



Influenza Surveillance in North American Commercial Swine Populations

Bryan S. Kaplan, PhD

Postdoctoral Research Associate

Department of Infectious Diseases

St. Jude Children's Research Hospital

Memphis, TN USA

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Study 1, 2009-2011

- Objectives:
 1. Characterize presence of influenza virus
 2. Isolate virus for characterization
- June 2009 - December 2011
- 33 Midwestern farms housing 1,000-13,000 pigs 3-30 weeks of age
 - 17 IA, 4 IL, 8 IN, 4 MN
- 30 Nasal swabs collected monthly for 12-24 consecutive months



Study 1, 2009-2011

Results:

- 16,170 nasal swabs collected from 540 groups
- 746 swabs (4.6%) positive for Influenza A virus
- 178 viruses isolated
- 136 nearly complete (≥ 5 segments) genomes

Table 3

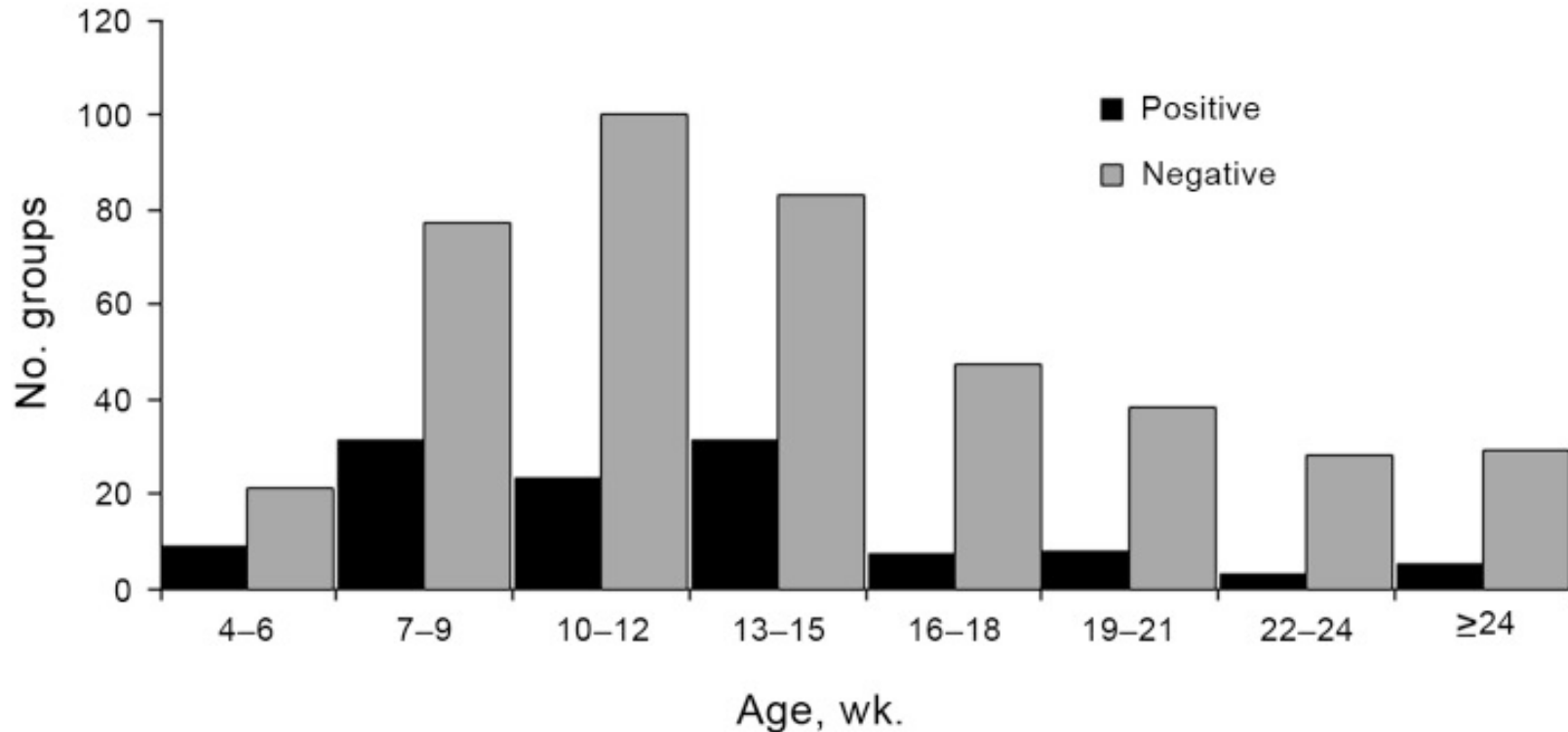
Relationship between group influenza status with age and season in for influenza virus, midwestern United States, June 2009–December 2

Variable	Estimate	Odds ratio (95% CI)	p value
Intercept	-1.330	NA	<0.01
Season			
Fall (referent)	NA	NA	NA
Spring	0.741	2.0 (1.1– 3.8)	0.01
Summer	0.657	1.9 (1.0–3.5)	0.03
Winter	-0.072	0.9 (0.4–1.8)	0.83
Age	-0.041	0.9 (0.9–1.0)	0.09

*Repeated measures logistic regression multivariable analysis. Generalized χ^2 di freedom = 0.92. NA, not applicable.

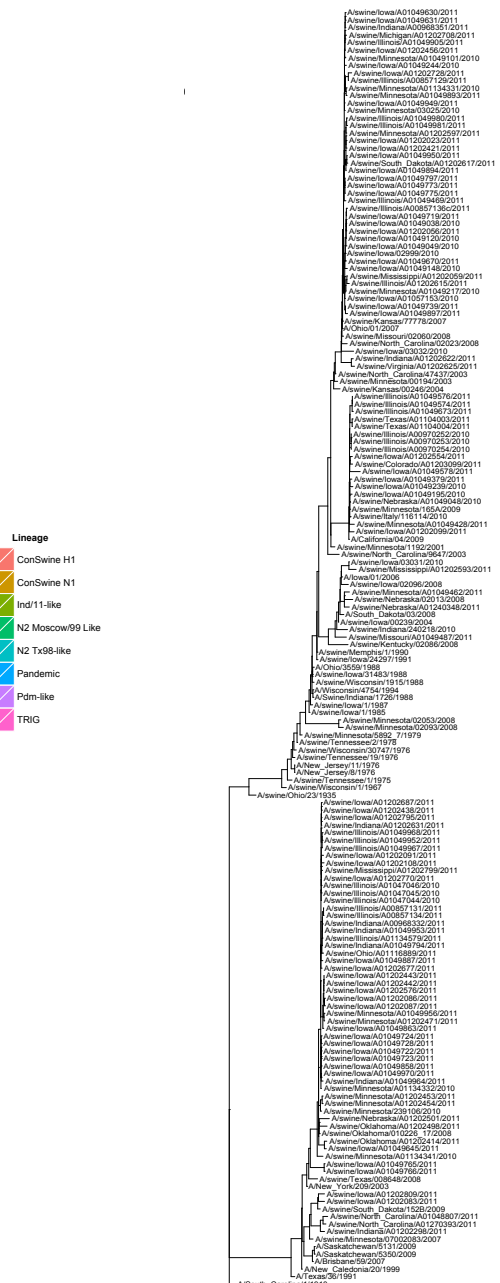
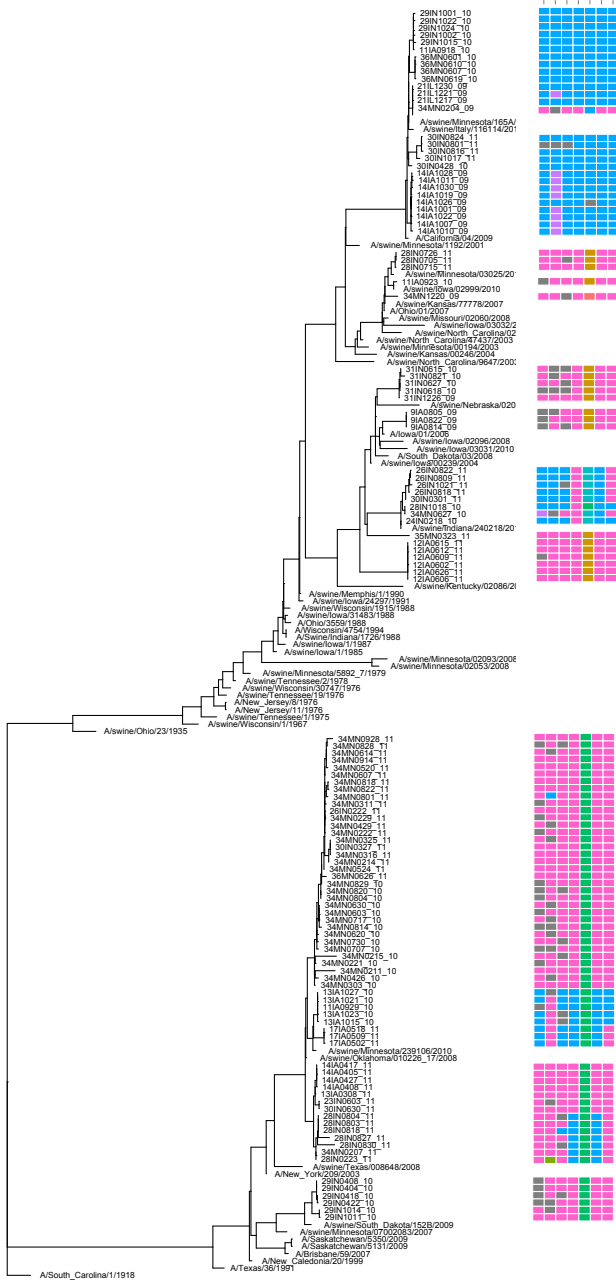


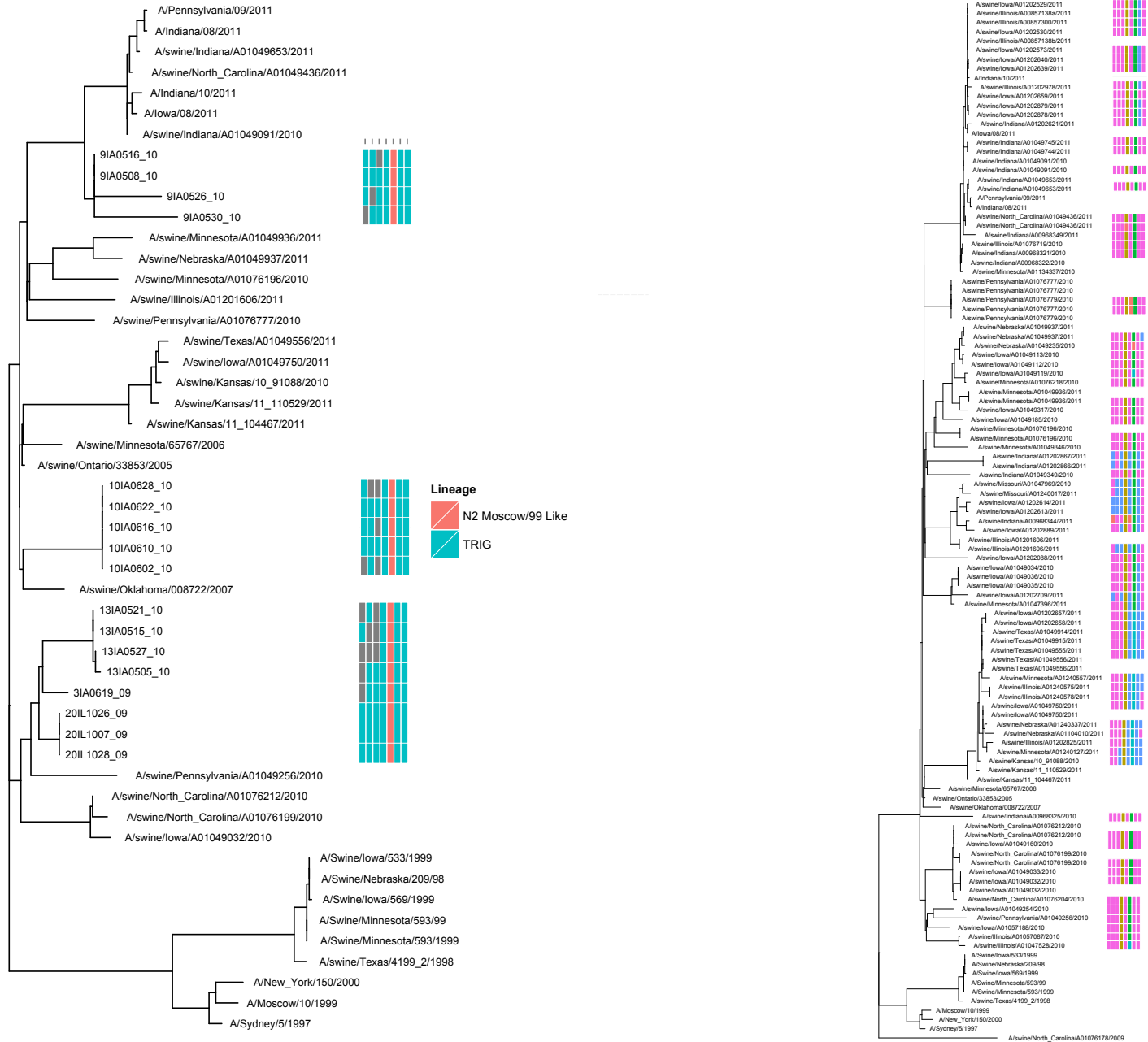
Study 1, 2009-2011



Corzo CA, Culhane M, Juleen K, Stigger-Rosser E, Ducatez MF, Webby RJ. Active surveillance for influenza A virus among swine, midwestern United States, 2009–2011. *Emerg Infect Dis.* 2013

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A/swine/Minnesota/05/1999



Study 1, 2009-2011

- Conclusions:
 - Positive ≠ Clinical Signs
 - Spring and Summer higher activity
 - Age
 - Active surveillance = Passive surveillance for capturing genomic diversity



Study 2, 2012-2014

Objective: Detail Influenza prevalence, diversity, and transmission in closed swine production systems

1. Determine incidence of IAV within farms in closed production systems
2. Animal Reservoir (Gilts and/or Piglets)
3. Farm Reservoir (commercial, developer, multiplier)
4. Transmission/evolutionary dynamics

Study length: 2 years (09/2012-06/2014), 26 sampling periods

Sampling: Breeding farms: 30 nasal swabs, Market Farms: 60 nasal swabs (30 piglets, 30 gilts) monthly.

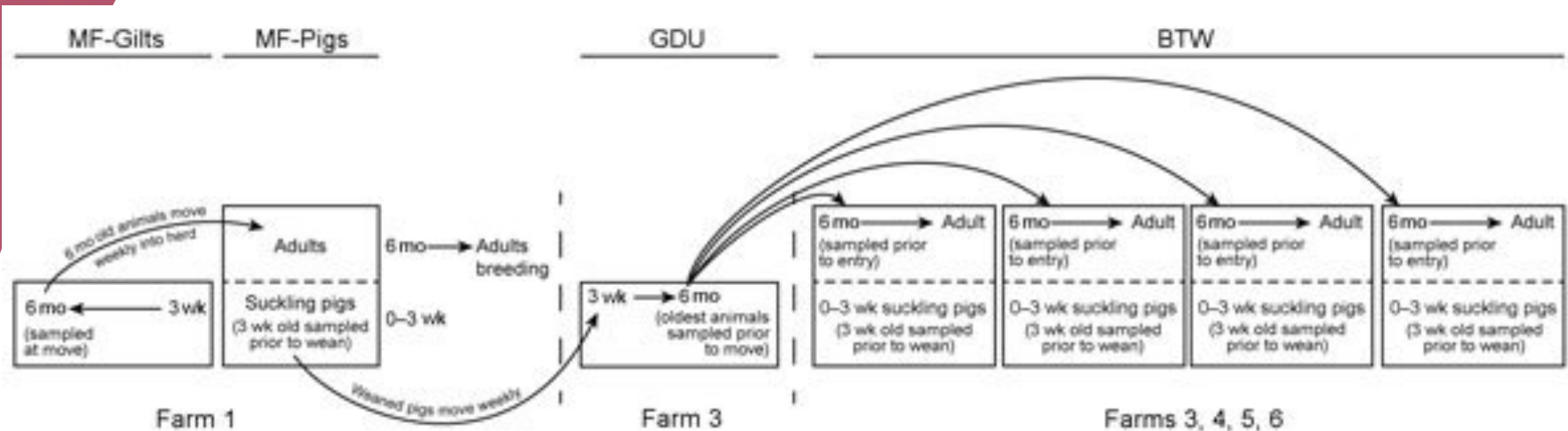
Monthly nasal swabs from 7 farms (1 genetic gilt developer, 1 multiplier, 1 commercial gilt developer, 4 commercial sow farms): ~1320 swabs per month.

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Study 2, 2012-2014

Closed, Coordinated swine production systems



Kaplan BS, DeBeauchamp J, Stigger-Rosser E, Franks J, Crumpton JC, Turner J. Influenza virus surveillance in coordinated swine production systems, United States. Emerg Infect Dis. 2015 Oct

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Study 2, 2012-2014

Totals:

- Overall Breakdown:
 - 23,138 swabs from September, 2012 to June 2014.
 - Negative: 21,928 swabs, 94.8%
 - Positive: 1,210 swabs, 5.2%
- Age Breakdown
 - Adult: 12,433, 53.7%
 - Weanling: 10,705, 46.3%

Type	# Samples	# Positive	% Positive	% Total Flu
MF- Gilts	2423	100	4.1	8.3
MF- Pigs	2487	173	7.0	14.3
GDU	2202	153	6.9	12.6
BTW	16026	784	4.9	64.8

Age	# Samples	# Flu Positive (%)	P-value
Adult	12433	550 (4.4)	0.002
Weaned	10705	660 (6.2)	0.002



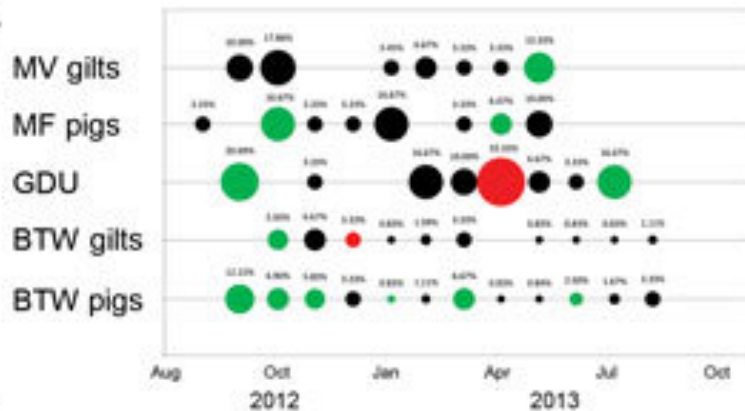
Study 2, 2012-2014

Factor		P value	Adjusted OR (95% CI)
Age	Juvenile	0.004	1.3 (1.1-1.6)
	Adult		ref
State	IL	<0.001	1.9 (1.4-2.6)
	OK		ref
Farm Type	Multi Farm	0.011	0.7 (0.5-0.9)
	GDU	<0.001	1.6 (1.2-2.1)
	BTW		ref
System	2	<0.001	1.7 (1.3-2.3)
	1		ref

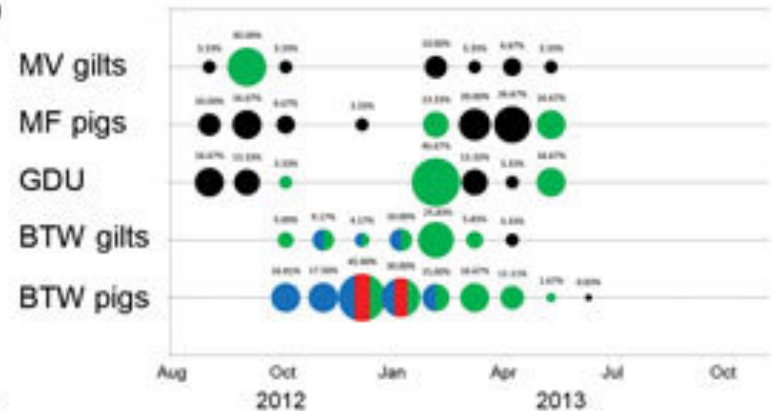


Study 2, 2012-2014

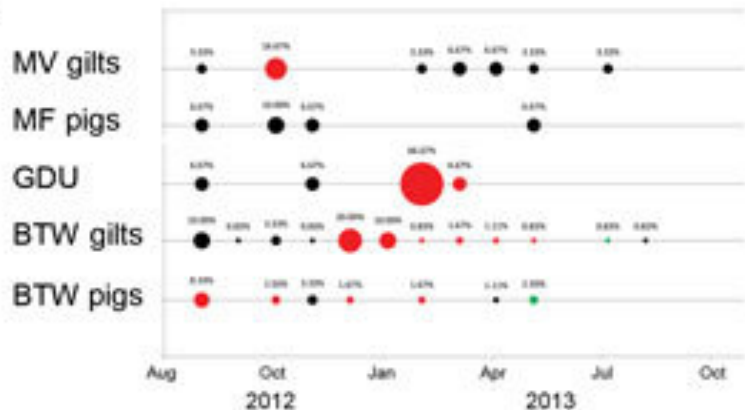
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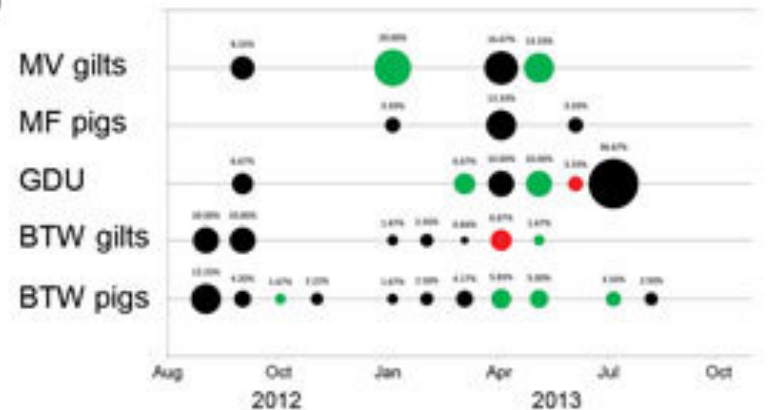
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C



D



Kaplan BS, DeBeauchamp J, Stigger-Rosser E, Franks J, Crumpton JC, Turner J.
Influenza virus surveillance in coordinated swine production systems, United States.
Emerg Infect Dis. 2015 Oct

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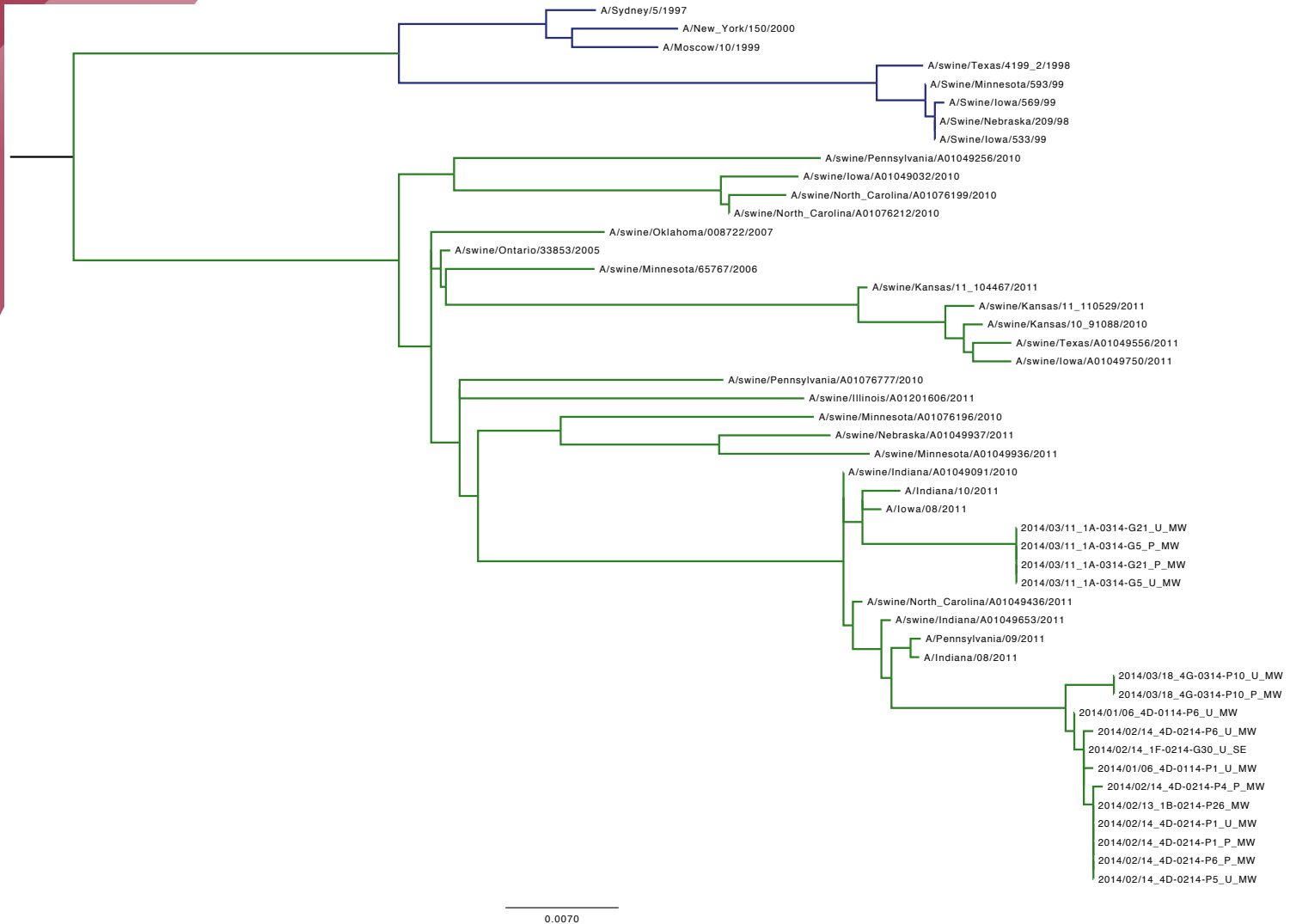


Study 2, 2012-2014





Study 2, 2012-2014

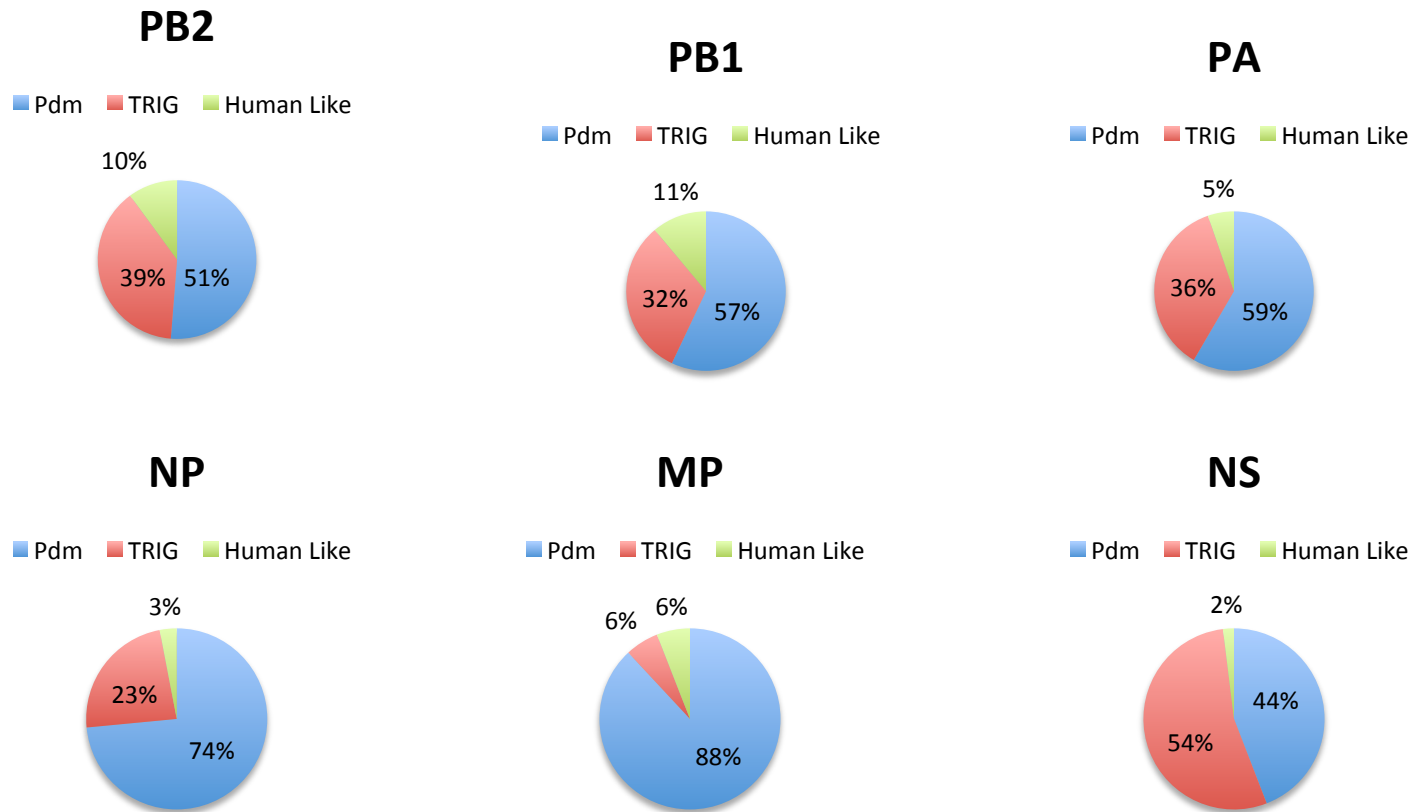


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Study 2, 2012-2014

Internal Gene Segment Lineage



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Study 2, 2012-2014

- IAV detected on all farms types and age groups in all productions systems
- Juvenile pigs (3 wks- 6mos) have higher prevalence of IAV than adult gilts (≥ 6 mos)
- GDU have highest prevalence of IAV
- Detection of multiple subtypes is rare (8/588 groups sampled)
- High levels of genetic diversity detected



Study 3, 2015-2017

Longitudinal influenza surveillance in Swine Breeding Herds

A. Objectives:

1. Understand the dynamics of intra-herd IAV transmission and viral genetic diversity in individual animals
2. Measure the systemic humoral immune response of individual animals and correlate systemic immune response to viral genetic diversity in individual.
3. Determine risk to farms importing replacement animals.

B. Methods:

1. 18 cohorts (20 animals) from 4 farms (IL & OH) will be serially sampled bi-monthly for 10 months.
2. 7,200 nasal swabs and serum samples
3. 120 swabs/sampling (5,040 total) from piglets for background



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Centers of Excellence for Influenza Research and Surveillance (CEIRS)