

USDA Influenza A Virus Surveillance Program in Swine

Presented to:

OFFLU SWINE INFLUENZA GROUP

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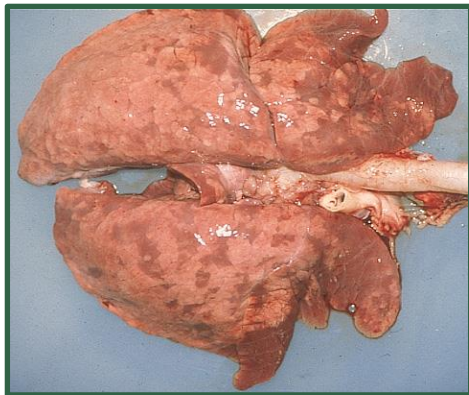


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3 Streams:

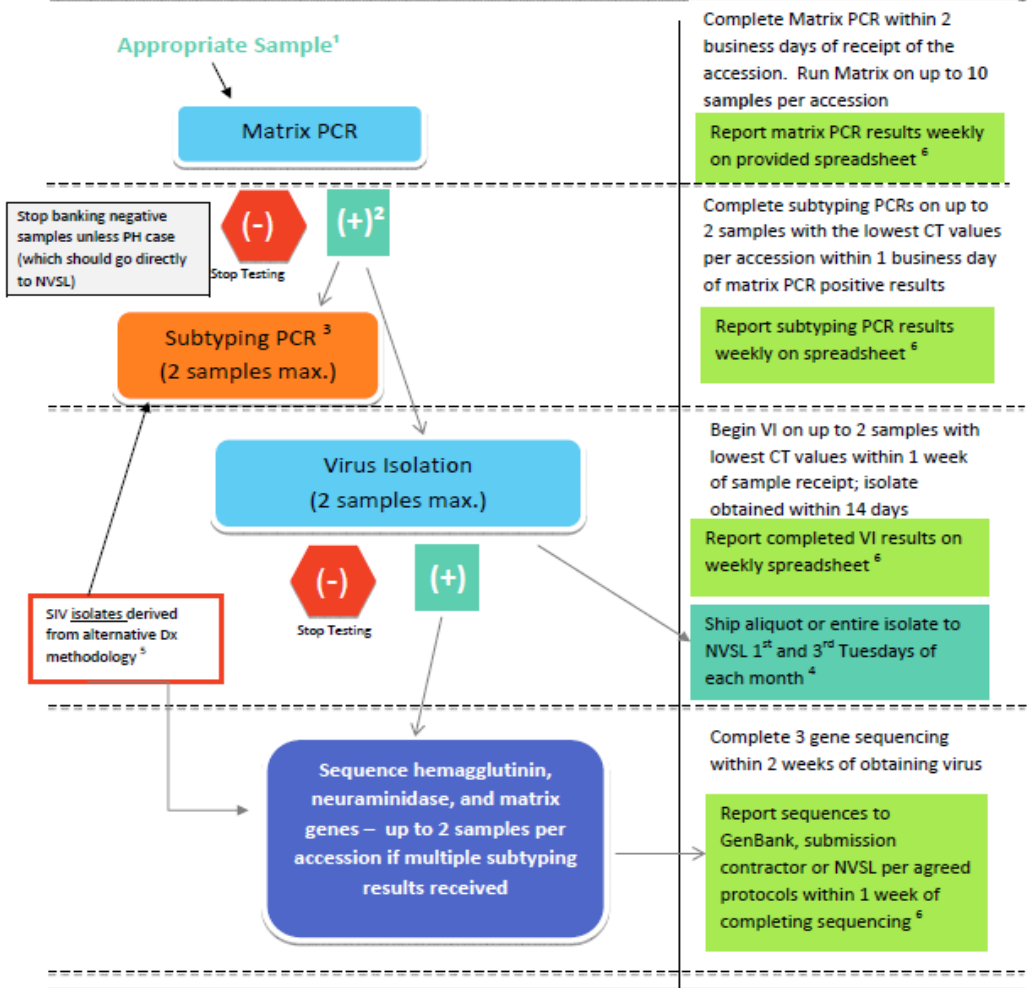
1. Sick pig submissions – NAHLN system – 99+%
2. Pigs related to PH investigations of novel flu cases
3. Swine exhibiting ILI at commingling events such as auctions, markets, fairs, or other swine exhibition events.



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Appendix C: Testing Guidelines, Forms, Submission Instructions

Swine Influenza Virus Testing Algorithm for NAHLN Laboratories



Total time from sample receipt to sequence reporting:
45 Days



Sample Submission Options:

1. Identified (6.3%):

- Only with written permission by swine owner
- Participating NAHLN lab will record producer and submitting veterinarian identifiers
- Can be shared with APHIS-VS

2. Anonymous (93.7%):

- Only state of accession origin is shared with APHIS-VS
- Dataset is blinded to producer information, submitting vet, testing lab

Under both options - capture reason for submission, age of swine, sample type, clinical severity (if shared)

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Data Disclaimers:

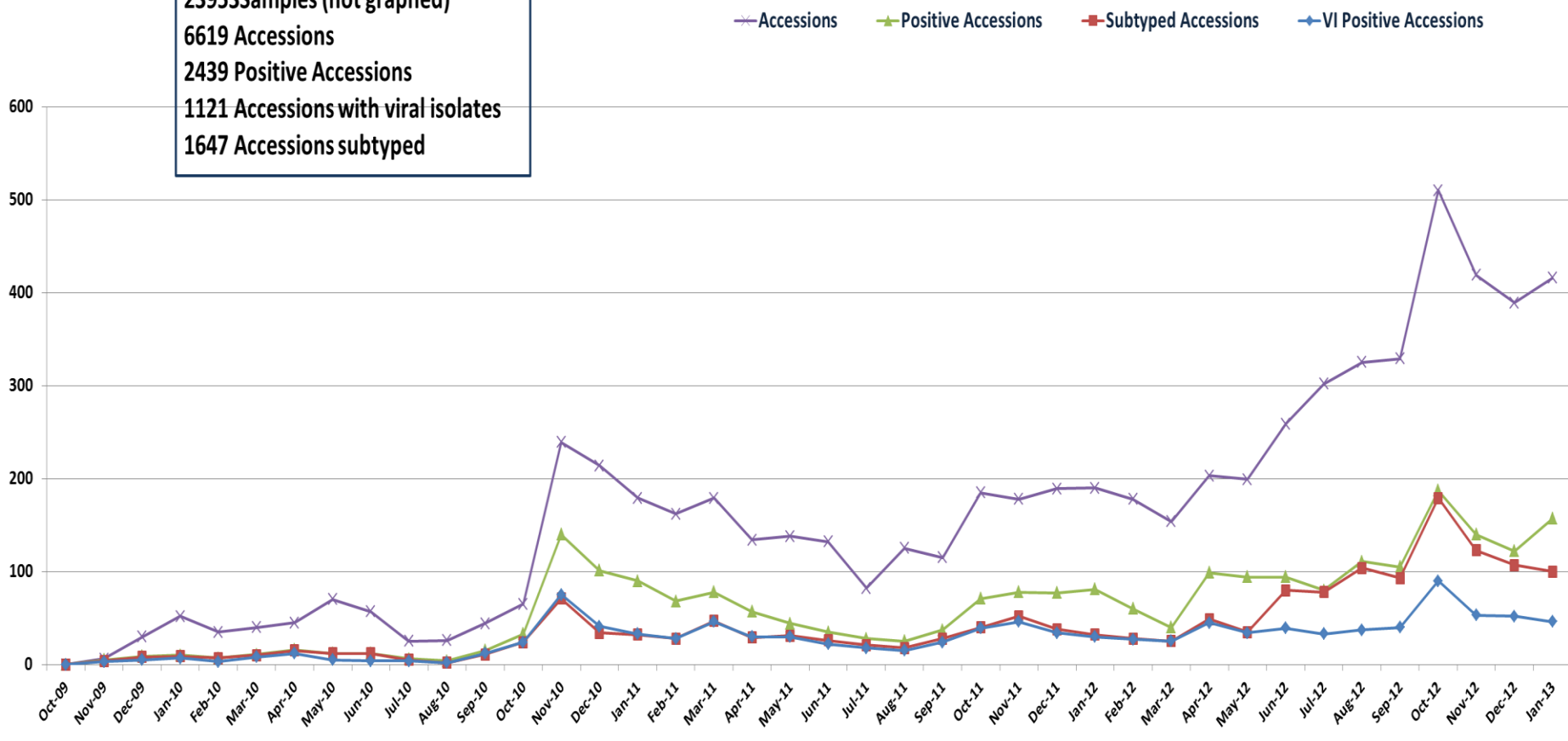
1. Surveillance is voluntary, passive, and anonymous
2. Does not indicate disease prevalence by
 - a. time
 - b. location
 - c. subtype
3. State-level data summaries are not disclosed externally (internal state stakeholders may get state-specific data)



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USDA SIV Surveillance Program Isolation and Characterization Activities - 10/1/2009-1/31/2013

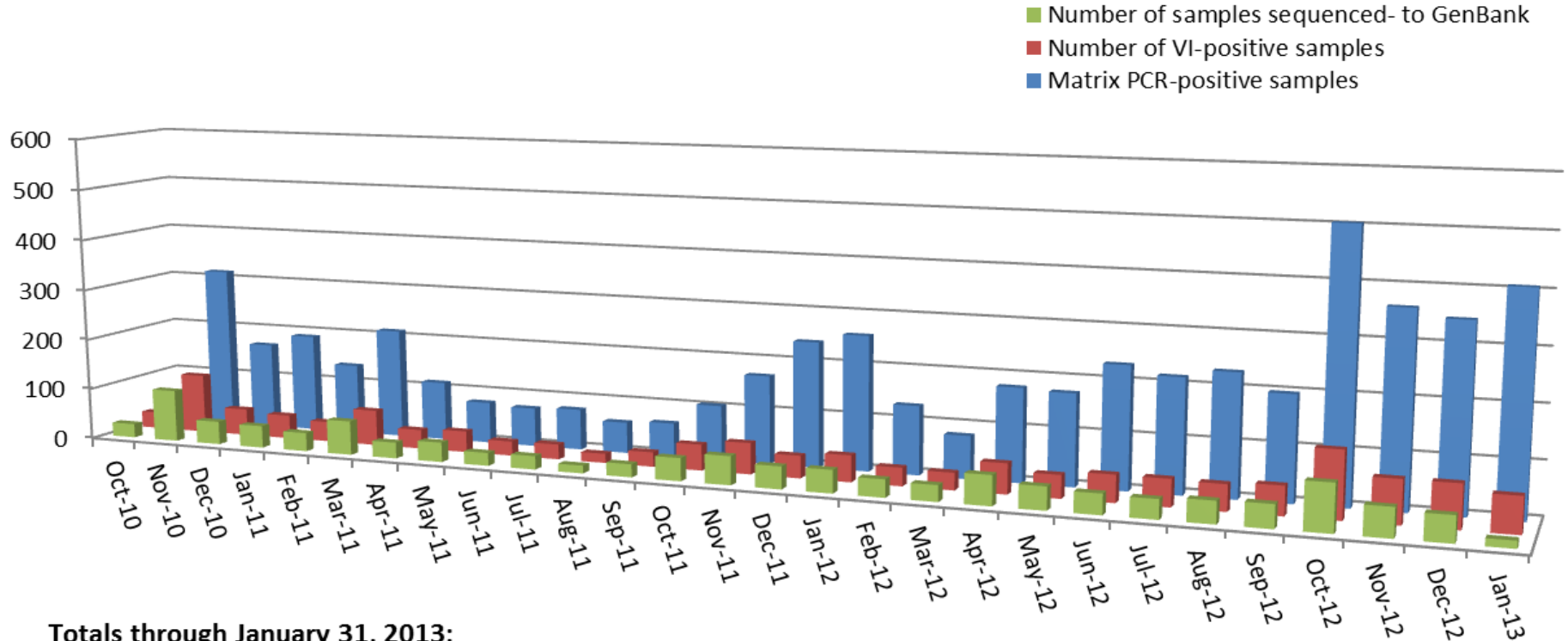
23953 Samples (not graphed)
6619 Accessions
2439 Positive Accessions
1121 Accessions with viral isolates
1647 Accessions subtyped



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USDA Influenza A Virus in Swine Surveillance Program GenBank Accessions by Month

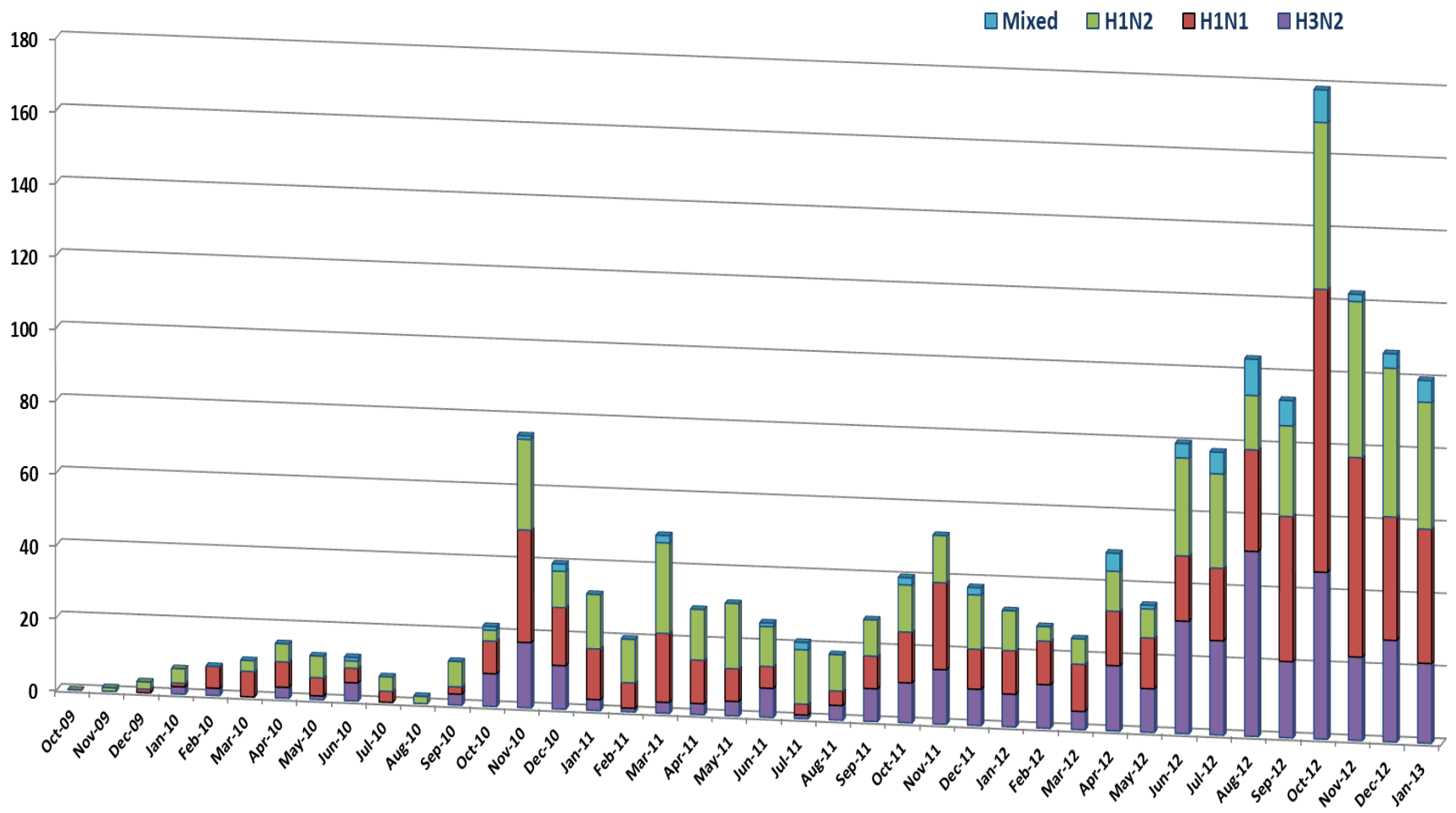


Totals through January 31, 2013:

Matrix Positive Samples:	5498	
VI Positive Samples:	1540	28.0%
Sequenced Samples:	1304	84.7%

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USDA SIV Surveillance Program - Subtypes Identified by Month - 10/1/2009-01/31/2013



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NVSL Roles

Repository

- ~1600 viruses
- Shipped-international, biologics companies, research, PH

Full genome sequencing

- Random viruses received
- Representatives of each subtype (H1N1, H3N2, H1N2)
- Representatives from each submitted state

Confirmatory testing

Public health investigations

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Influenza at the Human-Animal Interface-2012 Fairs

PCR screening

- Matrix
- Pandemic matrix
- Subtyping
- H3N2pM

Sequencing via ion torrent

- Direct from nasal swabs
- Virus

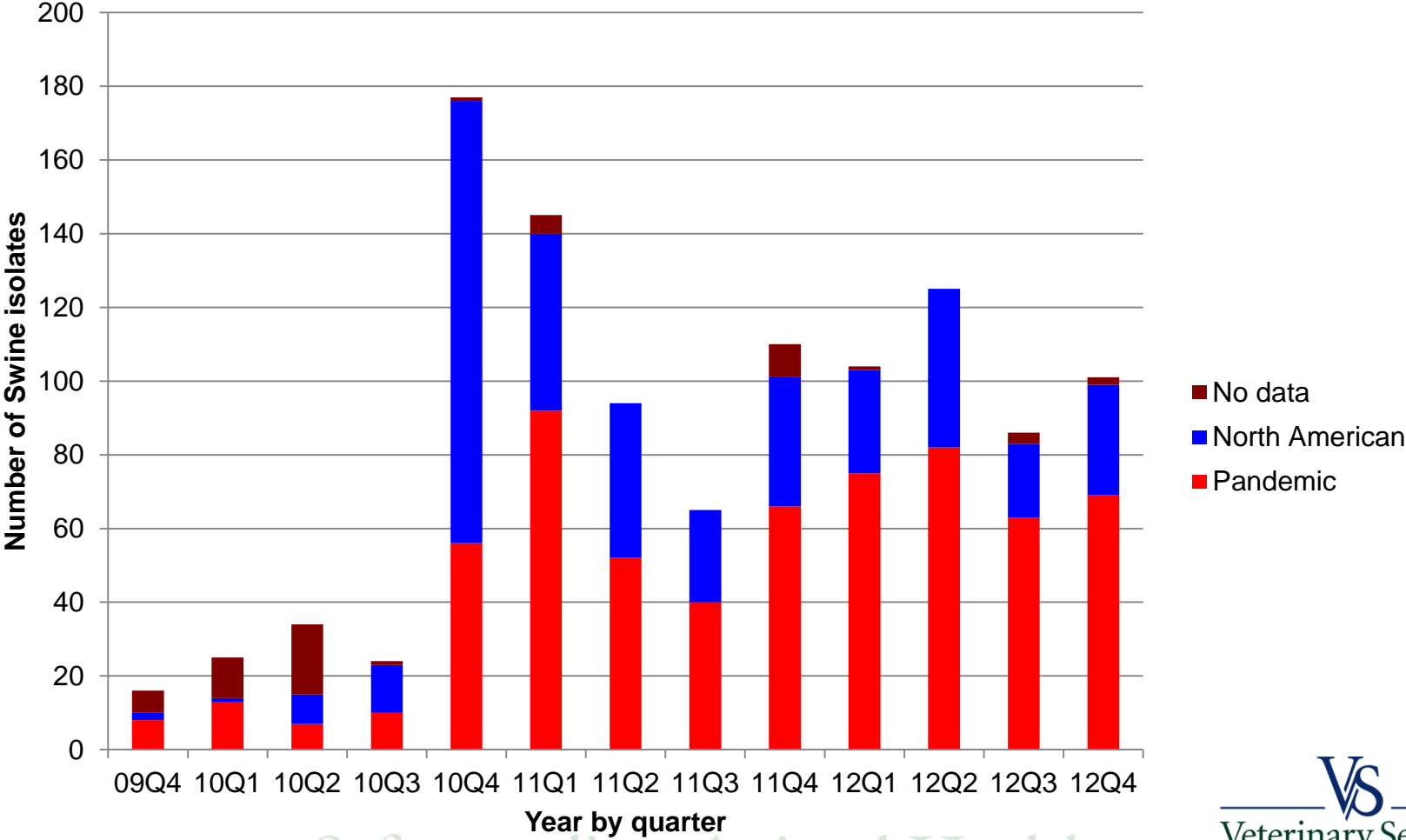
Shared information

- State/Federal animal health
- State/Federal public health



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Matrix lineage 2009-2012



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Case Count: Detected U.S. Human Infections with H3N2v by State since August 2011

<http://www.cdc.gov/flu/swineflu/h3n2v-case-count.htm>

Current as of March 30, 2013

* Case in Utah occurred in April 2012

States Reporting H3N2v Cases	Cases in 2011	Cases in 2012
Hawaii		1
Illinois		4
Indiana	2	138
Iowa	3	1
Maine	2	
Maryland		12
Michigan		6
Minnesota		5
Ohio		107
Pennsylvania	3	11
Utah		1*
West Virginia	2	3
Wisconsin		20
Total	12	309

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Gaps in Current Effort



- Data representativeness
 - By geography – farm-state-U.S.
 - By veterinary clinic
 - By production system (interstate movement not tracked)
- Isolated data - cannot observe changes over time within populations
- Many sequences still not shared – autogenous vaccines, non-participants

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Summary:

- Influenza A in swine currently very dynamic
- Multiple insertions of human-origin strains into the U.S. swine IAV population since 1998
- Intact human viruses not recovered from swine
- Widespread reassortment documented
- The USDA IAV-S Surveillance Program is an opportunity to monitor changes nationally
- Genomic analysis of collected data is intensifying
- Better understanding of within herd and area IAV ecology needed but is not a current function of this program



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It Takes A Village.....Thank You!

- Producers, practitioners, NAHLN labs for supporting the surveillance and fair investigations
- State Animal Health Officials
- Local, State, and Federal Public Health
- Veterinary Services personnel
- Agricultural Research Services personnel

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