

Supplementary Table 1. Case history reported from 35 porcine cases submitted to the Iowa State University Veterinary Diagnostic Laboratory that detected a MN99-like H1 or TX98-like H3 hemagglutinin sequence.

HA no.	HA clade	Prod. system	Site	Month	State	Prod. stage	Specimen*	PCR Ct	PCR subtype	Co-detection
1	C-I	A02139351†	S1	Jan	IA	Nursery	Isolate	18.1	H3N2	ND
2	C-I	PS1	S2	Feb	KY	Finisher	Oral fluid	30.0	H3N2	ND
3	γ 2- β -like	PS2	S3	Feb	OH	Adult	Nasal swab	32.1	H1/3N1/2	H3-2010.1
4	γ 2- β -like	PS3	S4	Feb	MT	Nursery	Lung	25.1	H1N1/2	Unknown‡
5	γ 2- β -like	PS4	S5	Mar	SD	Nursery	Isolate	20.5	H1N1	ND
6	C-I	PS5	S6	Apr	IA	Nursery	Lung	27.1	H3N2	ND
7	γ 2- β -like	PS6	S7	Apr	NE	Nursery	Oral fluid	24.9	H1N1	ND
8	C-I	PS7	S8	Apr	IA	Nursery	Lung	25.3	H3N2	ND
9	γ 2- β -like	A02157797	S9	Apr	IL	Grower	Isolate	19.7	H1N1	ND
10	C-I	A02157798	S10	Apr	TN	Nursery	Isolate	16.1	H3N2	ND
11	C-I	PS8	S11	Apr	IA	Nursery	Nasal swab	25.3	H1/3N1	H1- α
12	C-I	PS9	S12	Apr	MO	Unknown	Oral fluid	30.2	H3N2	ND
13	γ 2- β -like	A02157974	S13	Apr	NE	Nursery	Isolate	23.9	H1N1	ND
14	C-I	PS8	S14	Apr	IA	Nursery	Oral fluid	29.1	H3N1	ND
15	γ 2- β -like	PS10	S15	Apr	NE	Nursery	Oral fluid	24.6	H1N1	ND
16	C-I	PS5	S16	May	IA	Nursery	Lung	34.4	H3N2	ND
17	C-I	PS9	S17	May	MO	Nursery	Nasal swab	25.1	H1/3N1/2	H1- γ
18	C-I	PS8	S18	May	IA	Grower	Oral fluid	27.4	H3N1	ND
19	C-I	PS7	S19	May	IA	Nursery	Oral fluid	33.5	H3N2	ND
20	C-I	PS9	S20	May	MO	Nursery	Oral fluid	29.4	H1/3N1/2	H1- γ

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21	C-I	PS7	S21	May	IA	Nursery	Oral fluid	31.2	H3N2	ND
22	C-I	PS7	S21	May	IA	Grower	Lung	26.9	H3N2	ND
23	C-I	PS11	S22	May	IL	Unknown	Nasal swab	24.0	H1/3N1/2	Unknown
24	C-I	PS12	S23	June	IA	Nursery	Nasal swab	23.7	H3N2	ND
25	γ 2- β -like	PS13	S24	July	NE	Finisher	Oral fluid	27.7	H1H3	H3-2010.1
26	γ 2- β -like	PS14	S25	July	OH	Grower	Oral fluid	29.1	H1N1	ND
27	γ 2- β -like	PS6	S15	Aug	NE	Nursery	Oral fluid	32.7	H1N1	ND
28	γ 2- β -like	PS10	S7	Aug	NE	Nursery	Oral fluid	22.0	H1N1	ND
29	γ 2- β -like	A02254795	S26	Aug	IA	Nursery	Isolate	16.0	H1N1	ND
30	C-I	PS15	S27	Aug	MO	Unknown	Oral fluid	25.4	H1/3N2	H1- γ
31	γ 2- β -like	PS6	S15	Aug	USA	Nursery	Oral fluid	26.0	H1N1	ND
32	C-I	PS16	S28	Aug	MN	Nursery	Oral fluid	29.9	H3N2	ND
33	C-I	PS9	S29	Sept	MO	Unknown	Oral fluid	29.9	H1/3N1/2	H1- γ
34	C-I	A02257614	S30	Sept	MO	Finisher	Isolate	18.0	H3N2	ND
35	C-I	PS17	S31	Oct	MI	Finisher	Oral fluid	34.0	H3N3	ND

HA = hemagglutinin; IA = Iowa; IL = Illinois; KY = Kentucky; MI = Michigan; MN = Minnesota; MO = Missouri; MT = Montana;

ND = not detected; NE = Nebraska; OH = Ohio; PCR Ct = reverse-transcription real-time PCR cycle threshold; PS = production system; SD = South Dakota; S = site; TN = Tennessee.

* Sequencing specimen.

† A0xxxxxx: USDA surveillance bar code.

‡ Unknown indicates that multiple subtypes may be live attenuated influenza vaccine virus or wild-type.

Supplementary Table 2. Clinical metadata reported from 35 porcine cases submitted to the Iowa State University Veterinary Diagnostic Laboratory that detected a MN99-like H1 or TX98-like H3 hemagglutinin sequence.

HA no.	HA clade	Clinical signs	Lung lesions*	Histopathology	PCR Ct PRRSV	PCR Ct PCV-2	PCR Ct MHP	Bacteria
1	C-I	Respiratory disease	Edema	Necrotizing bronchiolitis	18.6	ND	27.7	<i>P. multocida</i> ; <i>S. suis</i>
2	C-I	NR	NA	NA	ND ^g	ND	ND	<i>H. parasuis</i>
3	γ 2- β -like	NR	NA	NA	ND	NR	ND	NR
4	γ 2- β -like	Respiratory disease	Consolidation	Necrotizing bronchiolitis	ND	NR	NR	NR
5	γ 2- β -like	Respiratory disease	NR	Necrotizing bronchiolitis	15.2	ND	NR	<i>H. parasuis</i>
6	C-I	Wasting	Congestion, pleuritis	Broncho-pneumonia	ND	NR	NR	<i>H. parasuis</i>
7	γ 2- β -like	Respiratory disease	Congestion, hemorrhage	NA	NR	NR	NR	NR
8	C-I	Respiratory disease	None reported	Necrotizing bronchiolitis	ND	30.7	ND	<i>B. bronchiseptica</i> ; <i>S. suis</i>
9	γ 2- β -like	Respiratory disease	NA	Necrotizing bronchiolitis	29.2	NR	NR	<i>P. multocida</i>
10	C-I	Respiratory disease	Consolidation	Necrotizing bronchiolitis	ND	NR	NR	NSG
11	C-I	Respiratory disease	NR	Necrotizing bronchiolitis	NR	NR	NR	<i>H. parasuis</i>
12	C-I	NR	NA	NA	ND	NR	NR	NR
13	γ 2- β -like	Respiratory disease	Consolidation	Necrotizing bronchiolitis	NR	NR	NR	NSG
14	C-I	Respiratory disease	Consolidation	Broncho-pneumonia	28.3	ND	NR	<i>S. suis</i>
15	γ 2- β -like	Respiratory disease	NA	NA	NR	NR	NR	NA

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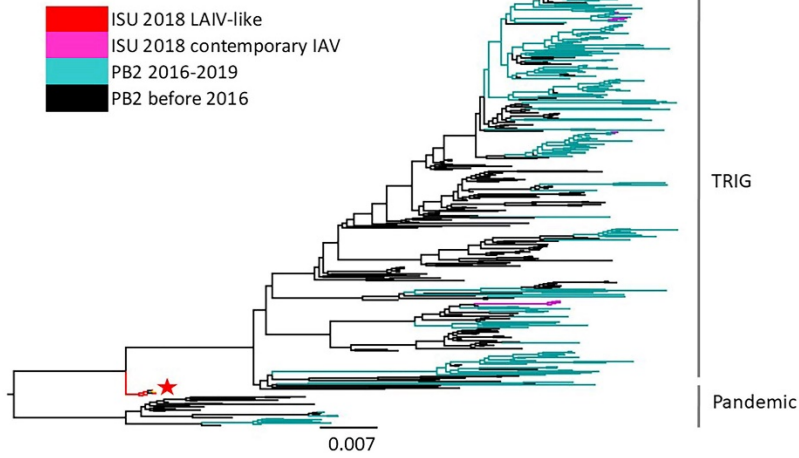
16	C-I	Respiratory disease	Consolidation	NR	ND	NR	NR	<i>B. bronchiseptica</i>
17	C-I	NR	NA	NA	NR	NR	NR	NR
18	C-I	Respiratory disease	NA	NA	25	NR	NR	NR
19	C-I	NR	NA	NA	NR	NR	NR	NR
20	C-I	NR	NA	NA	ND	NR	NR	NR
21	C-I	NR	NA	NA	NR	NR	NR	NR
22	C-I	Respiratory disease	Consolidation	Necrotizing bronchiolitis	ND	ND	ND	<i>P. multocida; H. parasuis</i>
23	C-I	NR	NA	NA	NR	NR	NR	NR
24	C-I	NR	NA	NA	NR	NR	NR	NR
25	γ 2- β -like	NR	NA	NA	NR	NR	NR	NR
26	γ 2- β -like	NR	NA	NA	ND	NR	NR	NR
27	γ 2- β -like	NR	NA	NA	NR	NR	NR	NR
28	γ 2- β -like	NR	NA	NA	NR	NR	NR	NR
29	γ 2- β -like	Respiratory disease	Consolidation	Necrotizing bronchiolitis	26.1	NR	NR	<i>S. suis</i>
30	C-I	NR	NA	NA	ND	NR	ND	NR
31	γ 2- β -like	NR	NA	NA	NR	NR	NR	NR
32	C-I	Respiratory disease	Consolidation	Necrotizing bronchiolitis	ND	ND	ND	<i>S. suis</i>
33	C-I	NR	NA	NA	NR	NR	NR	NR
34	C-I	Respiratory disease	Congestion	Necrotizing bronchiolitis	ND	NR	23	NSG
35	C-I	NR	NA	NA	NR	NR	NR	NR

HA = hemagglutinin; MHP = *Mycoplasma hyopneumoniae*; NA = not applicable; ND = not detected; NR = none reported; PCR Ct = reverse-transcription real-time PCR cycle threshold value; PRRSV = porcine reproductive and respiratory syndrome virus.

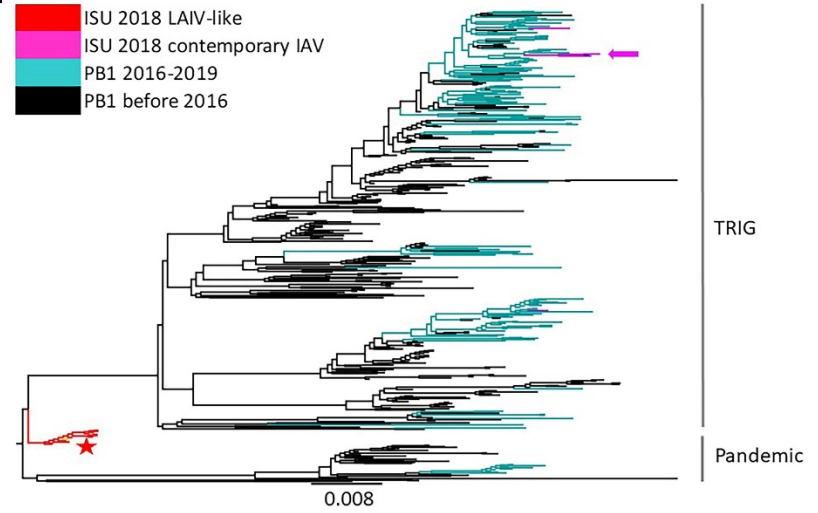
* Lung lesions indicate macroscopic lung lesions.

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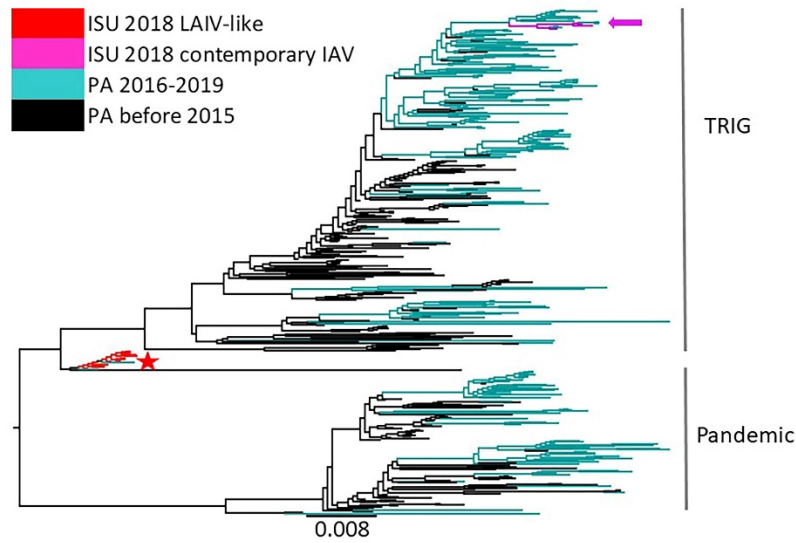
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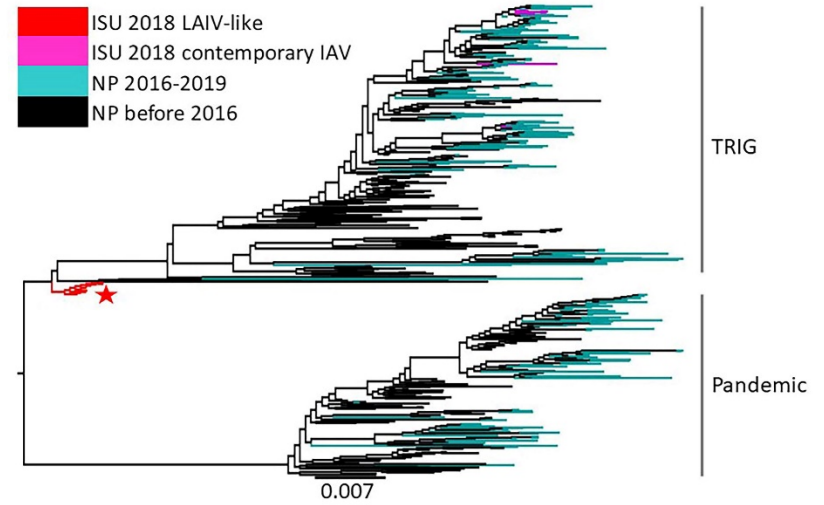
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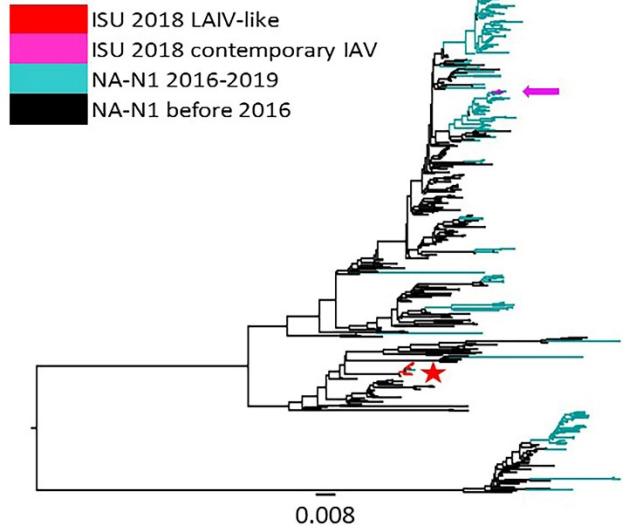


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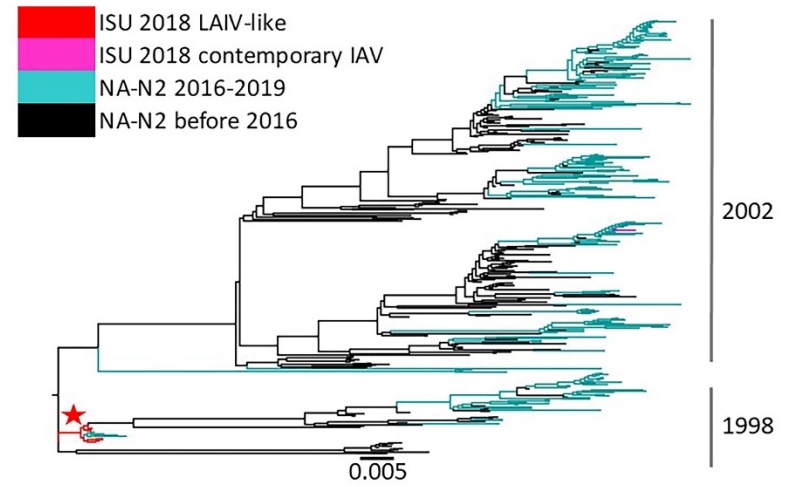


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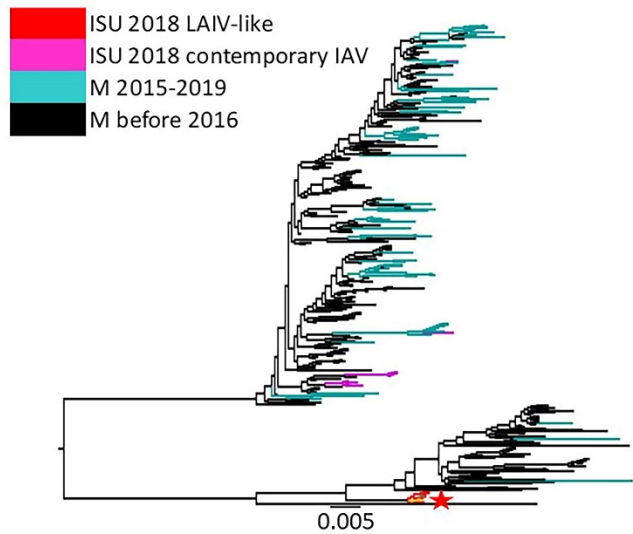
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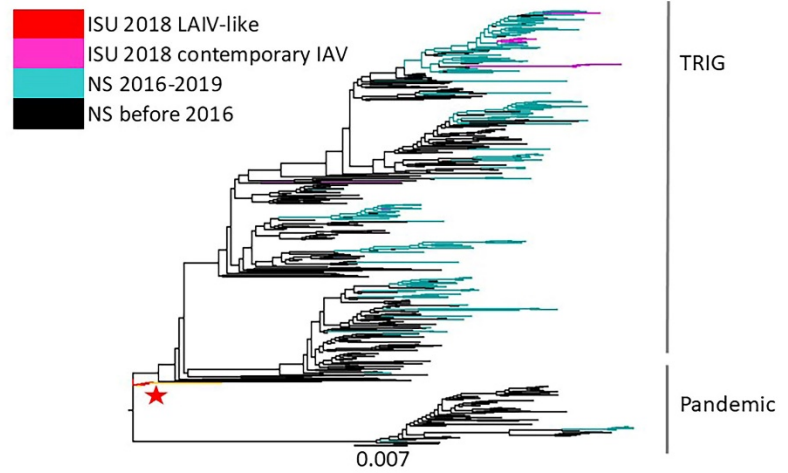
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Supplementary Figures 1–8. Maximum-likelihood phylogenetic tree of the neuraminidase and internal genes generated from the whole genome sequences represented in Figure 3 and including TX98 (CY095675) and live attenuated influenza vaccine (LAIV) internal gene segments, contemporary triple reassortant internal gene (TRIG) segments, contemporary 2009 H1 pandemic internal gene segments, and contemporary influenza A virus (IAV) neuraminidase clades. TX98-like or Mn99-like gene segments are represented in red and form their own cluster regardless of gene segment. TX98 and LAIV sequences are shown in yellow and are indicated with a red star. Co-detections with contemporary IAV are designated with a magenta arrow. Turquoise color demonstrates IAV gene segments from 2015 to 2019. Black demonstrates IAV gene segments before 2016. **Supplementary Figure 1.** Polymerase basic 2 (PB2) phylogenetic tree. **Supplementary Figure 2.** PB1 phylogenetic tree. **Supplementary Figure 3.** Polymerase acidic (PA) phylogenetic tree. **Supplementary Figure 4.** Nucleoprotein (NP) phylogenetic tree. **Supplementary Figure 5.** N1 neuraminidase (NA) phylogenetic tree. **Supplementary Figure 6.** N2 NA phylogenetic tree. **Supplementary Figure 7.** Matrix (M) phylogenetic tree. **Supplementary Figure 8.** Nonstructural (NS) phylogenetic tree.