



*OFFLU swine influenza virus meeting
27 – 28 March 2017
FAO Headquarters, Rome, Italy*

USDA SURVEILLANCE PROGRAM FOR INFLUENZA A VIRUS IN SWINE

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Three data streams

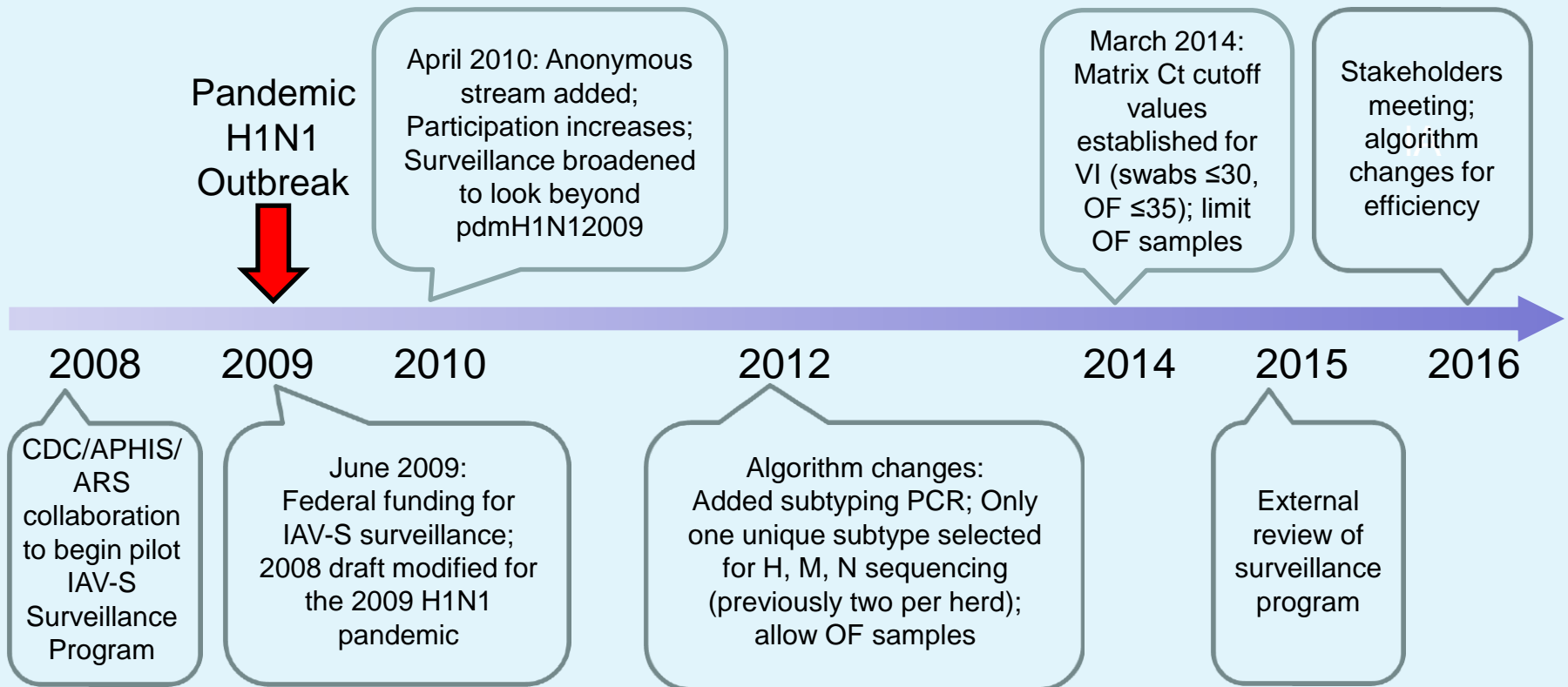
1. Case-compatible swine accessions submitted to the NAHLN system
 - Pigs on farm exhibiting influenza-like illness
 - >99% of samples
2. Swine populations epidemiologically linked to a human case of IAV
3. Swine exhibiting influenza-like illness (ILI) at commingling event such as auctions, markets, fairs, or other swine exhibition events.



Data disclaimers

- Surveillance is voluntary, passive, and anonymous
- No measure of disease prevalence by
 - Time
 - Location
 - Subtype
- State-level data summaries are not externally disclosed
 - Internal state stakeholder may receive state-specific data

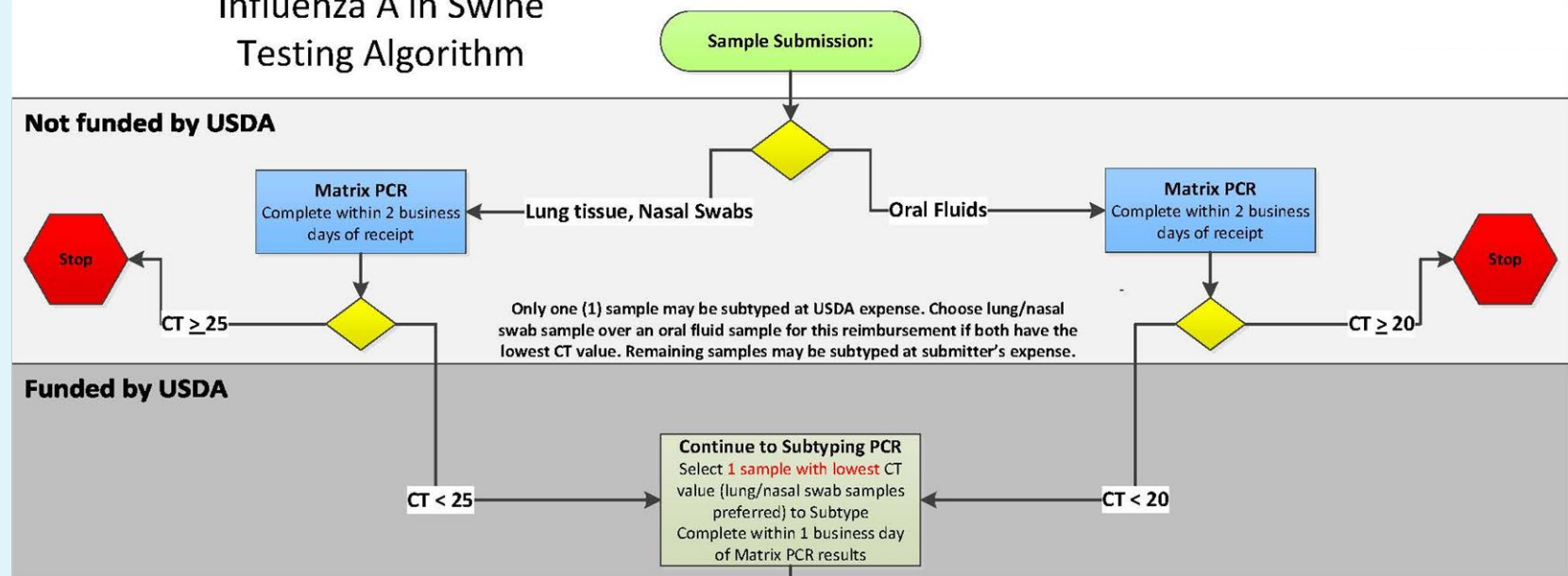
Surveillance Program Timeline History



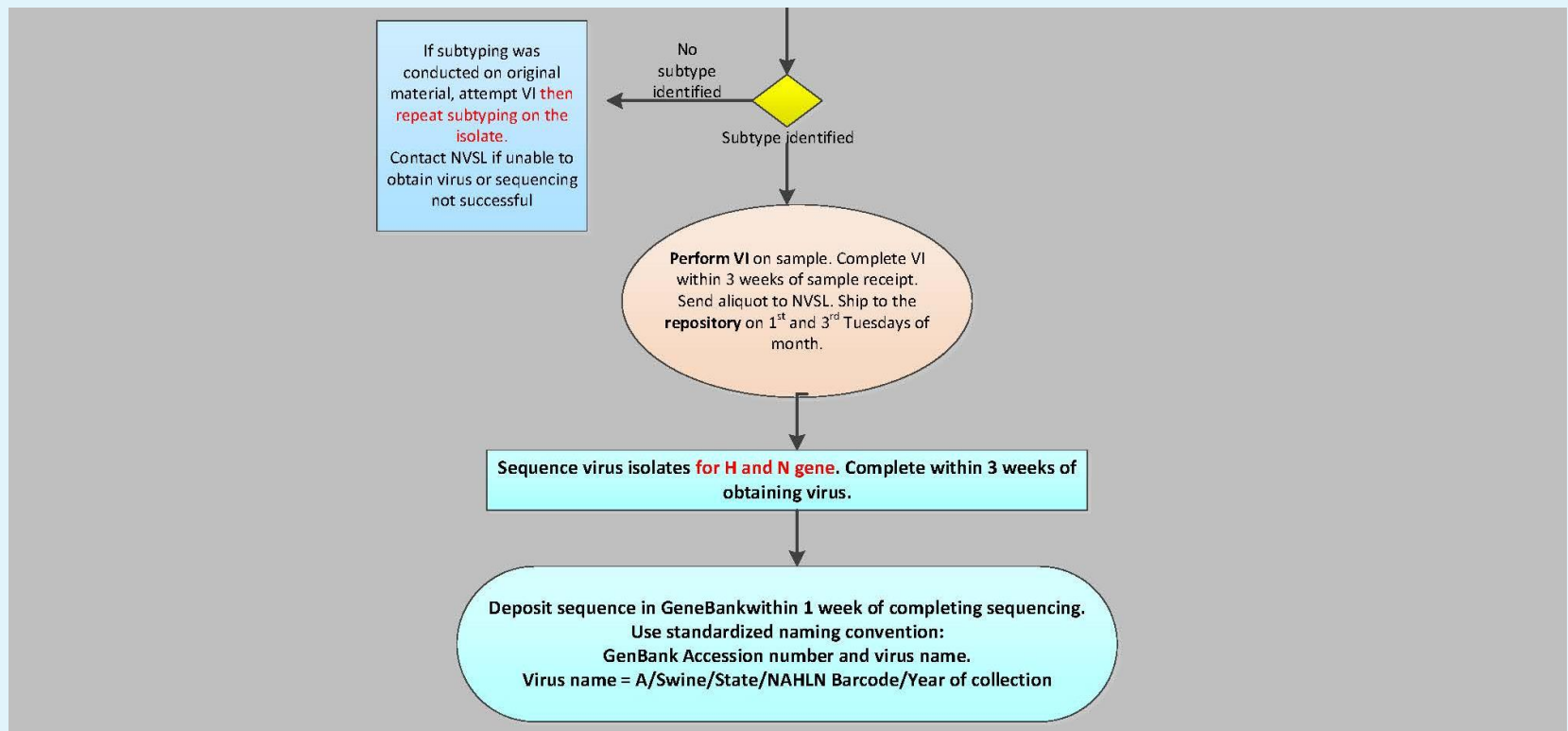
Budget and program modifications

1. Original program funding expected to be depleted soon
2. Stakeholder outreach for program efficiencies
3. Stakeholder meeting in May 2016 in Ames, IA
 - Program goals and objectives revisited
 - Conserve remaining funding until new funding could be identified
 - Discuss suggested modifications to improve efficiencies
4. Virus isolates are key
 - Research, diagnostics and vaccine development
 - Insight into strain variation across U.S. swine
 - Look at antigenic changes (better inform vaccine development)

Influenza A in Swine Testing Algorithm



- Matrix PCR cost no longer borne by the program
- Lower CT cutoff values for further covered testing
- Select only one sample per herd for subtyping



Matrix gene sequencing of select isolates at NVSL via whole genomic sequencing

Number of IAV laboratory accessions and samples tested in swine FY 2010 through Q4 FY 2016.

Measure Names
■ Number of accessions
■ Number of samples

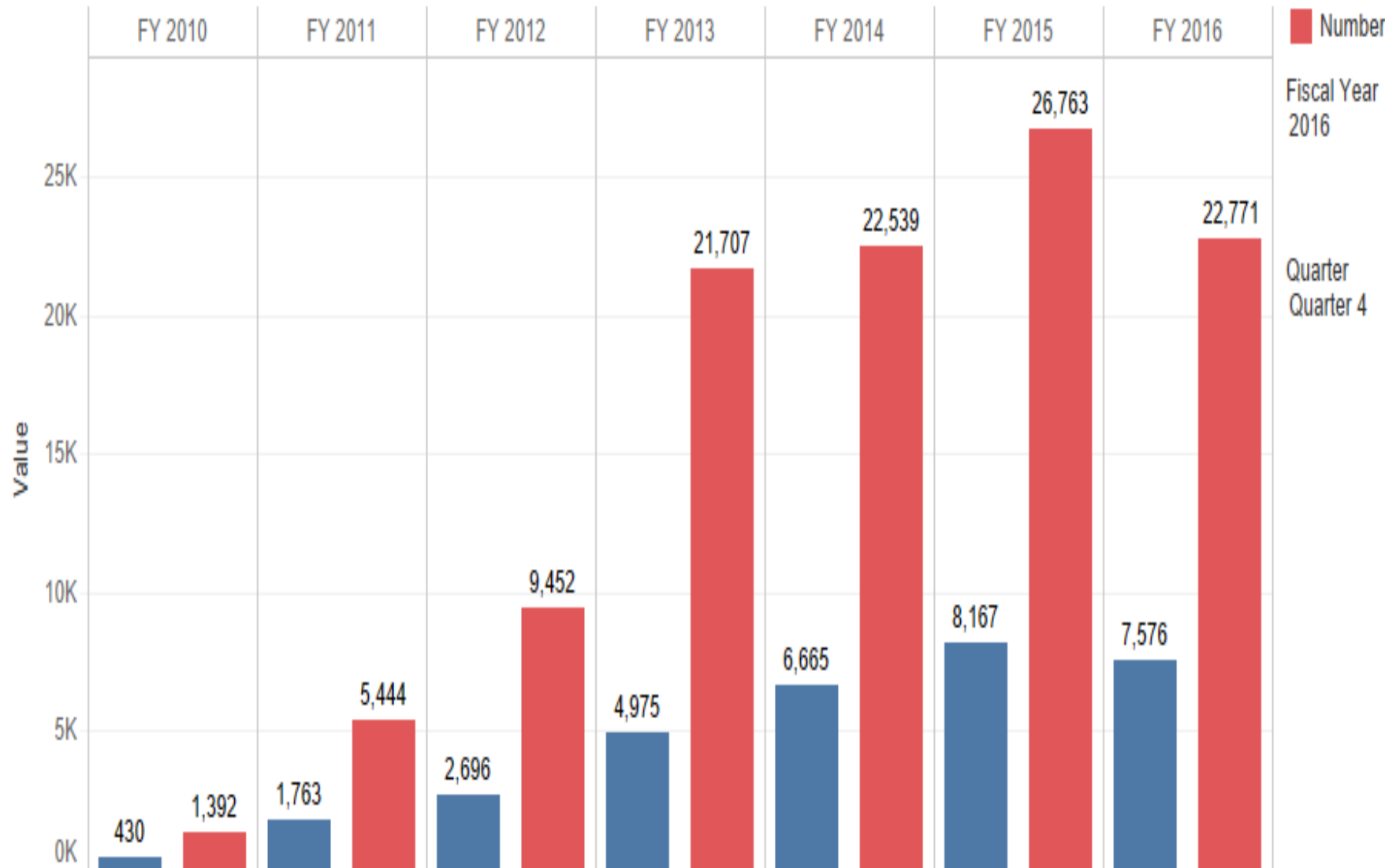
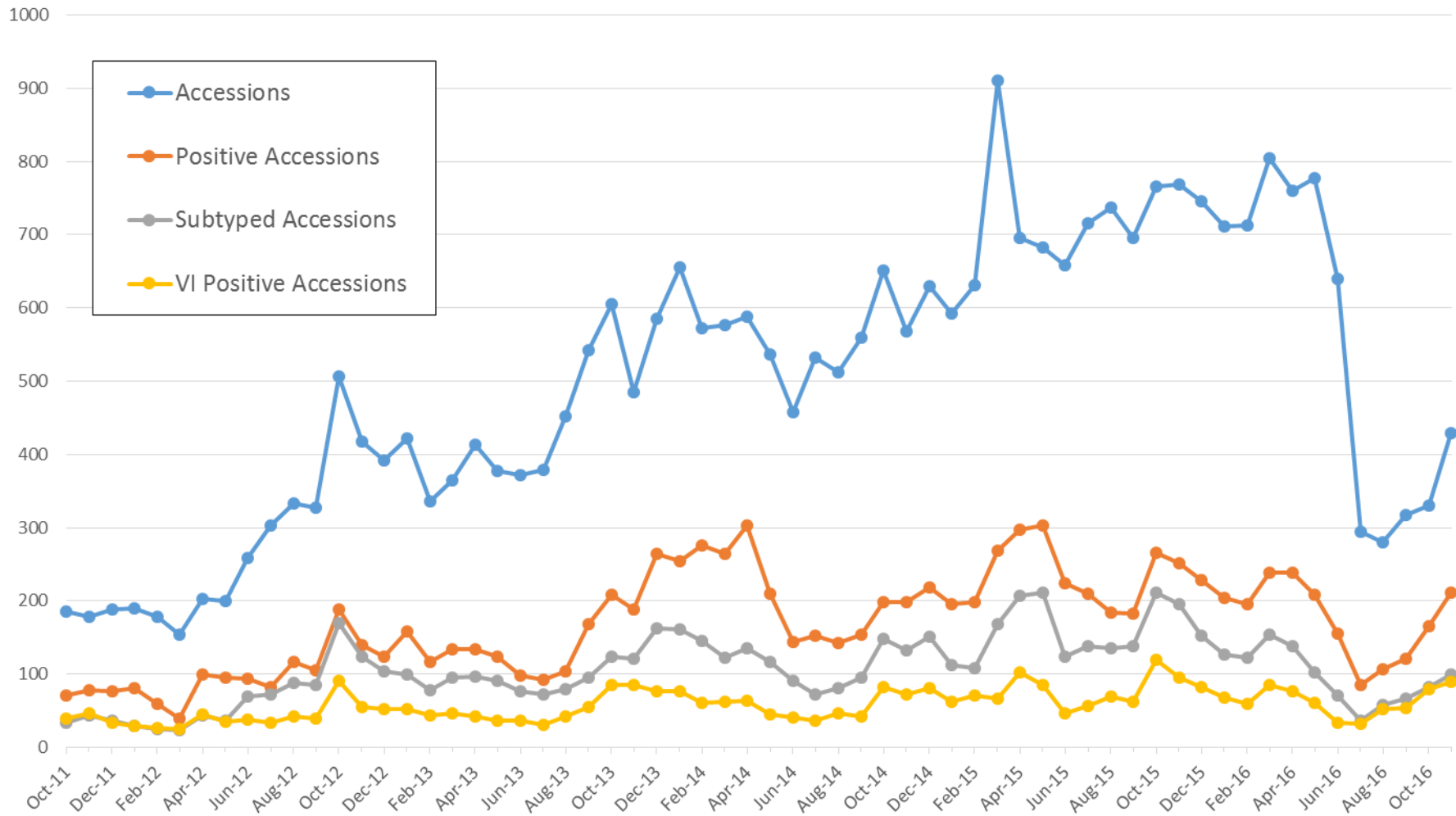


Figure courtesy of Dr. Ellen Kasari & CEAH

Number of accessions collected, subtyped, with matrix positive test results and with virus isolation positive results, October 2011 through November 2016



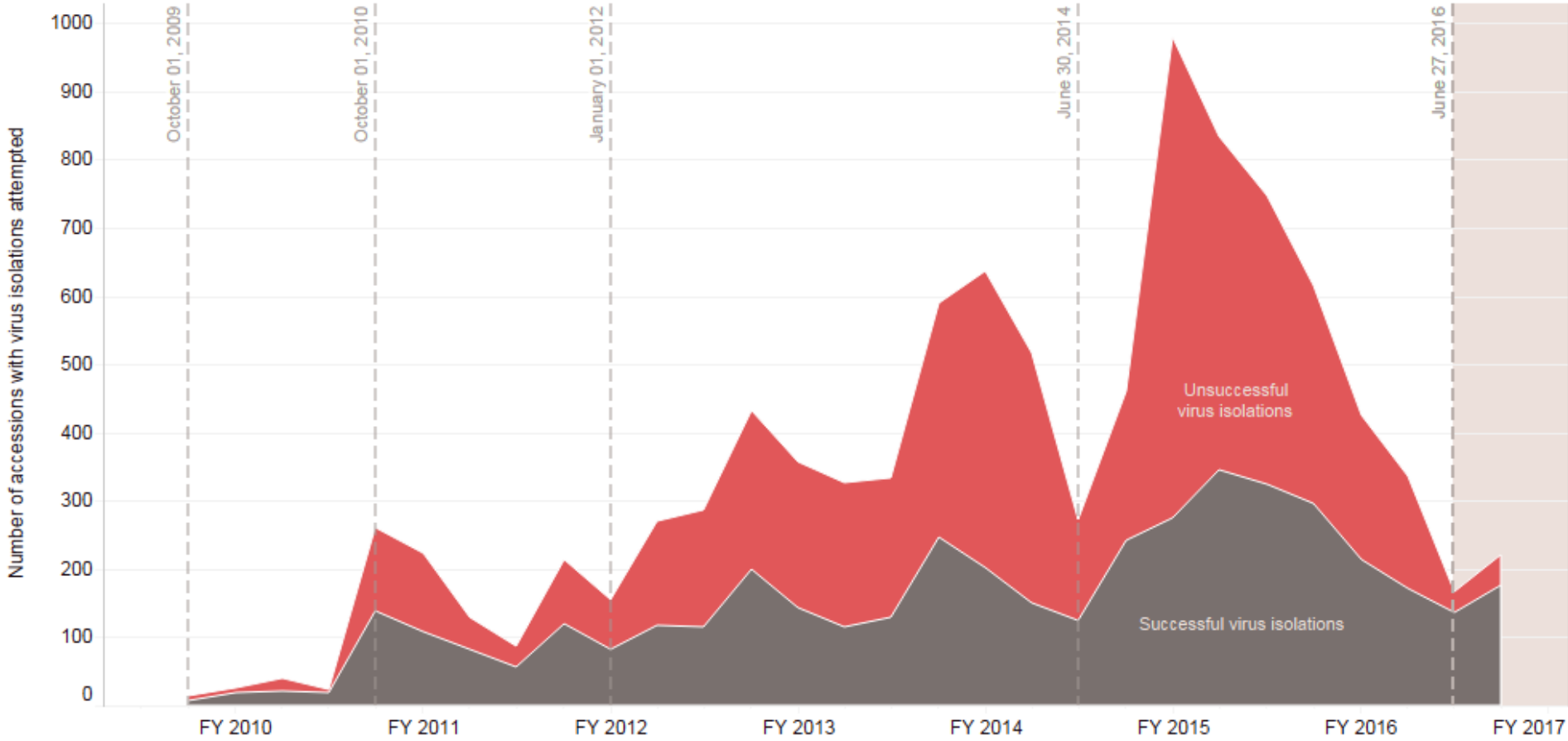
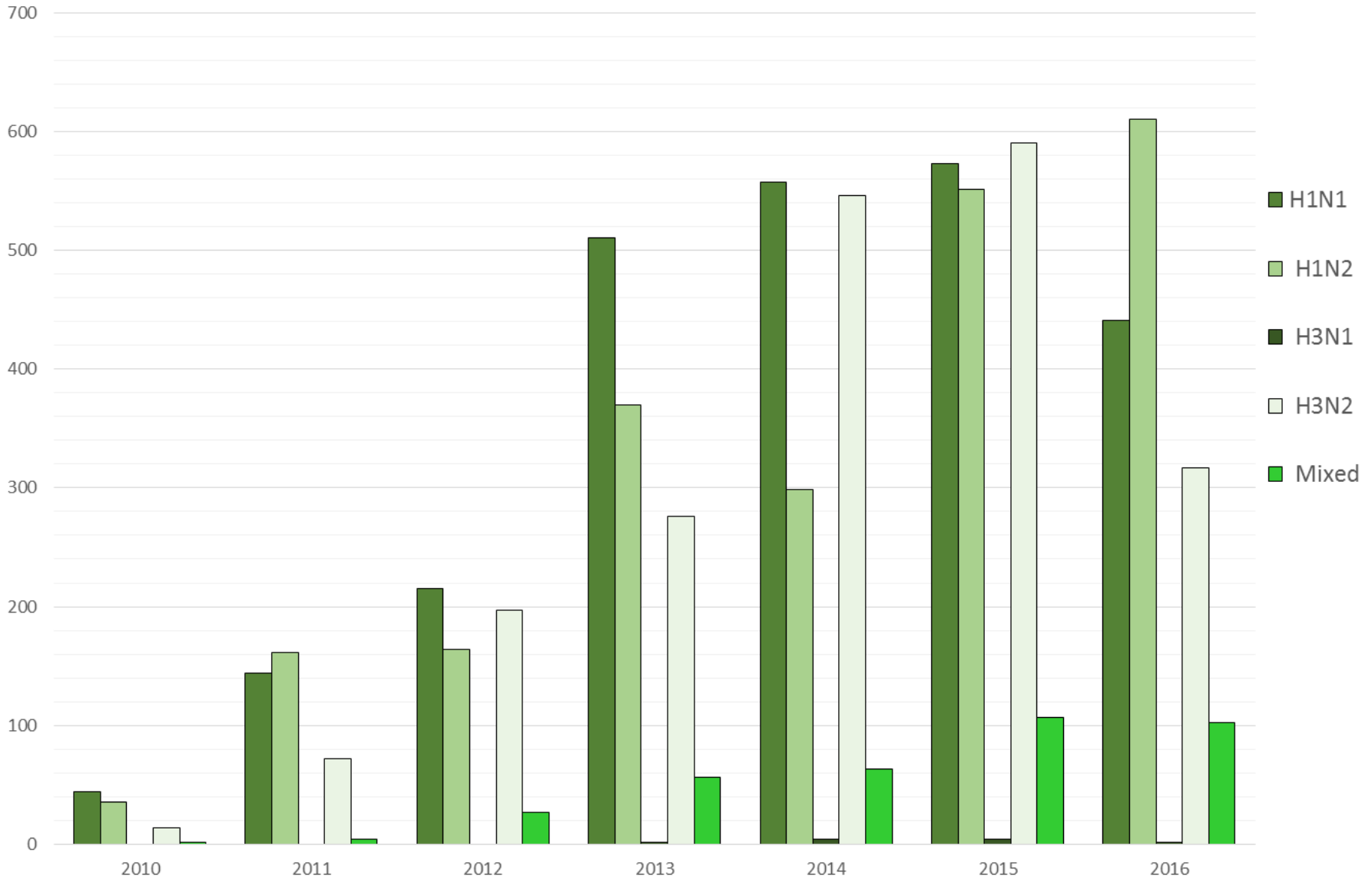


Figure courtesy of Dr. Ellen Kasari & CEAH



Accessions with each virus subtype present FY 2010 through FY 2016



NVSL Roles

- Repository Maintenance
 - ~6100 viruses (representing 37 states)
 - Shipping isolates to research laboratories, biologics companies, public health organizations, domestically and internationally
- Whole genome sequencing of select isolates of interest
- Confirmatory testing
- Assisting in public health investigations

County Fair-associated Zoonotic Transmissions

- July - August 2016
- Seven county fairs
 - Ohio – 4
 - Michigan – 3
- Eighteen human infections reported
 - Variant H3N2 influenza A virus
 - Linked to swine exposure at those fairs
- Swine sampled at each fair
 - Positive for H3N2 virus
- Human viruses were genetically related to the swine viruses detected from the same fairs

Summary

1. Program changes implemented June 27, 2016
 - Impact to the program – **74% cost savings**
 - New algorithm has been posted to web
2. Data management and analysis moving forward
3. 26/33 (79%) of the H3's in FY17-Q1 are Human-like H3s
 - Human-like H3 has now been identified in 11 states
 - Human-like H3 at the 2016 Michigan and Ohio county fairs

Acknowledgements

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