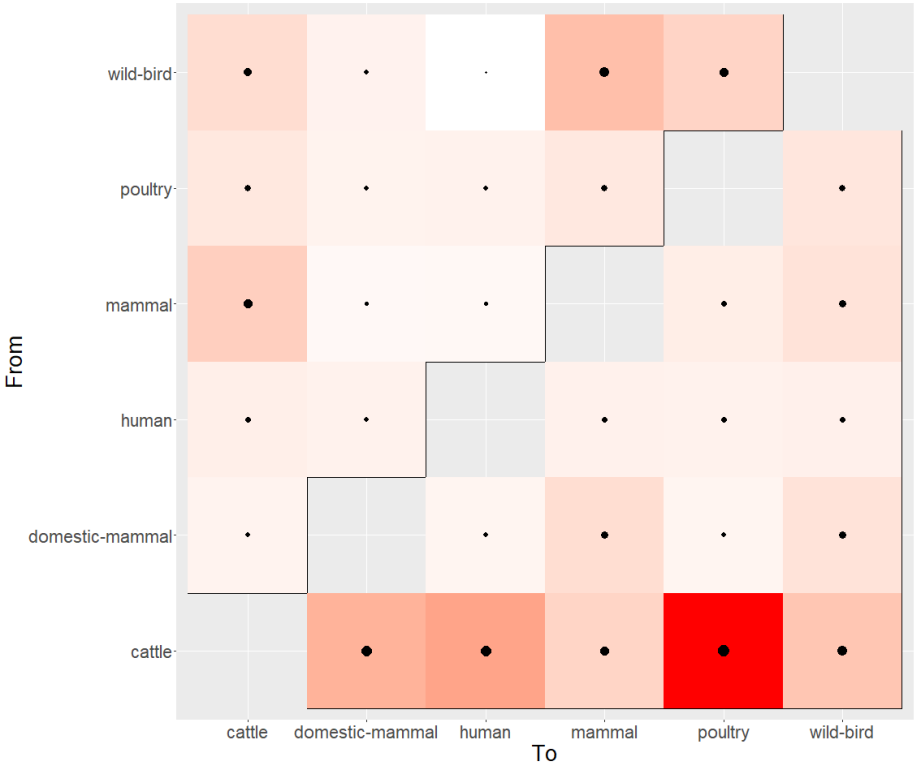
In dairy cattle, then back into other hosts



HA tree

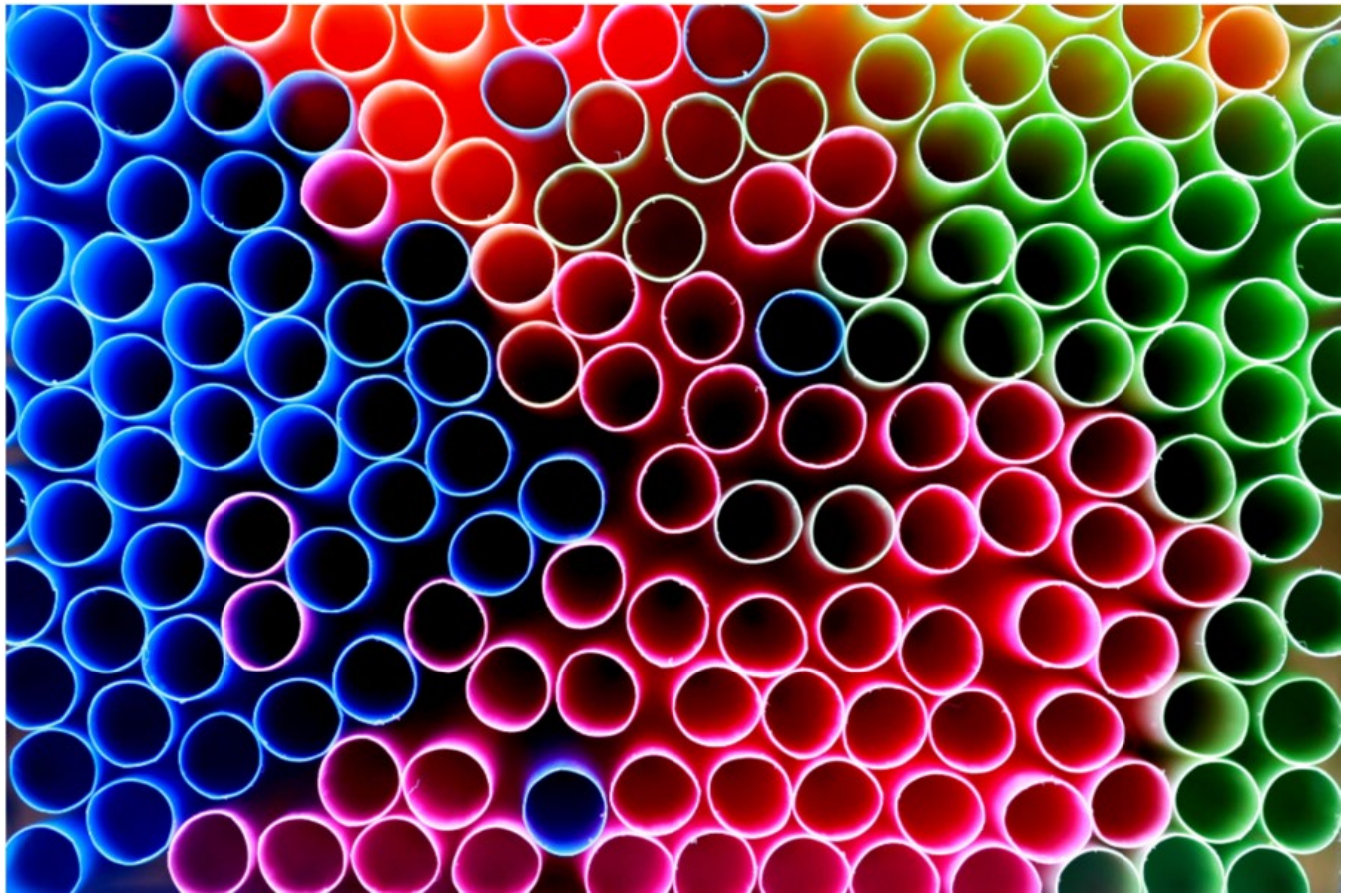
More than 10 cattle to other host transmission events

- Poultry, wild birds and peridomestic mammals
- Low-frequency within host variation and purifying selection



smot: https://github.com/flu-crew/smot

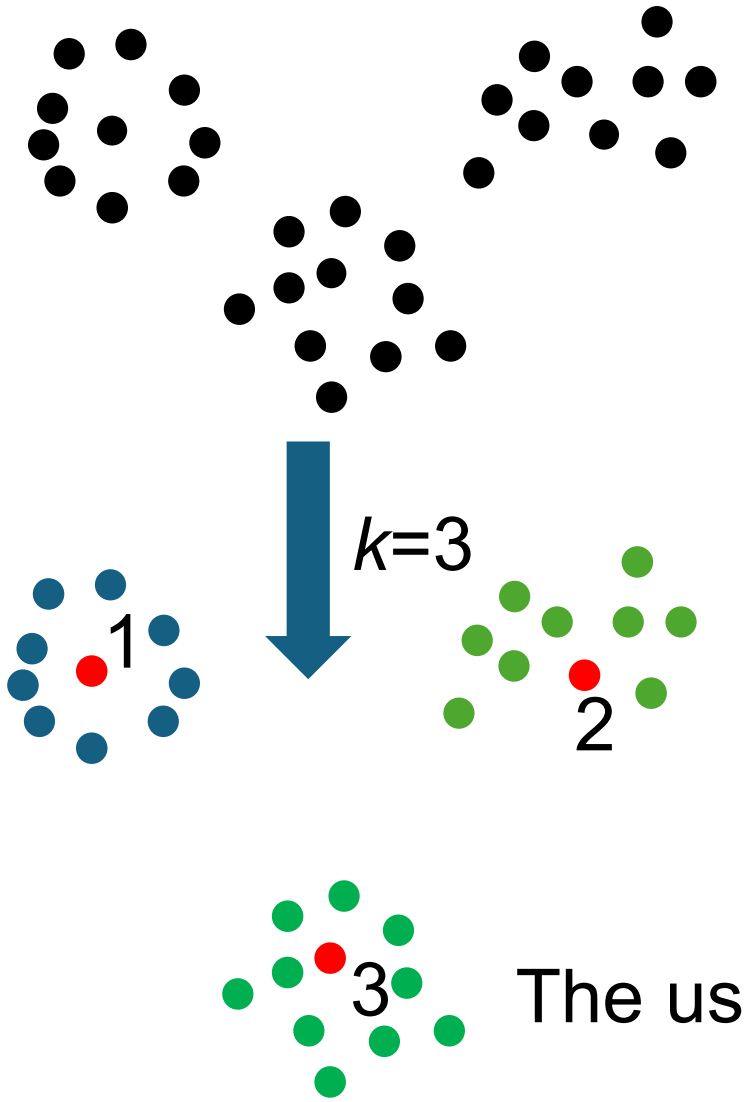
PARNAS: an objective selection of representative strains



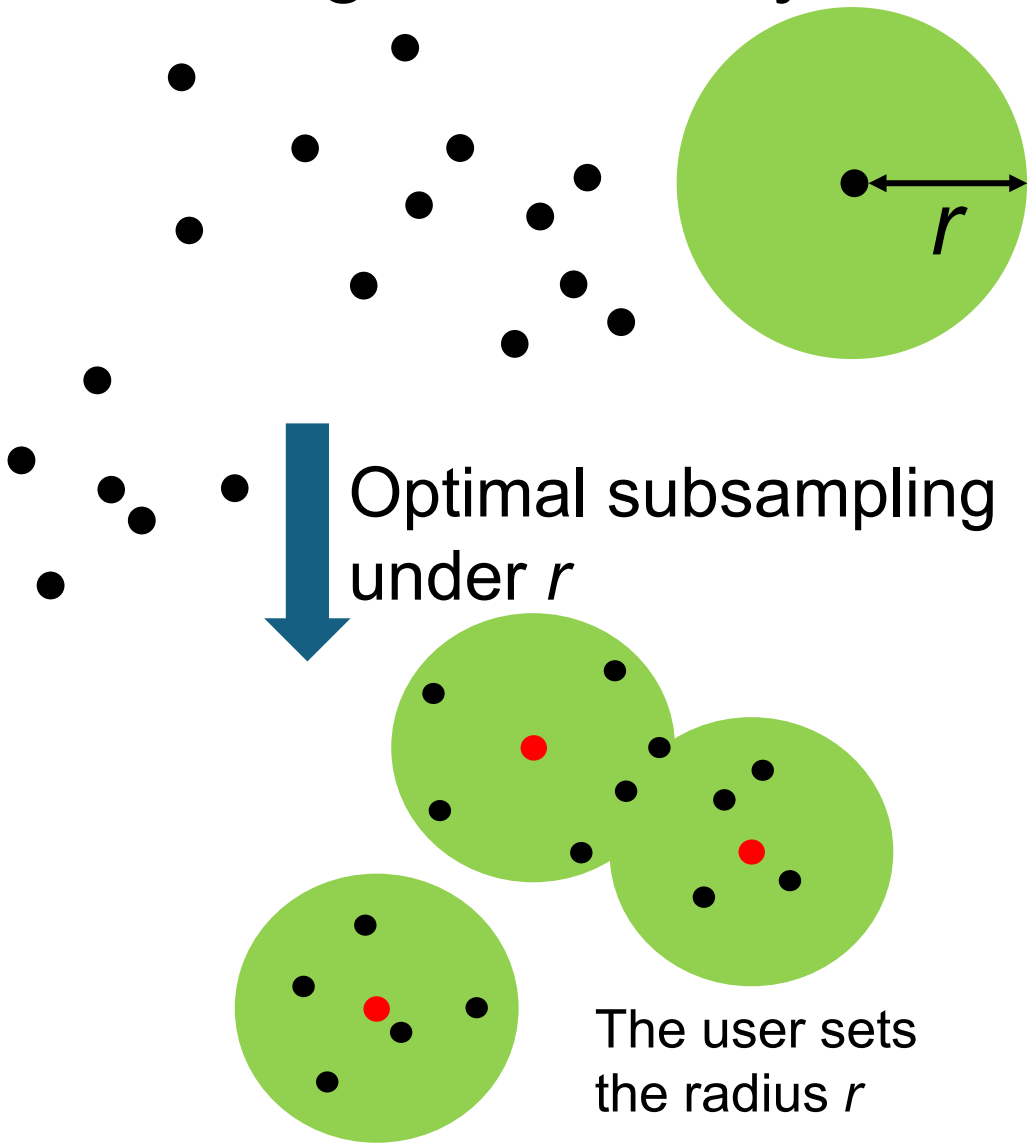
Markin et al. (2023) Systematic Biology: https://github.com/flu-crew/PARNAS

The main PARNAS sampling strategies

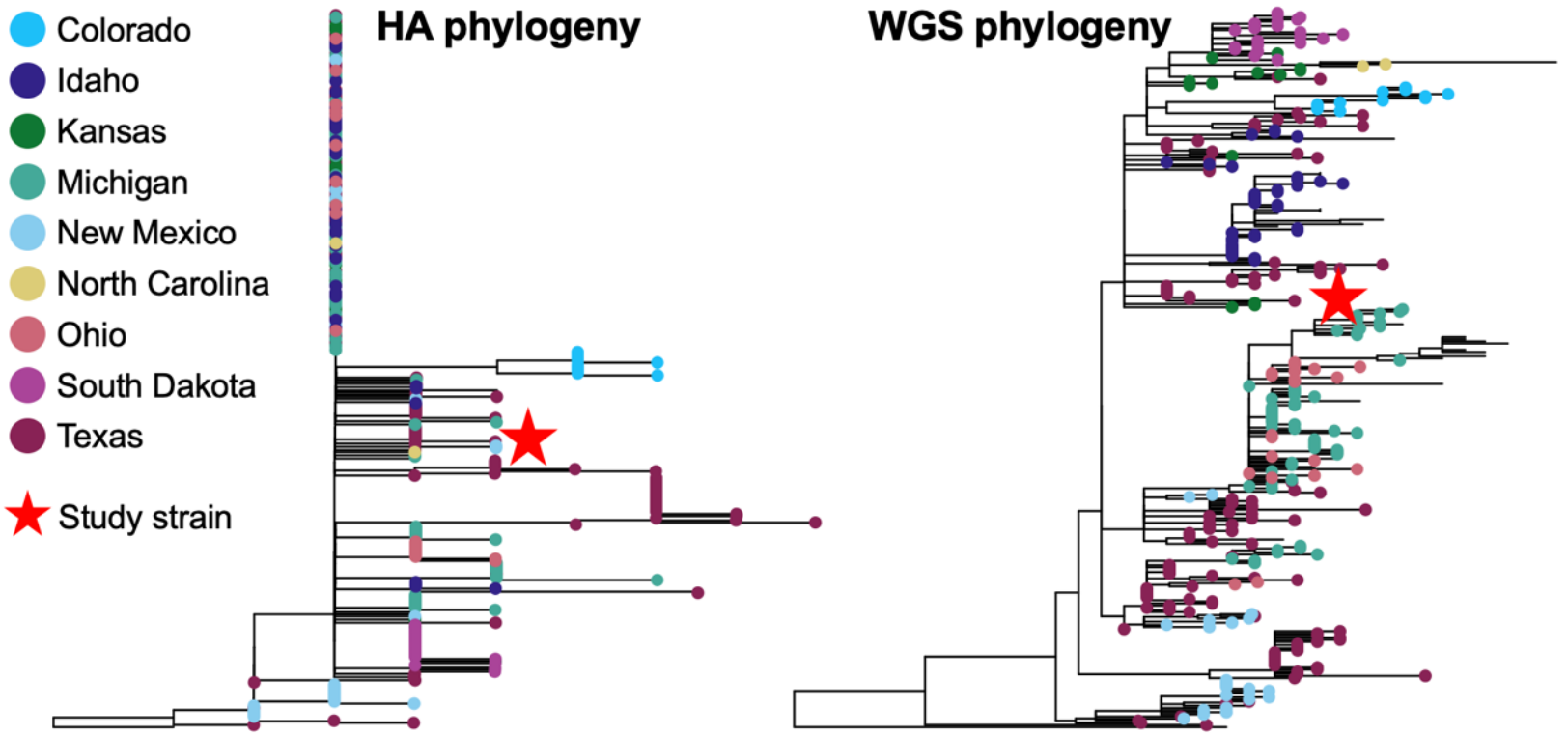
1) Selecting *k* best representatives



2) Covering all diversity



Despite ~6 months of transmission, there is minimal evolution



- The representative strain remains 99.94% similar across the genome; 2 synonymous substitutions in the HA
- A/dairy cattle/Texas/24-008749-002/2024 (can be requested from the National Veterinary Services Laboratories)

NADC flucrew

- Amy Baker
- Tavis Anderson
- Bailey Arruda
- Meghan Wymore Brand
- **Alexey Markin**
- Megan Thomas
- Carine Souza
- Debora Goulart
- Nick Otis
- Katharine Young
- Celeste Snyder
- Giovana Zanella
- **Garrett Janzen**
- **Blake Inderski**
- Sid Grover
- **Sanket Wagle**
- **Sriram Vijendran**
- **Carl Hutter**
- **Thao Nguyen**

Collaborators

- **USDA-APHIS-NVSL**
- **Mia Kim Torchetti**
- **Suelee Robbe-Austerman**
- **Kristina Lantz**
- **IRD/BV-BRC team**
- **Phil Gauger**
- **Oliver Eulenstein**
- **Michael Zeller**
- **Zeb Arendsee**
- **Joe Thomas**
- **Lauren Abrahamsen**
- **Nicola Lewis**
- **Daniela Rajao**
- **Daniel Perez**
- **Bryan Kaplan**
- **Brian Kimble**
- **OFFLU**
- **John Barnes/CDC**
- **Han Di/CDC**
- **Todd Davis/CDC**

Funding: USDA CEIRR CENTERS OF EXCELLENCE FOR INFLUENZA RESEARCH AND RESPONSE CDC