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Tracing the Source of Influenza A Virus Zoonoses in Interconnected Circuits of Swine Exhibitions

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Background. Since 2011, influenza A viruses circulating in US swine exhibited at county fairs are associated with >460 zoonotic infections, presenting an ongoing pandemic risk. Swine "jackpot shows" that occur before county fairs each summer intermix large numbers of exhibition swine from diverse geographic locations. We investigated the role of jackpot shows in influenza zoonoses.

Methods. We collected snout wipe or nasal swab samples from 17 009 pigs attending 350 national, state, and local swine exhibitions across 8 states during 2016–2018.

Results. Influenza was detected in 13.9% of swine sampled at jackpot shows, and 76.3% of jackpot shows had at least 1 pig test positive. Jackpot shows had 4.3-fold higher odds of detecting at least 1 influenza-positive pig compared to county fairs. When influenza was detected at a county fair, almost half of pigs tested positive, clarifying why zoonotic infections occur primarily at county fairs.

Conclusions. The earlier timing of jackpot shows and long-distance travel for repeated showing of individual pigs provide a pathway for the introduction of influenza into county fairs. Mitigation strategies aimed at curtailing influenza at jackpot shows are likely to have downstream effects on disease transmission at county fairs and zoonoses.

Keywords. swine; United States; zoonoses; farms; prevalence; influenza A virus; public health; animals; transmission; human-animal interface; pandemic risk.

The diverse pool of influenza A viruses (IAV) in animals presents an ongoing threat to human health [1–3]. Swine are mixing vessels for the evolution of genetically novel IAVs with genetic components from multiple host species [4]. The 2009 H1N1 influenza pandemic was of swine origin, highlighting the pathway for zoonotic IAV emergence provided by swine systems [3, 5, 6]. The 2009 pandemic furthered understanding of how global swine production facilitates the evolution of novel IAVs with zoonotic potential [7–9], and how specific human–animal interfaces can be targeted to prevent interspecies spillover events. Over the last decade, the United States (US) has recorded the highest number of swine-origin zoonotic IAV infections worldwide. Since 2011, novel reassortant IAVs of swine origin (H1N1v, H1N2v, and H3N2v subtypes) have been associated with >460 zoonotic infections in the US [10]. While swine workers are at a higher risk for zoonotic IAV from swine [11, 12], and zoonotic cases are sporadically linked to commercial swine, the vast majority of these infections were in youth swine exhibitors at county fairs [13–15]. An estimated 150 million people attend fairs in North America annually [16], providing a conduit for numerous people to interact with swine and their pathogens.

Agricultural fairs, which include county fairs, facilitate commingling among hundreds of swine for up to a week, creating an environment conducive to the rapid spread of IAV between animals as well as an interface for zoonotic transmission. The pigs at fairs are raised primarily by youth exhibitors and their families for the purpose of being shown at fairs and other shows through agricultural education programs such as 4-H and Future Farmers of America (FFA). In the Midwestern United States, where most swine-origin zoonotic IAV infections have occurred, county fairs occur primarily during June-October. Although county fairs are typically restricted to pigs from that county, swine exhibitors report attending an average of 3.1 shows in a year and showing the same pig multiple times [17]. Many of the additional exhibitions belong to circuits of "jackpot" shows that are held throughout the year. Swine are permitted to attend jackpot shows and return to their home farms afterward, potentially facilitating long-range dissemination of IAVs (Figure 1). Exhibitors with pigs attending multiple shows prior to their arrival at county fairs may be the source of the diverse IAVs detected in pigs that subsequently infect humans.
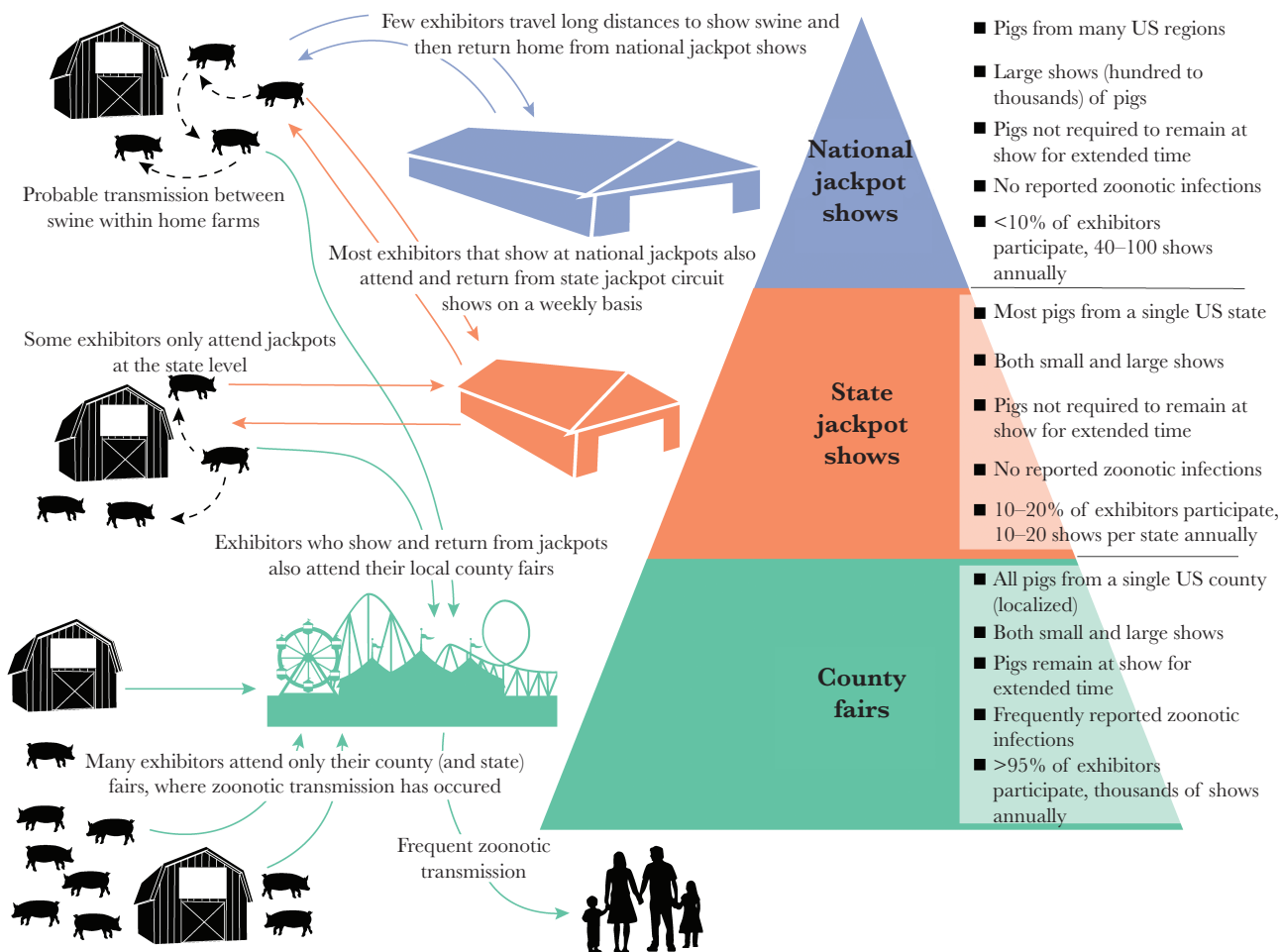
Figure 1. Characteristics of the 3 exhibition swine show types included in this study. National jackpot shows (blue) are the least frequent show type, with a small subset of all swine exhibitors traveling to attend. Attracting exhibitors from all over the US, national jackpot shows are very large, often with thousands of pigs in attendance. Circuits of state jackpot shows (orange) are organized in each state and occur every weekend for many weeks, allowing exhibitors to show every weekend and return home before showing the same or multiple pigs the following week. State jackpot circuits attract a subset of exhibitors from primarily within their individual state, but with typical interstate travel for some exhibitors. County fairs (green) occur in nearly every county within our study range, allowing only pigs from within that county to attend, and with nearly all youth swine exhibitors attending their local county fair.

Zoonotic infections have not been traced directly to jackpot shows. However, the occurrence of jackpot shows prior to the agricultural fair season positions them to serve as key upstream sources of the zoonotic viruses later isolated from humans. We conducted active IAV surveillance to determine IAV detection frequency at jackpot shows and county fairs and to elucidate the role of jackpots in disseminating IAVs in the exhibition network.

MATERIALS AND METHODS

Surveillance in Exhibition Swine

During 2016–2018, we conducted IAV surveillance in exhibition swine at jackpot shows across 8 US states (Arizona, Georgia, Illinois, Indiana, Iowa, Kentucky, Michigan, and Ohio) and at county fairs in Ohio, Indiana, and Michigan, due to the frequency of zoonotic IAV cases in these states [10]. Swine sampling was approved by The Ohio State University Institutional

Animal Care and Use Committee (protocol 2009A0134-R2). State fairs differ from both county fairs and jackpot shows in their broader regionality, longer duration, and greater size. Many state fairs host multiple shows for different categories of exhibition swine. Due to the variability both within state fairs and between states regarding their structure and regulations, state fairs could not be appropriately grouped with jackpots or county fairs and were censored from our analyses.

With permission from organizers overseeing each show, we collected 20 nasal swabs [16] or 24 snout wipes [18] at county fairs, 200 snout wipes at state jackpots, and 400 snout wipes at national jackpots, on the last day of each show. Samples were systematically collected from pigs and spatially distributed throughout the barn without consideration for clinical signs of IAV. Samples were placed on dry ice for transportations immediately after sampling. The sample sizes for county fairs were chosen to ensure ≥95% probability of detecting of IAV at

a prevalence of ≥ 0.15 at a typical-size fair. We targeted more samples at jackpot shows to account for shorter show durations (ie, less viral amplification). The required number of shows at which we sampled was calculated to detect the expected difference in proportion of positive shows between jackpots and county fairs with 80% power. To evaluate the geographic distribution of swine at jackpot shows, we recorded US postal codes corresponding to the location of the farm on which each pig was raised. We did not record identifying information for pigs or exhibitors to preserve exhibitor anonymity.

We screened viral RNA extracted from the samples with real-time reverse-transcription polymerase chain reaction (rRT-PCR) using the VetMAX-Gold SIV Detection Kit (Life Technologies) with the 7500 Fast Real-Time PCR System (Life Technologies) according to the manufacturer's protocol. We conducted virus isolation on all rRT-PCR–positive samples using Madin–Darby canine kidney cells [19]. We sequenced representative IAV isolates from each positive exhibition as previously described [20–22] and used full genome sequence data for antigenic subtype classification. All sequences are available in GenBank; accession numbers are listed in Supplementary Table 1.

Statistical Analysis

All statistical analyses were conducted using R version 4.0.1 [23]. Exhibition-level IAV status was designated using the results of IAV rRT-PCR tests of nasal swab and snout wipe samples. Exhibitions were designated as IAV positive when ≥ 1 sample tested positive. We estimated exhibition-level IAV prevalence by dividing the number of individual swine that tested PCR positive for IAV by the total number of swine sampled. In statistical analyses with multiple comparisons, we used the Benjamini–Hochberg procedure to control the false discovery rate.

Influenza Infection Association With Exhibition Type and Location

The association of IAV status with exhibition type and location was measured using Fisher exact tests and post hoc tests with Monte Carlo resampling (10 000 replicates), in which the nominal variables were exhibition type or state, respectively, and IAV presence or absence. For spatial geographic analyses, we focused on state jackpots and county fairs in the 3 most densely sampled states in our dataset: Ohio, Michigan, and Indiana. To determine if exhibition type or location was associated with influenza prevalence, we conducted general independence tests with Monte Carlo resampling (10 000 replicates) (*coin* package) [24]. For post hoc comparisons of prevalence between exhibition types or between US states, we used pairwise permutation tests (*rcompanion* package) [25].

Risk Factors of Influenza Detection at Exhibitions

We recorded epidemiologically relevant metadata for each exhibition, including GPS coordinates, sampling date, date of entry for exhibitors, exhibition size (≤ 200 swine or >200 swine), and whether other exhibitions had tested positive within the 14 days prior and the corresponding distances of these exhibitions. We defined exhibition duration as the number of days between the required arrival date for swine exhibitors and the date pigs were sampled [26]. For each year, we calculated pairwise geographic distances and pairwise differences in entry date between all exhibitions. We obtained total swine population sizes for US counties from the 2017 US Department of Agriculture's Census of Agriculture [27]. For jackpot shows, we computed distances in miles between show locations and the home zip codes of participants.

Bayesian Logistic Regression

We used a Bayesian approach to model the probability of county fairs and state jackpots testing positive for IAV. We excluded national jackpots from this analysis because all were IAV positive. Model covariates included show entry date (measured as the number of days from 1 January of each year), exhibition type (county fair or state jackpot), show size (≤ 200 swine or >200 swine), and the number of swine residing in each show's respective county. In 10 separate models, we included a covariate for whether IAV was detected at any exhibition within a 25-, 50-, 75-, 100-, or 200-mile radius within the prior 2 weeks (yes or no). Continuous variables were mean-centered and scaled prior to model fitting.

We fit logistic generalized linear regression models using Markov chain Monte Carlo (MCMC) with Stan [28] via the *rstanarm* package [29]. Weakly informative Student *t* priors (degrees of freedom = 7, location = 0, scale = 2.5) were placed on intercept and coefficient effect sizes. For each model, we ran 4 MCMC chains, each for 2000 iterations (including a burn-in period of 1000 iterations that was discarded), producing a total posterior sample size of 4000. We verified convergence by inspecting trace plots and confirming that all parameters had sufficiently low $\hat{R}$ values (all $\hat{R} < 1.1$) and sufficiently large effective sample sizes (>15% of the total sample size). To evaluate each model's predictive performance, we computed approximate leave-one-out cross-validation using Pareto smoothed importance sampling (*loo* package) [30, 31]. We used leave-one-out information criterion to estimate differences in model out-of-sample predictive accuracy and "stacking" of predictive distributions to compute model weights [32].

RESULTS

IAV Surveillance in Exhibition Swine

Across the 3 years, we collected nasal swab and snout wipe samples from >17 000 exhibition swine at 350 exhibitions in 8 US states (Figure 2). The majority of samples (n = 11 071 samples) were collected at state and national jackpot shows (45 and 14 exhibition events, respectively), and 5938 samples were collected from swine at 291 individual county fair events.
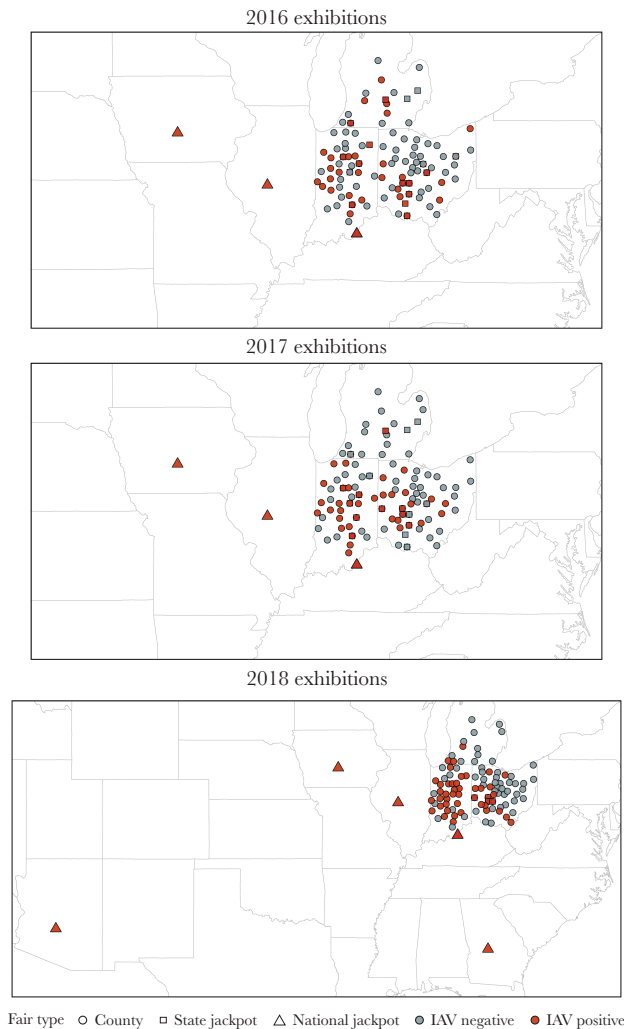
2016 exhibitions

2017 exhibitions

2018 exhibitions

Fair type ○ County ▢ State jackpot △ National jackpot ● IAV negative ● IAV positive

Figure 2. Maps of swine exhibitions sampled in 2016, 2017, and 2018. Each point represents a swine exhibition sampled for this study. The color of the point indicates whether pigs at the exhibition tested polymerase chain reaction (PCR) negative for influenza A virus (IAV, gray) or at least 1 pig tested PCR positive for IAV (red). The shape of the point indicates the type of exhibition (county, state jackpot, or national jackpot).

Across all 3 years, 15.3% (2602/17 009) of the pigs tested positive for IAV (Table 1), and IAV-positive swine were detected at 44.3% of all exhibitions. Large national jackpot shows were held throughout each year (January–December) with a median duration of 3 days, whereas state jackpots primarily occurred in May and June and were typically 1–2 days (Supplementary Figure 1). County fairs took place from June to September with a median duration of 5 days (Supplementary Figure 1).

The national jackpot shows included in our study took place in Iowa, Illinois, Georgia, Kentucky, and Arizona, and the samples from county fairs and state jackpot shows were collected in 3 Midwestern states with a high concentration of exhibition swine [17]: Ohio (162 exhibitions), Indiana (120 exhibitions), and Michigan (54 exhibitions) (Figure 2). We observed swine from diverse localities at state jackpots and an even greater

geographic distribution of exhibitor home farms at national jackpots (Figure 3; Supplementary Figures 2 and 3). Exhibition swine traveled the longest distances to attend national jackpot shows (Figures 3 and 4).

Across all years and exhibition types, we isolated viruses from 45.5% of our rRT-PCR–positive samples. Genotype analysis of 683 HA segment sequences revealed that we detected H1-α (1A.1.1), H1-δ1 (1B.2.2), H1-δ2 (1B.2.1), H1-γ (1A.3), H1-pdm (1A.3.3.2), H3-2000 (H3.1990.4), and H3-2010 (H3.2010.1)— global nomenclature based on [33]. The dominant genotypes detected at county fairs were also detected in similar proportions at the early national and state-level jackpots within each year, but we detected varying proportions of each genotype across years (Supplementary Table 2). All of the PB2 segments were TRIG lineage and selected for genetic distance analysis. Genetic distances between isolates were smaller within a single year compared to between study years (Supplementary Table 3), further supporting the notion that similar viruses propagate throughout shows in a given year, but patterns in dominant genotypes do not necessarily persist between show seasons.

IAV Detected in Swine at Majority of Jackpot Shows

IAV first appeared in state jackpot shows in May, then in national jackpot shows beginning in June, and ultimately in county fairs from June to October (Figure 4). IAV was frequently detected at state jackpot shows that took place in late June and early July, and sporadic zoonotic infections coincided with the peak of county fair season in July and early August (Figure 4). We detected IAV in a higher proportion of state and national jackpots (76.3%) compared to county fairs (37.8%) (Figures 4 and 5), and the probability of a swine exhibition having at least 1 IAV-positive animal was strongly associated with the exhibition being a jackpot show (Fisher exact test, $P = .0002$ and $P < .00001$). Among jackpot shows, we detected IAV in 68.9% of state shows and at every national show, even those held in regions with small local swine populations (Fisher exact test, $P = .03$; Figure 2).

Higher IAV Prevalence at County Fairs

The proportion of pigs testing positive for influenza varied across fair types and study years (Table 1; Figure 6A), with national jackpots having the greatest overall prevalence when data from the 3 years were combined (Fisher exact tests: state jackpot vs national jackpot, $P < .001$; county fair vs national jackpot, $P = .01$). However, these numbers represent averages across hundreds of fairs, and a more detailed examination reveals that county fairs and jackpot shows have different dynamics. County fairs tend to be highly bifurcated: Either there are no IAV-positive animals (62.2% of fairs), or >75% of animals are IAV-positive (13.7% of fairs). In contrast, state and national jackpot shows are consistently infected but generally at lower frequencies (13.9% of animals). Therefore, if we limit our

Table 1. Influenza A Virus Prevalence, Organized by Exhibition Type (County, State Jackpot, National Jackpot) and Year (2016, 2017, 2018)

Exhibition Type	2016[a,b]	2017[a,b,c]	2018[b,c]	Total Specimens[a,b,c]
County fair	19.7% (389/1973)	16.3% (322/1973)	17.9% (357/1992)	18% (1068/5938)
State jackpot	11.9% (313/2631)	9% (228/2543)	17.2% (102/594)	11.1% (643/5768)
National jackpot	11.1% (177/1600)	27.7% (442/1597)	12.9% (272/2106)	19.3% (831/5303)
Total specimens	14.2% (879/6204)	16.2% (992/6113)	15.6% (731/4692)	15.3% (2602/17009)

The numbers of positive specimens and all specimens tested are included in parentheses.

[a]Fisher exact test, county fair:state jackpot (adjusted $P < .05$).

[b]Fisher exact test, county fair:national jackpot (adjusted $P < .05$).

[c]Fisher exact test, state jackpot:national jackpot (adjusted $P < .05$).

analysis to exhibitions with at least 1 IAV-positive pig, county fairs had significantly greater IAV prevalence than state and national jackpots, both in the 3-year dataset (pairwise permutation tests, $P = .00008$ and $P = .003$) and when analyzing years separately (2016: $P = .00004$, 2017: $P = .07$, 2018: $P = .02$; Figure 6B). Among IAV-positive shows, the mean estimated prevalence was 16.8% for state jackpots, 16.2% for national jackpots, and 46.9% for county fairs. More than a third (36.3%) of IAV-positive county fairs had ≥75% pigs test positive, whereas only 1 IAV-positive jackpot show had ≥50% pigs test positive.

High Rates of IAV Detection in Indiana

Across all exhibition types, IAV was detected in 21.7% of pigs sampled at Indiana exhibitions (n = 3286), 13.1% at Ohio exhibitions (n = 6387), and 7.9% at Michigan exhibitions (n = 2033). When county fairs and state jackpot samples were aggregated separately, county fairs and state jackpot shows in Indiana exhibited higher estimated prevalence compared to their counterparts in Ohio and Michigan (Indiana: county fairs, 23.6%; jackpot shows, 17.8%; Ohio: county fairs, 15.5%; jackpot shows, 11.2%; Michigan: county fairs, 11.7%; jackpot shows, 5.2%), though these differences were not statistically significant (independence tests, $P > .05$). Exhibitions in Indiana had at least 1 IAV-positive animal more frequently (59.2%) than exhibitions in Michigan (25.9%) and Ohio (34.6%) (Fisher exact test, $P = .0001$ and $P = .0001$, respectively; Supplementary Figure 4). When we limited our analysis to exhibitions with at least 1 positive sample, there was not a
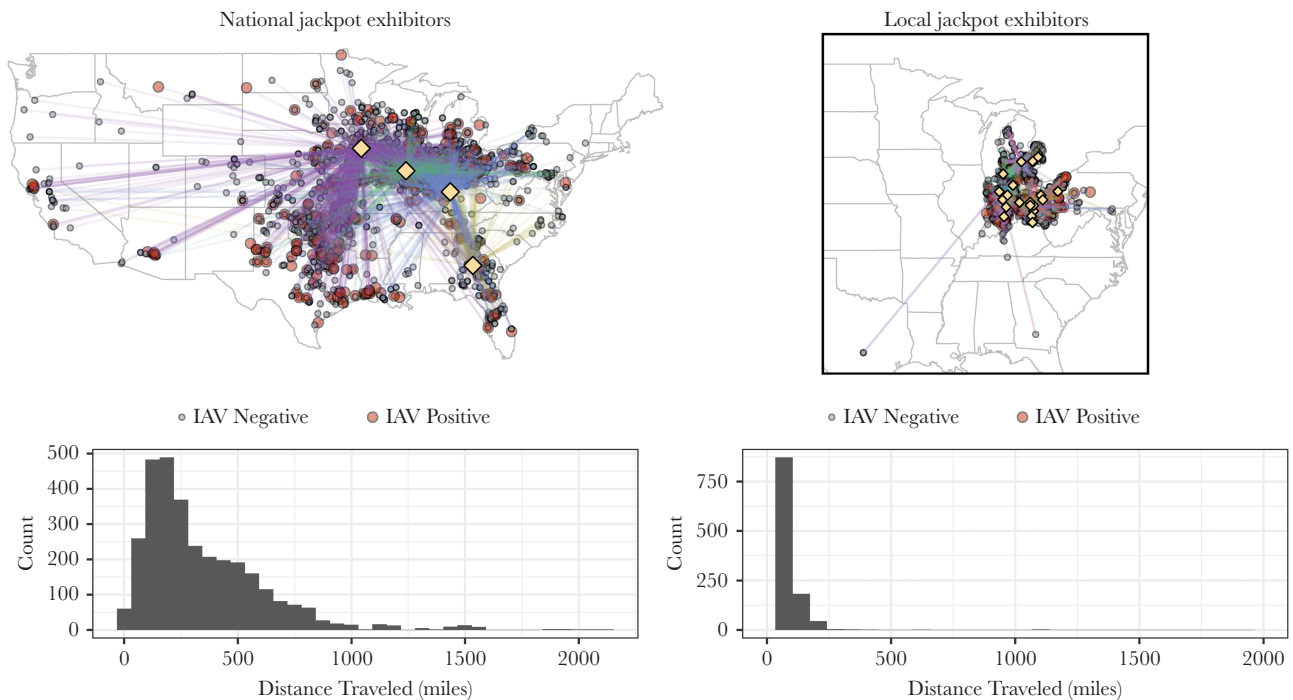

Figure 3. Geographic range of national and state jackpot exhibitors in 2016, 2017, and 2018. Each year, participants from 31–37 US states attended the national jackpot shows sampled in our study. The state jackpot shows in our study drew participants from 4–9 states. Circular points are the home zip code locations of sampled pigs, and point color indicates whether pigs from a particular zip code tested polymerase chain reaction (PCR) positive or PCR negative for influenza A virus (IAV). Yellow diamonds are the locations of jackpot shows. Lines are colored by show identity and connect shows to home zip codes. Histograms are binned distances (miles) traveled by exhibitors from their home zip code to show locations.
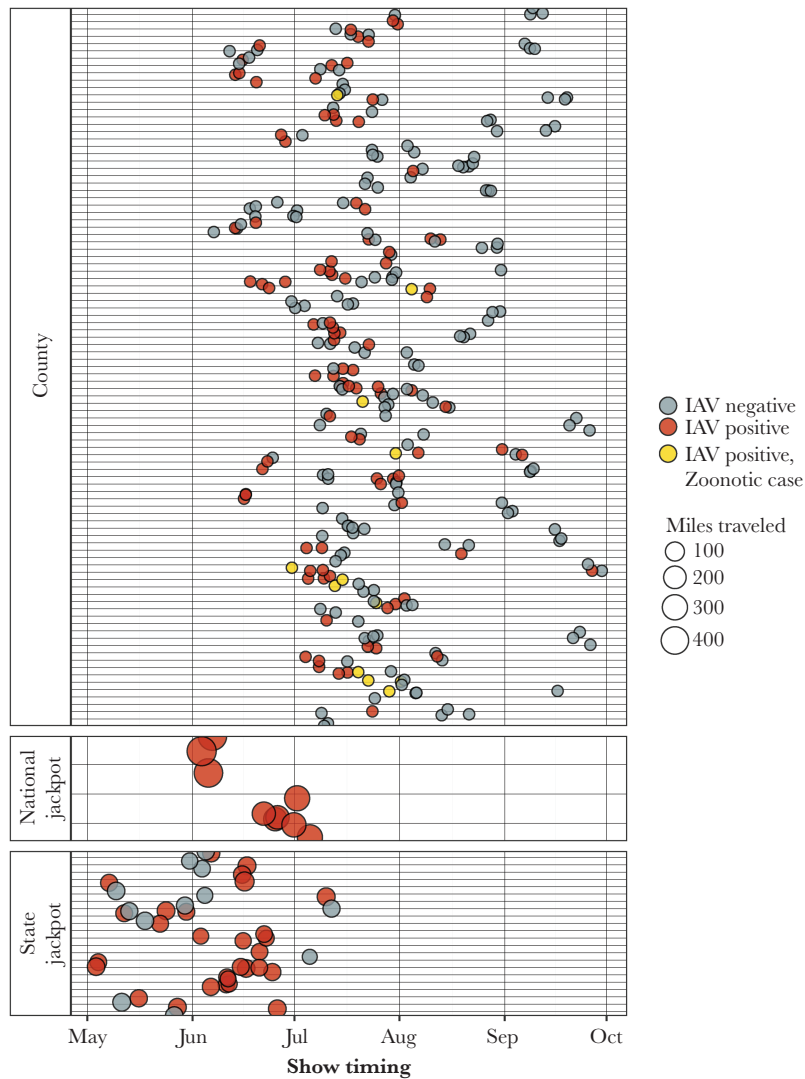
Figure 4. The timing of swine exhibitions organized by show type. Exhibitions that occurred from May to October during 2016–2018 are aggregated to show the relative timing (month-day) of swine exhibitions throughout the year. Point color indicates whether pigs sampled at an exhibition tested polymerase chain reaction (PCR) negative for influenza A virus (IAV, gray), if at least 1 pig tested PCR-positive for IAV (red), or if at least 1 pig tested positive for IAV and the exhibition was linked to a zoonotic infection (yellow). Point size indicates the average distance in miles traveled by exhibitors to attend that show based on the United States postal code of their home farm. Shows are arranged on the y-axis by longitude and jittered for clarity.

significant difference in prevalence across the 3 states (independence test, $P > .05$).

Risk Factors for IAV at Swine Exhibitions

We tested multiple predictors for whether an exhibition (county or state jackpot) tested positive for IAV. Overall, exhibition type was the strongest predictor. Jackpot shows had 4.35-fold higher odds of detecting an IAV-positive animal relative to county fairs (95% confidence interval, 1.2–16.61; Figure 5B; Supplementary Table 4). Larger show sizes (>200 swine), earlier timing during the show circuit, local swine population size, and whether a nearby show had tested positive for IAV within the prior 2 weeks were also associated with increased odds of detecting IAV (Figure 5B; Supplementary Table 4). Though the

probability of IAV detection increased with show duration, the size of the effect was marginal (Figure 5B; Supplementary Table 4). The model that included the infection status of any show type within 75 miles had the best predictive performance, with a classification accuracy of 70%.

DISCUSSION

For more than a decade, animal and public health officials have attempted to disrupt the transmission of IAVs from exhibition swine to youth exhibitors that occurs every summer. However, it is difficult to mitigate zoonotic transmission at county fairs where upwards of 70% of swine can be infected, and new preventive strategies are needed. Here, we demonstrate that IAVs are frequently detected in exhibition swine at jackpot shows
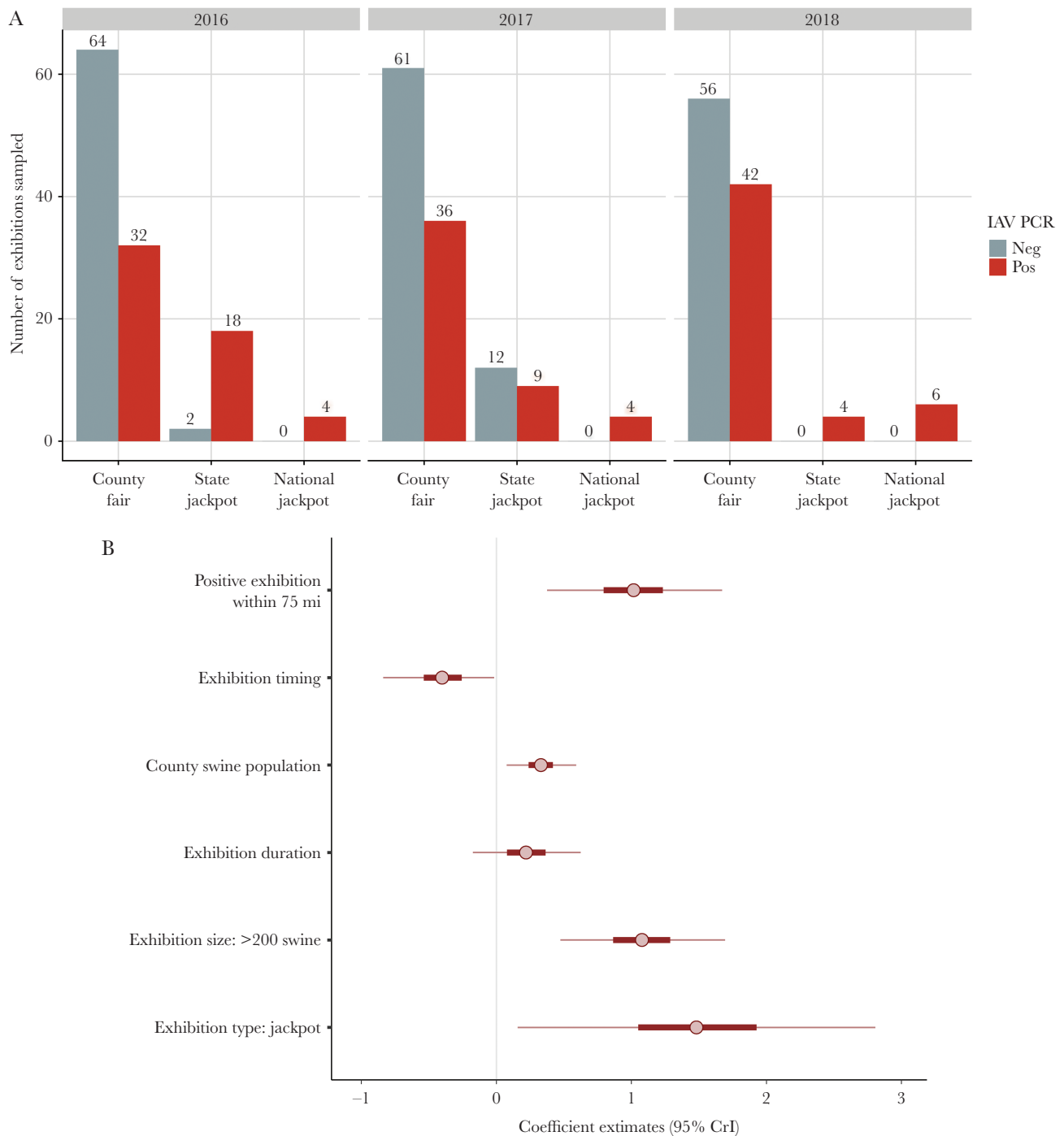
Figure 5. *A*, Number of swine exhibitions that tested polymerase chain reaction (PCR) positive or PCR negative for influenza A virus (IAV). Exhibitions were designated as IAV positive if ≥1 pig tested IAV positive using PCR. Gray bars correspond to IAV-negative exhibitions, and red bars correspond to IAV-positive exhibitions. *B*, Risk factors of exhibitions testing PCR positive for IAV (county fairs and state jackpots). Median coefficient estimates (circles) and posterior 50% and 95% credible intervals (CrI; inner and outer whiskers) were estimated using a Bayesian logistic regression model. Continuous predictors were mean-centered and scaled prior to model fitting

that occur upstream to county fairs and draw pigs from wide geographic catchments, presenting a new target for mitigation efforts. Critically, IAVs detected at jackpot shows have been connected to zoonotic transmission events that occur at subsequent county fairs. For example, an emerging H3N2 subtype that was recovered from our jackpot swine samples in 2016

was subsequently detected 1 month later in pigs and people at a county fair [14]. This study highlighted the potential of jackpot shows to seed IAV diversity into county fairs where public health risk is high. Likewise, an early-season national jackpot show in 2018 appeared to serve as a superspreading event that propagated H1δ-2 (H1N2v) IAVs throughout the
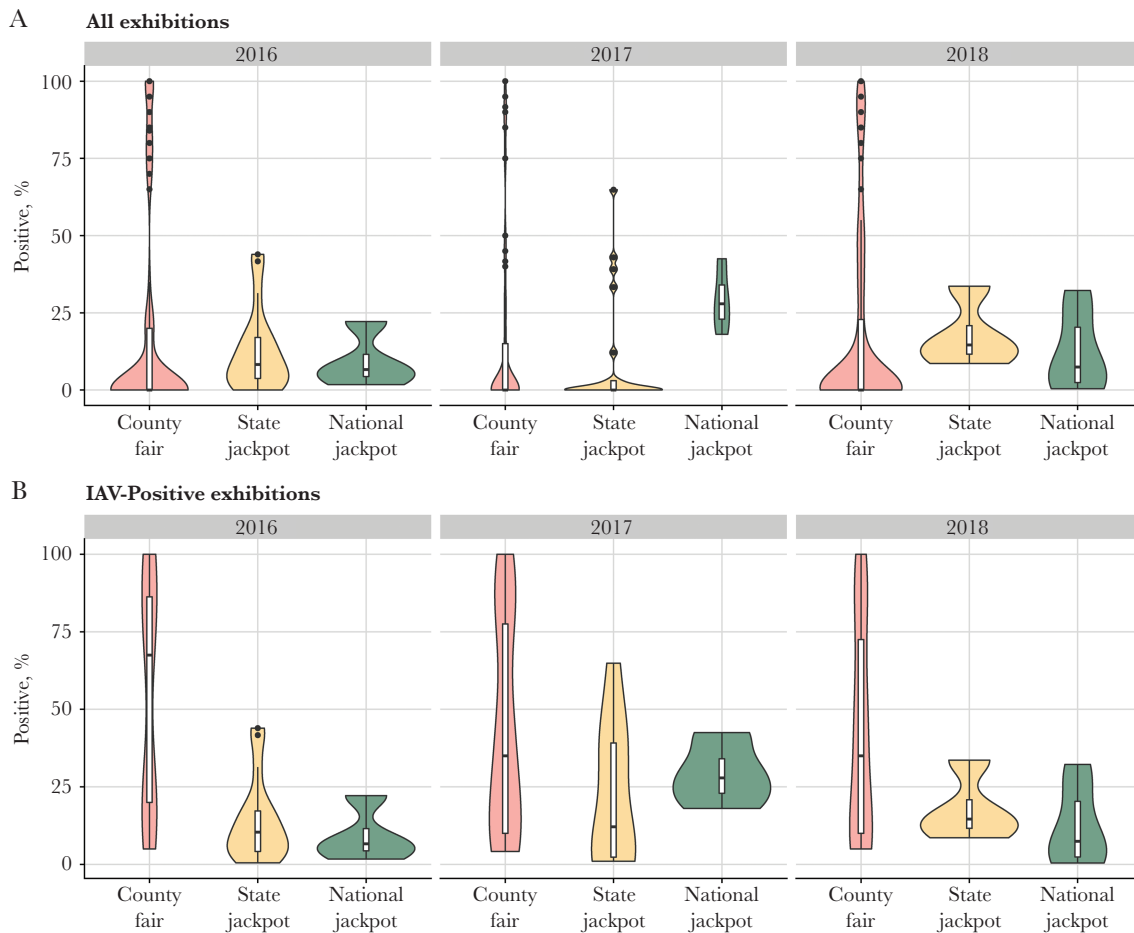
Figure 6. Influenza A virus (IAV) prevalence in all swine exhibitions (*A*) and IAV polymerase chain reaction (PCR)–positive swine exhibitions (*B*) in 2016, 2017, and 2018. Exhibitions were designated as IAV positive if ≥1 pig tested IAV positive using PCR. Violin plots show the distribution of exhibition prevalence and contain boxplots that visualize 5 summary statistics (the median, 2 hinges, and 2 whiskers). The lower and upper hinges correspond to the first and third quartiles (the 25th and 75th percentiles), and whiskers extend to points within 1.5 interquartile ranges of the lower and upper quartile for a distribution.

exhibition circuit; this lineage caused the majority of zoonotic cases reported later that summer [34]. In each year of our study, genotype analyses indicate that IAVs detected at jackpot shows contribute to IAV outbreaks at county fairs later in the show season. Altering the timing of critical jackpot shows may be effective at reducing introduction of zoonotic potential IAV into county fairs. To date, zoonotic transmission occurs primarily at county fairs. Characterizing entire networks of swine exhibitions that drive the dispersal of zoonotic IAVs into county fairs has uncovered new opportunities for mitigating an ongoing pandemic risk.

Although IAV prevalence is lower at jackpots, the likelihood of detecting at least 1 pig with IAV is higher at jackpot shows compared to county fairs. The structure of jackpot shows allows exhibition swine from widely scattered locations to commingle, return home, and show again repeatedly throughout the year, which explains the simultaneous detection of highly related IAVs at geographically dispersed county fairs [35]. Swine can shed IAV for at least 9 days postexposure and typically remain

infectious for at least 5 days [36, 37]. This duration of infection enables swine to carry and transmit IAV from shows week-to-week and within home farms. Because the timing of state jackpot shows overlaps with both national jackpot shows and county fairs, IAVs introduced into jackpot shows have a clear route to seed county fairs. The introduction of IAV at a county fair by a few pigs can spread rapidly among participating swine [38], which enables subsequent zoonotic transmission [14, 16]. Due to local control of show regulations, adoption of recommendations to mitigate zoonotic transmission of IAV is highly varied among the thousands of county fairs that occur annually in the United States. The jackpot show network offers public health control points that could be targeted to reduce IAV introductions at downstream county fairs.

The lower estimated prevalence of IAV within IAV-positive jackpot shows compared to county fairs accounts for the observed absence of zoonotic infections tied to jackpot shows. While county fairs are typically 5–7 days, many jackpot shows are short in duration (1–2 days), which does not likely afford

time for sustained IAV amplification within shows. Beyond duration, lower IAV prevalence in jackpots shows could arise from differences in swine husbandry between practiced jackpot exhibitors and county fair exhibitors who only show pigs annually. For example, a higher proportion of jackpot exhibitor survey respondents report vaccinating their pigs against IAV [39] than did county fair respondents in a different survey [17]. Throughout this study period, exhibitors likely had access to autogenous vaccines and commercially available live attenuated and whole inactivated influenza vaccines, but as of 2020, the only vaccine commercially available to exhibitors is a whole inactivated vaccine.

IAVs are funneled down from national jackpots into state jackpot circuits and from state jackpots into the subsequent county fairs [34]. At a national jackpot show associated with IAV dissemination [34], we recorded 11.2% Indiana zip codes across 3 years compared to 2.9% and 2.3% from Ohio and Michigan, respectively. More Indiana pigs attending national jackpot shows may correspond to an increased number of introductions into state jackpot shows and county fairs, resulting in the observed high proportion of positive shows in Indiana relative to Ohio and Michigan. In contrast, we did not detect significant differences in IAV prevalence within exhibitions between states, indicating that transmission dynamics of IAV within Indiana shows are typical of other localities.

Our predictive model of IAV infection at swine exhibitions found that the odds of detecting IAV increases with show size (the number of pigs present) and the size of the commercial swine population in a county. The association between show size and IAV infection is consistent with prior findings [26]; that is, larger shows often host open-class and breeding swine shows in addition to junior market shows, drawing a greater diversity of exhibitors. Commercial swine are considered the primary source of IAV diversity in exhibition swine [40] and are sometimes managed at the same location as exhibition swine. Exhibitor household members often have contact with swine other than their own, providing an interface for viral transmission between commercial and exhibition swine [17]. However, the commercial swine presence of a county may not be a reliable predictor of IAV infection at jackpot shows, which host a majority of swine exhibitors from outside of the county.

Despite being a small niche in the swine industry, IAV surveillance efforts have detected substantial viral diversity in exhibition swine [16, 38]. In US commercial swine populations, IAVs tend to cluster spatially, and IAV gene flow generally corresponds with the direction of swine transportation across states [41]. As the geographic diversity of farms participating in exhibitions increases, we expect the diversity of IAV detected to also increase. Presence of diverse IAVs within 1 exhibition could facilitate frequent coinfection and high reassortment potential in this population of exhibition swine.

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