U of Minnesota IAV-S Testing Summary

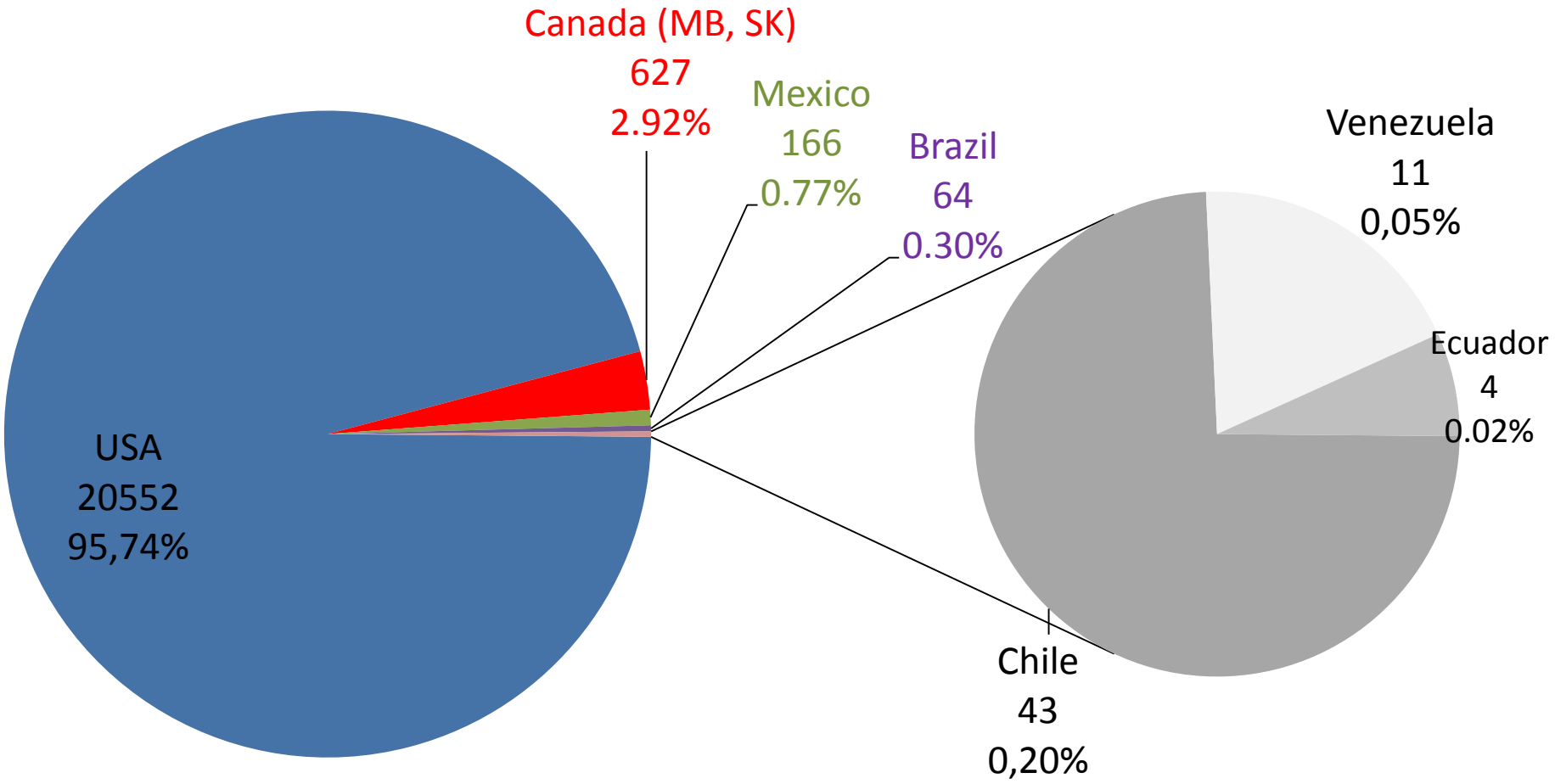
11-1-2014 to 11-30-2015

Marie Culhane

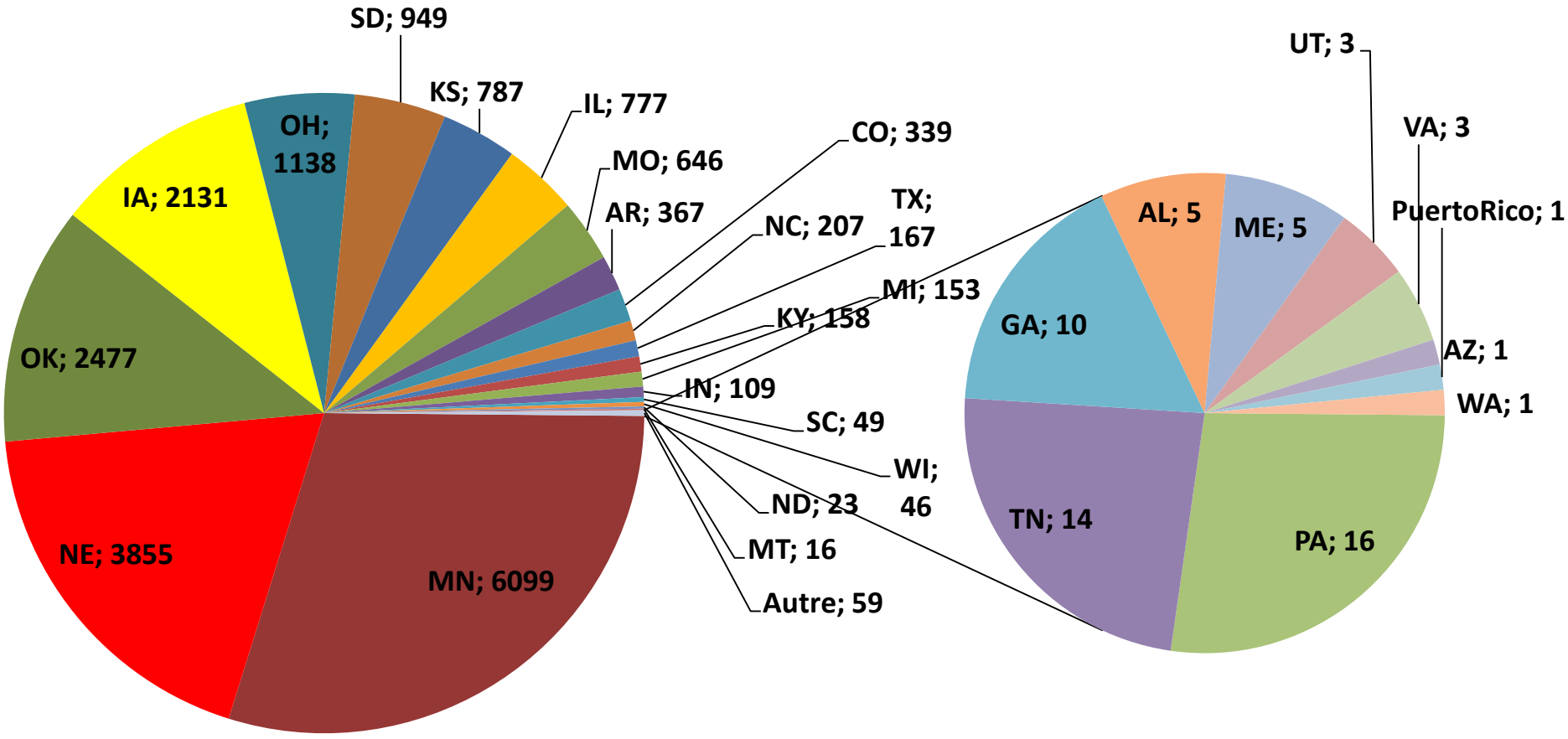
21,467 IAV-S rRT-PCR Matrix Gene Tests Performed between 11-1-2014 to 11-30-2015

- Samples from pigs in
  - 30 US States
  - 4 Canadian Provinces
  - 2 Mexican States
  - 4 South American Countries
    - Chile, Ecuador, Brazil, Venezuela
- 33% as part of USDA Flu Surveillance
  - 7016 of 21,467

Pig Locations



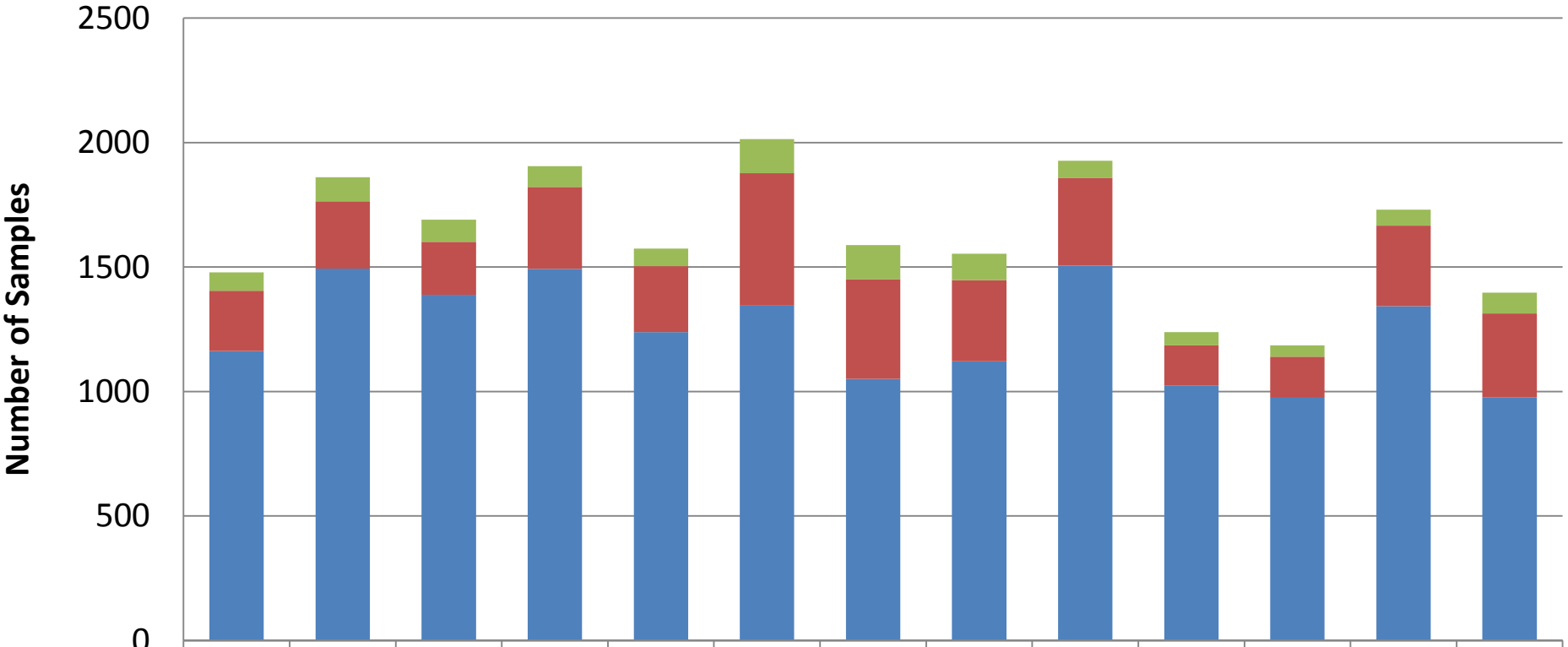
USA Pig Locations



Top States in US$ Hogs and Pigs Sold, USDA NASS 2012

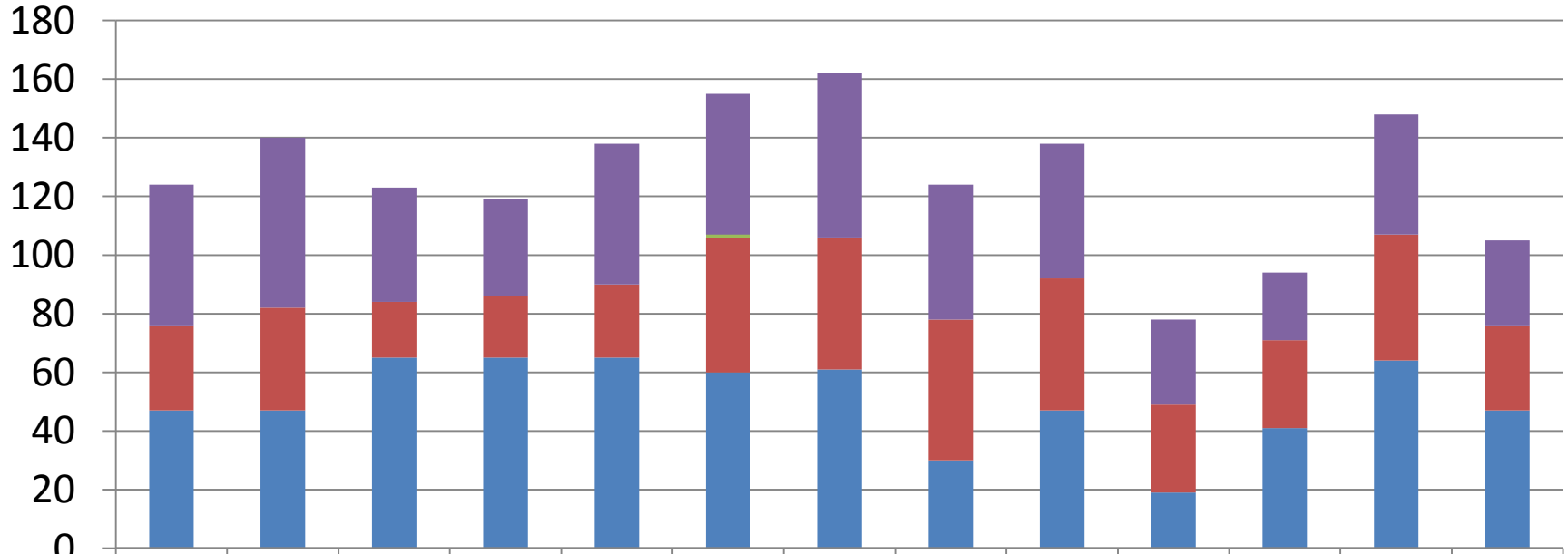
IA 6.8; **NC** 2.9; **MN** 2.8; **IL** 1.5; IN 1.3; **NE** 1.1; **MO** 0.9; **OH** 0.8; **KS** 0.7; **OK** 0.7

IAV-S rRT-PCR Matrix Gene Test Results
11-1-2014 to 11-30-2015



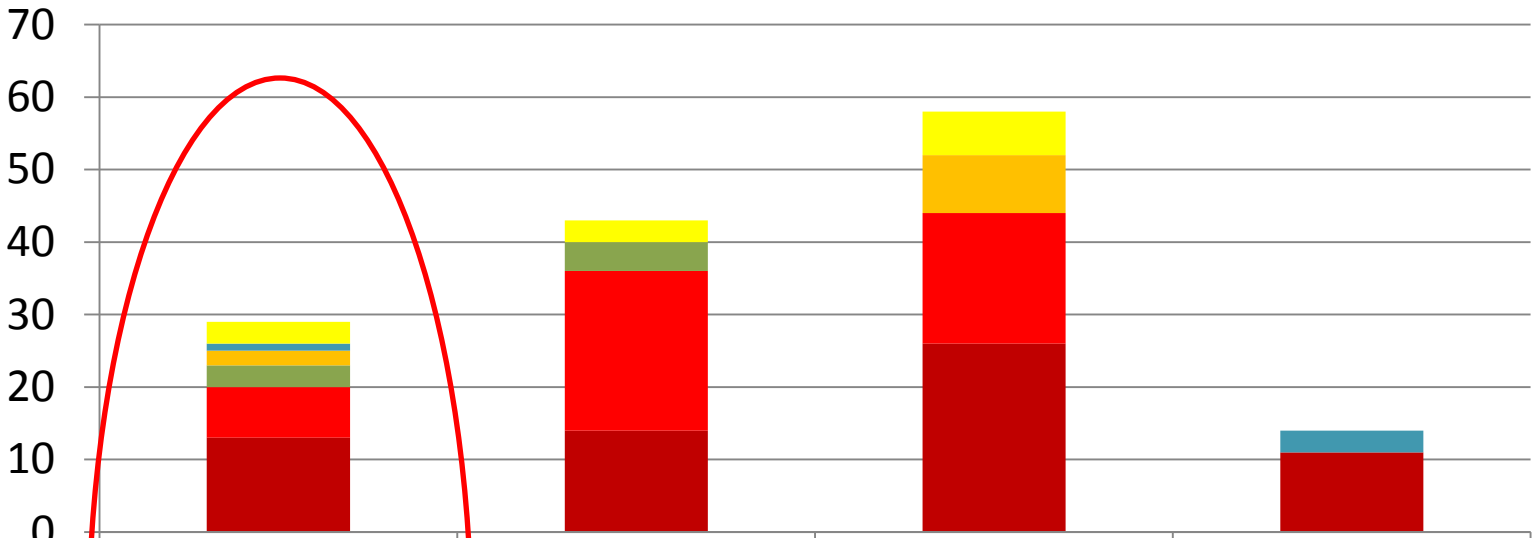
	2014		2015										
	11	12	1	2	3	4	5	6	7	8	9	10	11
Suspect	74	96	89	84	71	137	137	106	69	53	45	64	84
POSITIVE	242	270	213	329	265	532	400	326	353	161	165	323	336
Neg	1162	1494	1388	1492	1238	1345	1051	1121	1505	1024	975	1343	977

IAV-S Subtypes by Year and Month



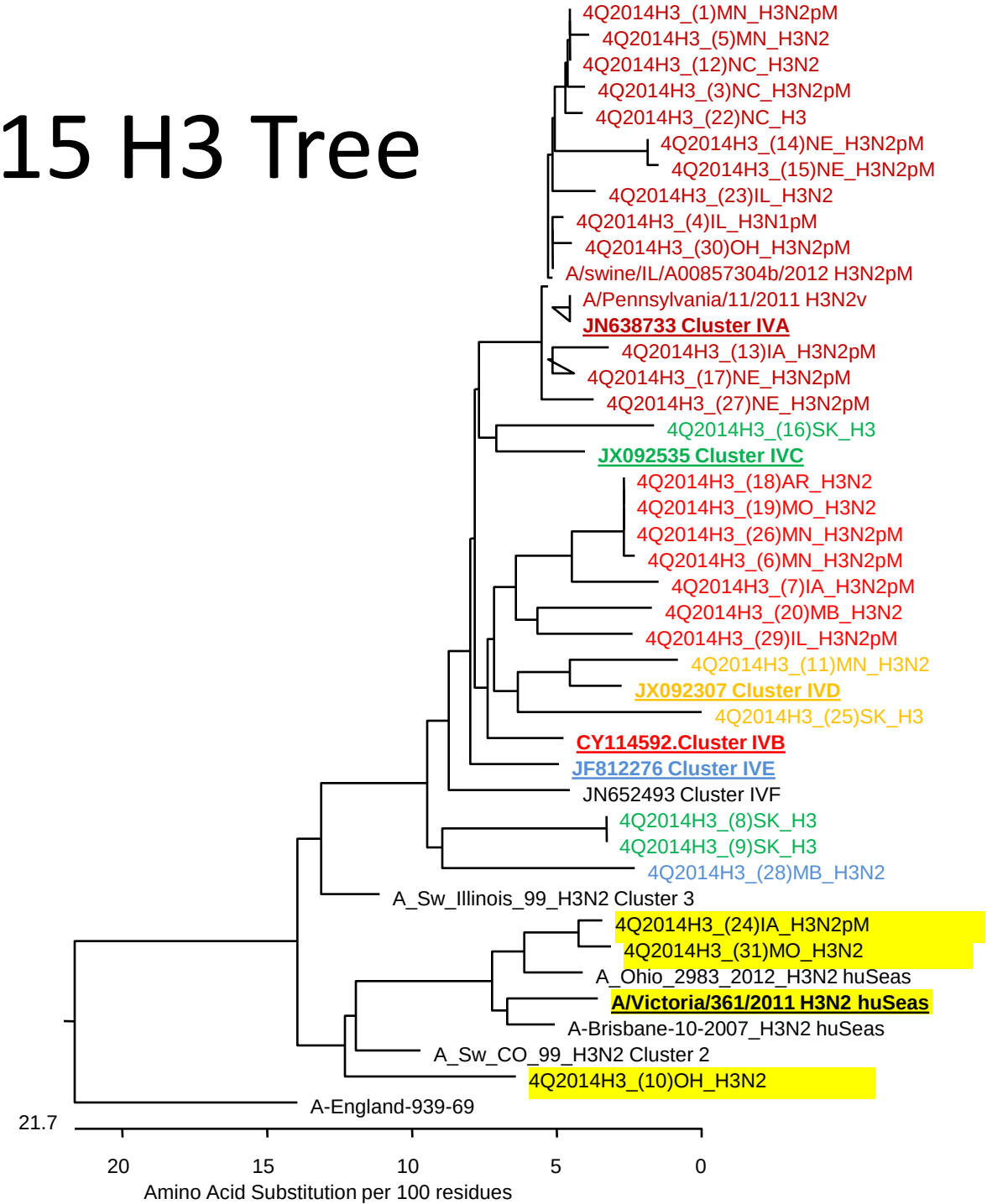
	11	12	1	2	3	4	5	6	7	8	9	10	11
	2014		2015										
H3N2	48	58	39	33	48	48	56	46	46	29	23	41	29
H3N1						1							
H1N2	29	35	19	21	25	46	45	48	45	30	30	43	29
H1N1	47	47	65	65	65	60	61	30	47	19	41	64	47

IAV-S H3 Genetic Clusters by Quarter

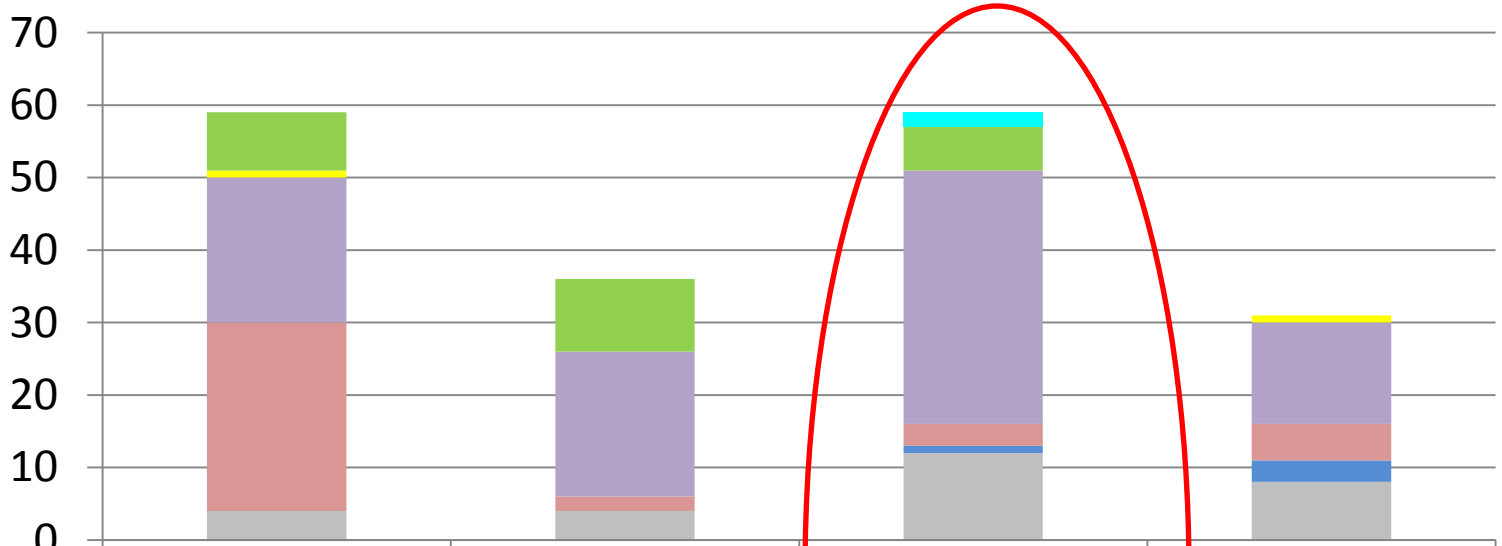


	4Q2014 H3	1Q2015 H3	2Q2015 H3	3Q2015 H3
otherH3	3	3	6	0
IVFH3	0	0	0	0
IVEH3	1	0	0	3
IVDH3	2	0	8	0
IVCH3	3	4	0	0
IVBH3	7	22	18	0
IVAH3	13	14	26	11

4Q2015 H3 Tree

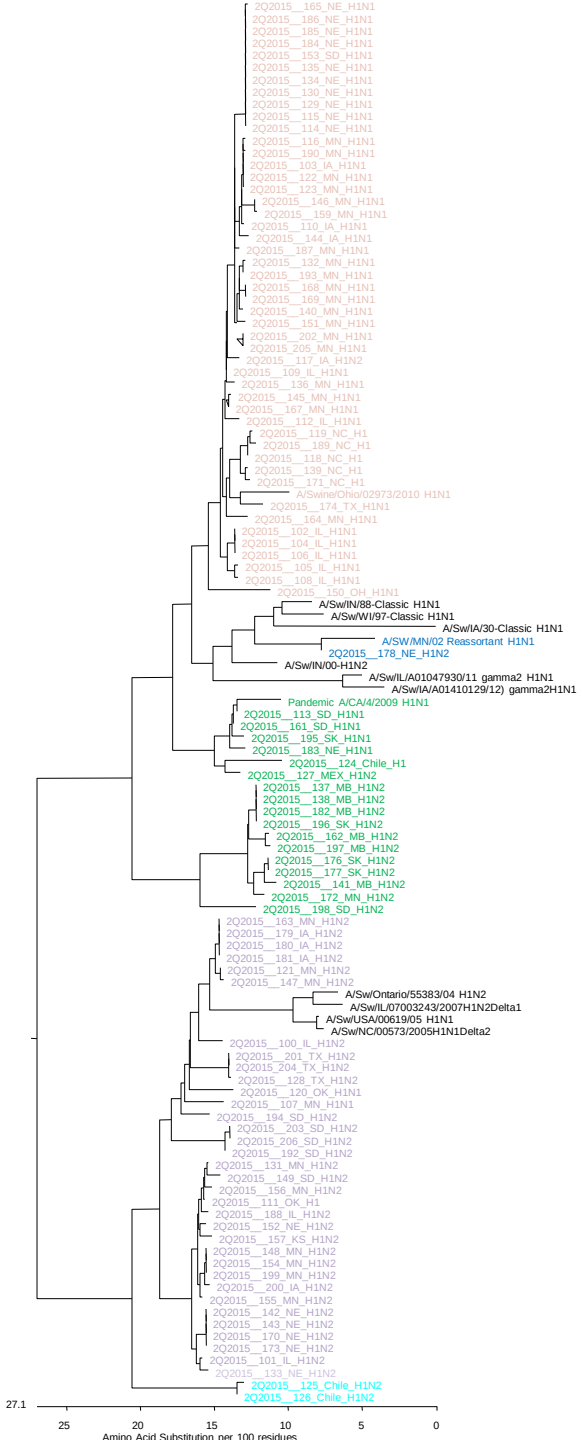


IAV-S H1 Genetic Clusters by Quarter

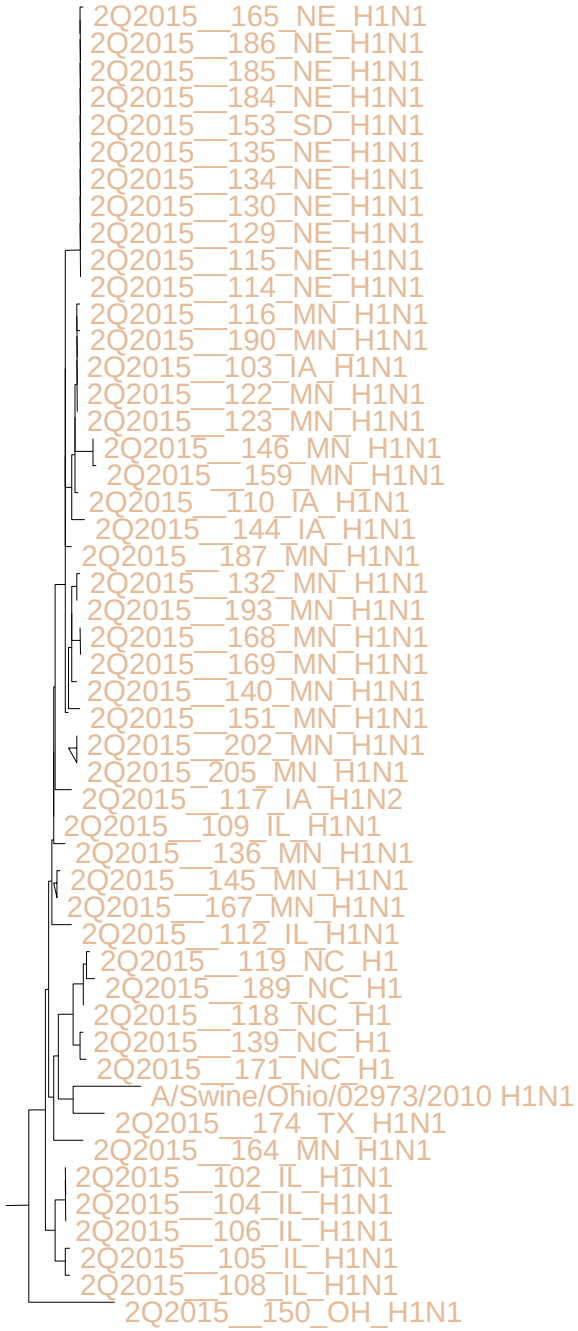


	4Q2014 H1	1Q2015 H1	2Q2015 H1	3Q2015 H1
otherH1	0	0	2	0
npdmH1	8	10	6	0
Delta2H1	1	0	0	1
Delta1H1	20	20	35	14
gammaH1	26	2	3	5
betaH1	0	0	1	3
alphaH1	4	4	12	8

2Q2015 H1 Tree All

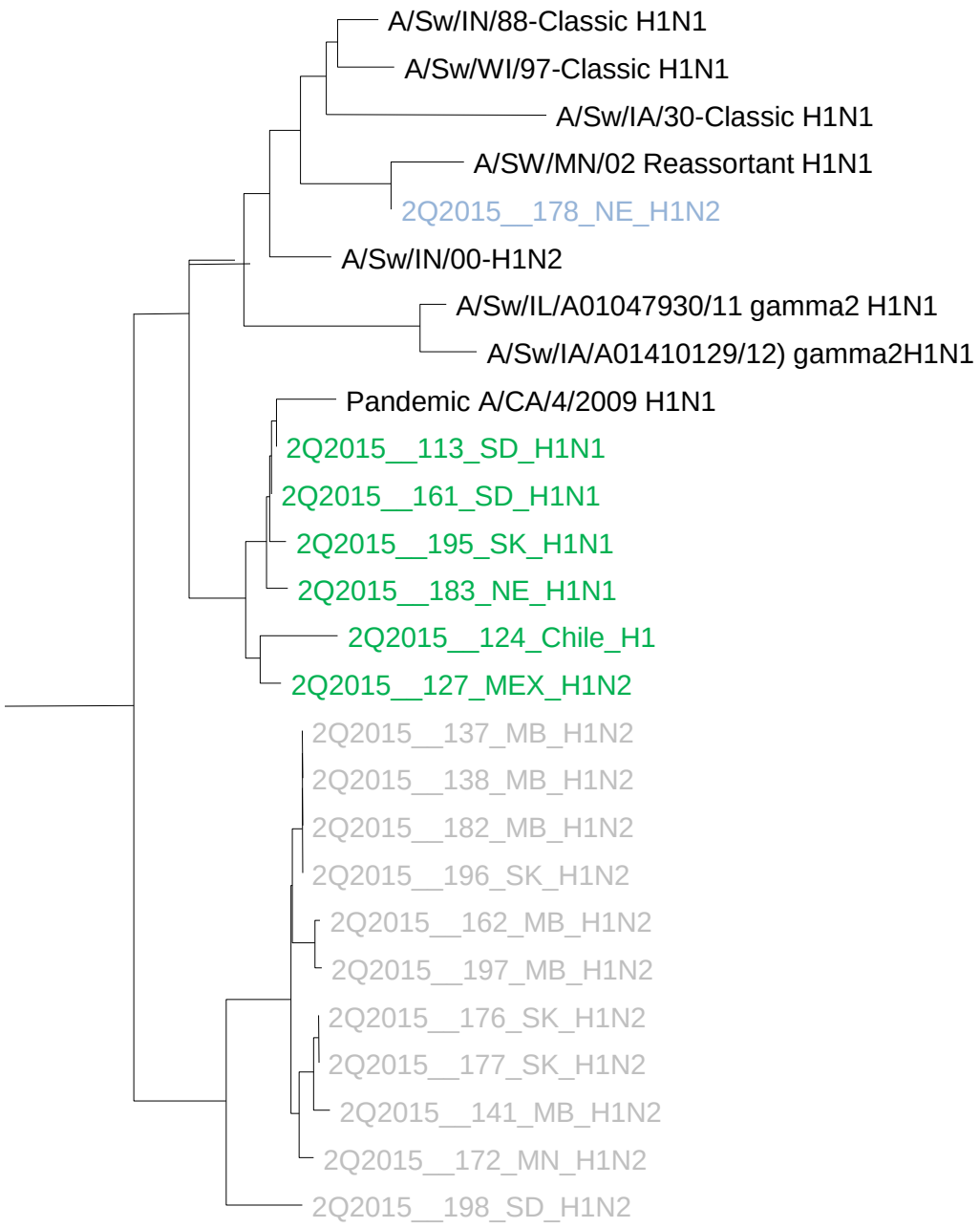


2Q2015 H1 Tree Gamma-cluster (NE, MN, IA, SD, IL, NC ,TX, OH)

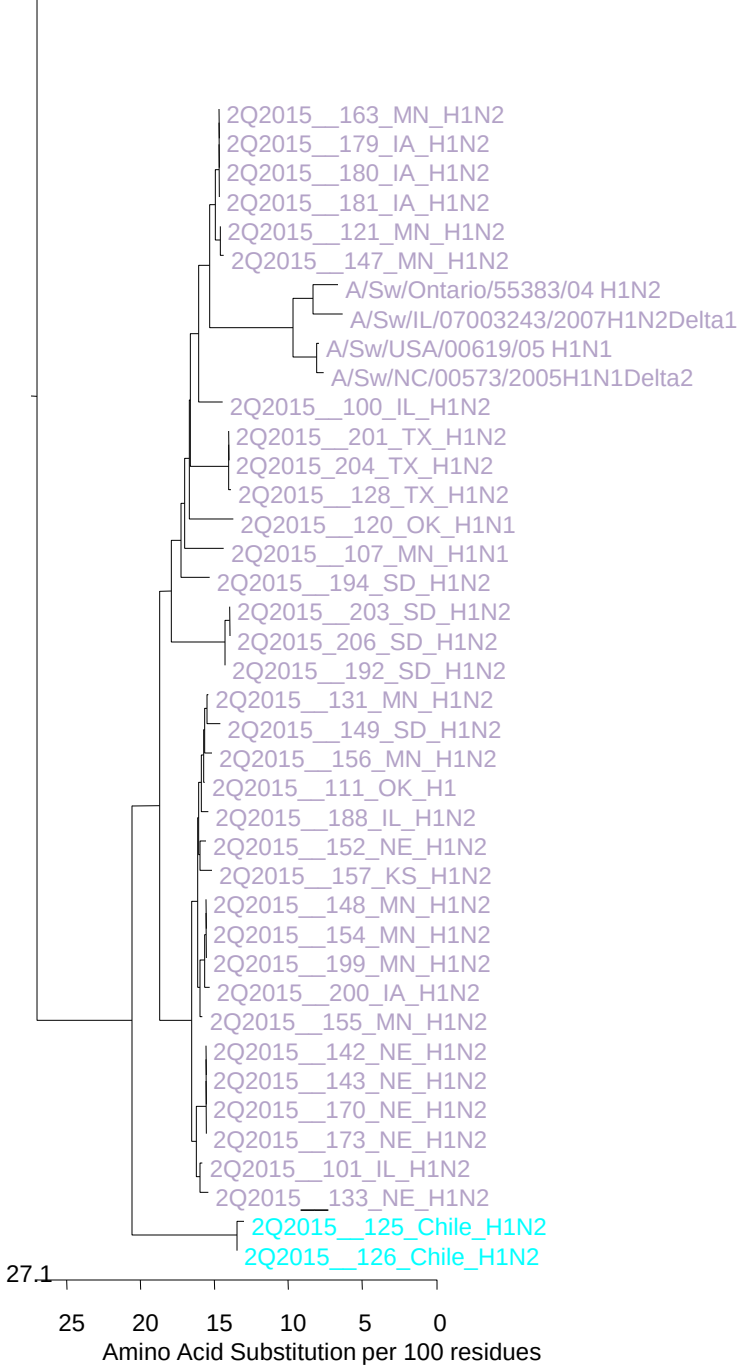


2Q2015 H1 Tree

Alpha (Canada, SD, MN); Beta (NE), and nPdm (Canada, Mexico, SD, NE)



2Q2015 H1 Tree Delta 1 and 2 (MN, IA, IL, TX, OK, SD, NE, KS) and Human Seasonal (Chile)



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Research

PMCID: PMC4551470

Novel Human-like Influenza A Viruses Circulate in Swine in Mexico and Chile

Martha Nelson, Marie R. Culhane, Albert Rovira, Montserrat Torremorell, Pedro Guerrero, and Julio Norambuena

Human-to-swine transmission, spatial migration via swine movements, and genomic reassortment are the key evolutionary mechanisms that generate this viral diversity. Additional antigenic characterization and whole-genome sequencing is greatly needed to understand the diversity and independent evolution of IAV in swine.