African swine fever (ASF) is a highly contagious hemorrhagic viral disease that affects domestic pigs and wild boars. Since its introduction into China in 2018 (1) and subsequently into many other countries in Asia (2), most of the global pig population has been exposed to the ASF virus (ASFV). In the absence of vaccines and treatments, ASF control relies heavily on on-farm biosecurity and on early detection and containment of infected premises (IPs). It is, therefore, essential to identify and target major ASFV transmission routes. However, only a few studies have assessed the contribution of different transmission routes to ASF epidemics (3–6), probably because detailed epidemiologic data are lacking. Although those studies have contributed to knowledge of risk factors for ASFV infection, their findings are limited by possible bias resulting from underreporting of outbreaks, absence of information about contact patterns between farms, or both.

After ASFV is introduced into domestic pigs, contact between farms may contribute greatly to virus spread (7). Vehicles connect farms through the movements of animals, persons, feed, or medical supplies. Such vehicle movements may create conditions for large ASF epidemics on pig farms, as has been reported for other animal diseases (8–10). However, despite their probable epidemiologic role, the role of vehicle movements in shaping ASF epidemics has not been assessed. Moreover, although the role of livestock movements in the dynamics of several animal diseases has been assessed in a large body of modeling studies (11,12), other types of contact between farms, such as those mediated by vehicles involved in farming activities, have rarely been explicitly accounted for.

In 2019, South Korea experienced its first ASF outbreak, which affected domestic pigs and wild boars in the northernmost part of the country. At least 1 pig was positive for ASFV by reverse transcription PCR (13) on 14 farms (IPs) from September 17 through October 9. ASFV infection was also confirmed by reverse transcription PCR for 26 wild boars from October 3 through November 20. We assessed the contribution of vehicle movements and wild boars to the spread of ASFV to pig farms during the 2019 epidemic in South Korea by combining ASF case data and vehicle movement data generated by nationwide global positioning system (GPS) tracking.
RESEARCH

Methods

Data

The Animal Plant and Quarantine Agency (https://www.qia.go.kr) provided the domestic pig farm registry and farm case data. The study population included all 6,340 registered pig farms (Figure 1). IPs were in 4 contiguous municipalities: Ganghwa Island (n = 5/35), Gimpo (n = 2/20), Paju (n = 5/93), and Yeoncheon (n = 2/80) (I3). Any 2 IPs were <84 km apart (median 28.5 km) (Appendix Figure 1, https://wwwnc.cdc.gov/EID/article/27/7/20-4230-App1.pdf). By October 16 (i.e., 1 week after the last reported IP), 62.7% (143/228) herds in affected municipalities had been depopulated (Figures 2, 3).

Most (71.4%) IPs raised >1,000 pigs (Appendix Figure 2). Premises were either commercial (n = 12) or backyard (n = 2) farms: 10 breeding and fattening, 2 breeding, and 2 fattening farms. All IPs, except for 1 backyard farm, were registered. Of the 14 IPs, 11 were detected through farmers’ reports of ASF-like clinical signs and 3 were detected by active surveillance. At the time of reporting, ≤5 pigs on each farm showed ASF-like clinical signs; these clinical signs were observed in ASFV-positive sows on 9 IPs.

Data on the movements of GPS-tracked vehicles involved in farming activities (e.g., private and government veterinary services; feed, manure, and livestock transport) were collated from the Korean

Figure 1. Spatial distribution of registered domestic pig farms in South Korea, indicating African swine fever–positive farms (IPs); ASFV-positive wild boars, confirmed during the study period (August 28–October 16, 2019); and pig farms visited by vehicles that had visited IPs ≥1 time during the study period. ASFV, African swine fever virus; IP, infected premises.
Animal Health Information System (https://www.kahis.go.kr). Given the low number of symptomatic pigs at the time of reporting and the estimated incubation period in pigs (4–13 days) (14), we assumed that the length of time between farm infection and reporting was <20 days. In addition, because the law required that vehicles be disinfected before entering farms and when entering and exiting a city, town, or village, we assumed that ASFV-contaminated vehicles remained infectious for <1 week. On the basis of these assumptions, we considered all movements made by vehicles that entered IPs from August 28 (20 days before the first report of an infected premise) through October 16 (a week after the last report of an infected premise).

The Ministry of Environment (https://me.go.kr) provided data on cases in wild boars. From the first report of ASFV infection in domestic pigs, surveillance efforts for wild boars progressively increased by providing financial incentives for wild boar hunting, trapping, and carcass reporting and by testing for ASFV all wild boars caught or found dead (Appendix Figure 3). We assessed spatial clustering of wild boar cases by using an elliptic version of the spatial scan statistic in SaTScan (https://www.satscan.org).

**Bayesian Modeling**

To test the hypothesis that vehicle movements and ASFV-infected wild boars were the main sources of infection for pig farms, we fit a model of ASFV transmission to the farm case data. A vehicle was considered potentially contaminating if it entered farm $i$ within $d$ days after having visited farm $j$ while farm $j$ was infectious. For a given farm on a given day, the overall force of infection was modeled as the sum of the risk for infection resulting from visits by potentially contaminating vehicles, the risk resulting from exposure to wild boars in the spatial clusters of ASFV-positive wild boars, and background risk. Two levels of background risk were considered, depending on the location of a farm: in municipalities where the virus had been detected or across the country. We estimated parameters by using a 2-stage Metropolis-Hastings Markov chain
Monte Carlo algorithm and, because infection dates were not observed, a data augmentation technique (15–17). The model accounting for the influence of vehicle movements and wild boars was compared with models accounting for only 1 of these epidemiologic factors or for only the constant background risk (null model) on the basis of their deviance information criterion (Appendix).

**Results**

**Vehicle Movement Patterns**

During the study period, 208 vehicles visited IPs, making 12,671 visits to 832 farms (infected and noninfected). A total of 156 vehicles made 2,824 farm visits within 3 days after having visited an IP (assuming that vehicles could remain contaminated for 3 days after visiting an IP); each vehicle made a median of 3 farm visits (interquartile range [IQR] 2–7). Of those farm visits, 255 (9.0%) involved other IPs and 2,569 (91.0%) involved 360 non-IPs (5.7% of farms in the country). The number of farm visits changed with the assumed duration of vehicle infectiousness (Figure 4), decreasing from 5 (IQR 2–9) to 2 (IQR 1–4) as the assumed duration of infectiousness decreased from 6 days to 1 day. However, the proportions of movements involving other IPs and non-IPs remained constant (Appendix Table 3). In terms of movements between IPs, 96 (37.6%) started from an IP within the 20-day period preceding the report of a suspected infection and reached another farm within 3 days, before the other farm reported a suspected infection. All these movements occurred between 5 (65.6%) IPs on Ganghwa Island or between 6 (34.4%) IPs off the island (Appendix Table 4). No vehicle movements were involved at 2 IPs (IP2 and IP11). Although another IP (IP14) was visited by such vehicles, the IP was not a source of potentially contaminating vehicle movements to other IPs, even with a vehicle infectiousness duration of 6 days (Appendix Figure 4).
Spatial Clustering of ASF-Positive Wild Boars

During September 21–November 20 in 95 of 226 municipalities, 1,292 wild boars were tested; the rate of testing increased over time (Appendix Figure 3). A total of 26 ASFV-positive wild boars were identified in Paju (n = 6/57), Yeoncheon (n = 8/130), and Cheorwon (n = 12/398) (Figure 5). Two clusters of ASFV-positive wild boars were identified. Of 36 wild boars tested in cluster 1 (10.7 km²), 10 were ASFV positive, and of 131 in the larger cluster 2 (1,209.4 km²), 13 were positive. Wild boars caught or found dead within these clusters were 21.8 (cluster 1) and 37.2 (cluster 2) times more likely to be ASFV-positive than were those outside these clusters (p<0.001 for all). Although there was no pig farm in cluster 1, there were 6 IPs and 112 non-IPs in cluster 2 (Figure 5). The distance between an infected premise and the nearest infected wild boar was 1.3–37.0 km (Appendix Figure 5).

The Model

For our results, we assumed that a vehicle remained infectious for 3 days after having left an IP. Changes in this parameter value did not largely affect interpretation of the results (Appendix).

When compared by using the deviance information criterion, the model accounting for vehicle movements and for exposure to wild boars in the spatial cluster was preferred over models accounting for only 1, or none, of those sources of infection (Table; Appendix Table 5). Indeed, exposure to these factors substantially increased the risk of farms becoming infected. The daily probability of infection on a farm increased 11.1-fold (95% highest density interval [HDI] 1.1–39.3) after the visit of a potentially contaminating vehicle, compared with a farm not visited by such a vehicle (Appendix Table 6). For a farm in the spatial cluster of ASFV-positive wild boars, the daily probability of becoming infected was 2.5 (95% HDI 1.0–7.7) times as high as for a farm outside this cluster (Appendix Table 6).

On the basis of the best-fit model, we estimated the force of infection exerted on IPs on their estimated infection dates and the proportion of ASFV incursions attributable to each transmission route. Vehicle movements accounted for 41.2% and exposure to wild boars in the spatial cluster for 24.0% of viral incursions; the background risk accounted for the remaining 34.8% (Appendix Table 7). The contribution of different transmission routes to ASFV incursion into IPs varied with the spatial location of the farms. Vehicle movements were the most likely route for ASFV introduction into IPs in the southwestern epidemic region. In contrast, ASFV was not likely to have been spread by vehicles in the northeastern epidemic region, where wild boars were estimated to be the main source of infection for IPs within the ASFV-positive wild boar cluster (Figure 5; Appendix Figures 6, 7). Indeed, the density of potentially contaminating vehicle movements differed greatly between these regions. After accounting for the posterior predictive
probability that an infected premise was already infected when a vehicle left it, the estimated number of potentially contaminating vehicle movements was 36.6 between IPs and 891.6 from IPs to non-IPs (Appendix Table 8). Of those movements between IPs, 94.3% reached IPs in the southwestern (4.3 visits/infected premise) regions and 5.7% reached IPs in the northeastern (0.3 visits/infected premise) regions. Also, among farms visited by potentially contaminating vehicles, the force of infection resulting from these vehicle movements was much higher for IPs than for non-IPs (Appendix Figure 8). Together, these findings indicate that a dense network of potentially contaminating vehicle movements was formed between a small group of farms, despite the short length of time between farm infection and reporting (median 4.3 days, 95% HDI 1.0–15.8) (Table). To avoid an infected farm spreading ASFV to >1 other farm through vehicle movements, the average number of vehicles visiting a farm in a day and the average number of farms visited by a vehicle in a day should be limited to 1.3 (Figure 6).

### Discussion

Our investigation of the role of vehicle movements and of wild boars in ASFV spread to pig farms during the 2019 epidemic in South Korea was made possible by the availability of vehicle movement data generated by integrated GPS tracking and case data on wild boars generated by enhanced ASFV surveillance. The model that accounted for the influence of vehicle movements and wild boars best explained the epidemic pattern, suggesting that both transmission routes contributed to ASFV spread.

Our model suggests that the main route of ASFV introduction into IPs in the southwestern epidemic region was through contaminated vehicles. Indeed, most IPs on Ganghwa Island and Gimpo were densely connected through vehicle movements. In particular, there were a large number of vehicle movements between the 5 IPs on Ganghwa Island (IPs 5–9) ≈1–9 days before a suspected ASFV infection was reported. These 5 IPs reported possible ASF outbreaks within a 4-day period; a small
number of pigs showed clinical signs at the time of reporting. This finding suggests that the high density of vehicle movements probably promoted virus transmission between these IPs. Vehicle movements may have increased ASFV spread more because of potentially less effective vehicle disinfection measures on the island. According to epidemiologic investigations, IPs on Ganghwa Island seemed to have insufficient disinfection facilities for vehicles and personnel. Moreover, although farms were relatively close together on this small island (total 302.4 km²), most vehicle disinfection stations were near 2 bridges connecting the island to the mainland. Therefore, vehicle movements on the island were likely to bypass these stations.

It is unclear how the virus reached the southwestern epidemic region. No potentially contaminating vehicle movements from other affected municipalities were recorded, even when the infectious period for a contaminated vehicle was extended to 6 days. No wild boars were caught or found dead, and they were therefore unavailable for ASFV testing in either municipality. Although the lack of boars for testing does not exclude the possibility that ASFV circulated in the wild boar population, the number of wild boars may be relatively small and the risk for ASFV spread from wild boars to domestic pigs may be very low in this region. Alternatively, ASFV could have been introduced through vehicle movements not captured in this study. We accounted only for vehicle movements between farms; we did not account for vehicle movements involving other types of premises (e.g., slaughterhouses) that could have acted as a source of infection.

Our results suggest that exposure to ASFV-positive wild boars was the main source of infection for pig farms in the northeastern epidemic region. First, all IPs except 1 (IP1) in Paju and Yeoncheon were located in a cluster encompassing almost all ASFV-positive wild boars found in those municipalities. Second, unlike IPs in the southwestern region, several IPs in Paju and Yeoncheon were not connected, or were only weakly connected, to other IPs through vehicle movements. However, the way in which ASFV could have spread from wild boars to domestic pigs remains unclear. Pietschmann et al. (18) showed that ASFV transmission was possible from wild boars to domestic pigs housed in separate pens. Such contact was, however, unlikely to have occurred in this setting because the pigs were kept indoors in all but IP11, a backyard farm. Also, potential biological vectors (Ornithodoros spp. ticks) have not been reported in South Korea (19,20). Although the exact mode of ASFV transmission remains unknown, the potential for ASFV spread from infected wild boars must be addressed by ASF prevention and control efforts, a view that is supported by a previous study that linked epidemics in wild boars and domestic pigs in the Russian Federation (3).

The nationwide GPS vehicle tracking system provided a unique opportunity to investigate the role of vehicle movements in virus dissemination between farms. Although the estimated length of time from farm infection to reporting was short and several movement restriction (standstill) periods were enforced, a large number of vehicles had already visited IPs during their estimated infectious period and could have spread ASFV to other farms. The types of vehicles and the purpose of the farm visits were not made available for this study. Vehicles involved in farming activities were required by law to be disinfected at multiple sites (e.g., the entry point of a city, town, or village) during the epidemic and routinely disinfected at the farm entrance. These findings suggest that disinfection may have been suboptimal. Therefore, restrictions on vehicle movements should be prioritized in the event

### Table. Posterior parameter estimates and posterior predictive length of time between infection and reporting of African swine fever, South Korea, 2019*

| Parameters | Median (95% HDI) | G-R | DIC |
|-----------|-----------------|-----|-----|
| Full model | | | |
| Potentially contaminating vehicle movement ($P_v$) | 53.9 (7.4–113.4) $\times 10^{-4}$ | 1.00 | 275.8 (null model: 284.6) |
| Wild boar cluster ($P_{B_w}$) | 8.2 (0.0–19.0) $\times 10^{-4}$ | 1.00 | |
| Background (country, $P_{B_c}$) | 0.03 (0.0–0.1) $\times 10^{-4}$ | 1.00 | |
| Background (epidemic region, $P_{B_e}$) | 5.4 (1.1–11.2) $\times 10^{-4}$ | 1.00 | |
| Mean of the gamma distribution ($\mu$) | 3.7 (1.0–8.8) | 1.00 | |
| Variance of the gamma distribution ($\beta$) | 44.6 (5.2–113.5) | 1.00 | |
| Length of time between infection and reporting ($D$)† | 4.3 (1.0–15.8) | | |

*DIC, deviance information criteria; G-R, Gelman-Rubin convergence diagnostic; HDI, highest density interval; $P_v$, risk for infection resulting from 1 potentially contaminating vehicle movement; $P_{B_w}$, daily risk for infection resulting from being located in an African swine fever virus–positive wild boar cluster; $P_{B_c}$, daily background risk (country); $P_{B_e}$, daily background risk (epidemic region).

†The distribution was obtained by simulating values from the gamma distribution, based on parameters $\alpha$ and $\beta$ randomly sampled from their joint distribution.
of virus introduction into areas where high on-farm biosecurity cannot be guaranteed. The availability of contact tracing data could reduce the negative effect of movement restrictions on farming activities by targeting those restrictions to premises that have been in contact with IPs. Active surveillance could also be focused on these premises, enabling even more timely case detection.

The background risk accounted for a substantial fraction of the force of infection exerted on several IPs. Swill feeding probably did not contribute to this background risk because it was banned at the start of the epidemic and, according to the outbreak investigations, did not seem to be practiced on IPs. Control measures were unlikely to have promoted ASFV dissemination. Pigs were culled within a few days after confirmation of diagnostic results, and carcasses were placed inside a fiber-reinforced plastic chamber and buried on the premise. Vehicles and personnel involved in these interventions were not allowed to visit non-IPs throughout the epidemic. Regular inspections of vehicles visiting feed and manure disposal plants suggested that most vehicles involved in farming activities were registered and therefore tracked by GPS. Nonetheless, some vehicle movements not captured in this study could have contributed to disease spread. For instance, we did not consider vehicle contamination from visiting other types of premises (e.g., slaughterhouses). Private vehicles were not GPS tracked, but outbreak investigations did not identify any connections between IPs through such vehicles. Wild boars may have also substantially contributed to the background risk. Although these findings strongly suggest that the prevalence of ASFV infection in wild boars was much higher within than outside the clusters, it was not possible to exclude the possibility that the virus might also have circulated at lower prevalence in wild boar populations outside the spatial clusters. This source of infection might have been plausible for some IPs for which most of the force of infection was attributed to background risk.

One limitation of this study is that the model did not consider the possible heterogeneity in the infectiousness of vehicles and the susceptibility of farms to ASFV infection. Farm visits may involve different types of contact with persons, equipment, and pigs, thereby presenting different transmission risks. In addition, farms with poor biosecurity could have been exposed to an increased risk for infection when visited by contaminated vehicles. The risk for infection from infected wild boars was also likely to have varied between farms because of different levels of on-farm biosecurity and proximity to wild boar habitats. In addition, although the model identified an excess risk for infection for farms within the spatial cluster of ASFV wild boar cases, the spatiotemporal heterogeneity in ASFV circulation among wild boars inside and outside the cluster may have been underestimated.

Another limitation is that the model assumed that the potential for a contaminated vehicle to transmit the infection remained constant throughout the vehicle’s period of infectiousness. Yet because vehicles were supposed to be disinfected when entering a farm, their infectiousness may have decreased over time with each additional farm visited. Accounting for this process would probably have increased the estimated probability of virus incursion after a visit from a potentially contaminating vehicle. However, this process is unlikely to have influenced our conclusions because the contribution of vehicle movements to ASFV spread was not affected by variations in the assumed duration of vehicle infectiousness.

Figure 6. Expected number of secondary farm cases of African swine fever (r) caused by 1 infected farm through the movements of vehicles, South Korea, 2019. r is computed as a function of the average daily number of vehicles visiting a farm (x-axis) and the average daily number of farms visited by a vehicle (y-axis). Different lines represent different thresholds for the proportion of iterations in which r was <1 (p = 1, 0.99, or 0.95). Vehicles were assumed to remain infectious for 3 days after leaving an infected farm. Appendix Figure 9 (https://wwwnc.cdc.gov/EID/article/27/7/20-4230-App1.pdf) shows the results with different assumptions on the duration of vehicle infectiousness.
The possibility that some wild boars were infected while on IPs cannot be completely excluded. However, ASFV was probably circulating among wild boars before pig farms were infected, given that the first wild boar case was detected in the demilitarized zone where no civilians and farms are present, and North Korea had already reported the disease. Subsequently, the delayed detection of ASFV in wild boars probably resulted from the lower sensitivity of surveillance in wild animals compared with domestic animals and from increased surveillance efforts among wild boars after disease detection on farms. In addition, since the end of the study period (November 21, 2019), ASFV infection has been confirmed in >700 wild boars and on 3 pig farms (2), suggesting that ASFV can continue to circulate among wild boars in the absence of virus circulation among domestic pigs.

Our models did not account for within-farm transmission dynamics. Farm infectiousness was likely to vary over time, influencing between-farm transmission dynamics. However, given that a small number of pigs showed ASF-like clinical signs on all IPs at the time of reporting or detection, and that herds were culled within 1 or 2 days, the effect may have been limited.

In conclusion, our findings suggest that the movement of contaminated vehicles and infected wild boars contributed to the spread of ASFV to pig farms in South Korea. Although the ongoing circulation of ASFV in wild boars poses an ongoing risk for virus spillover onto pig farms, vehicle movements have the potential to cause large chains of transmission between farms. Therefore, the timely implementation of movement restrictions is critical for the rapid and effective management of ASFV epidemics. In this regard, the tracking of vehicles involved in farming activities could guide the targeting of restrictions to those at high risk for infection because of their recent contacts. High on-farm biosecurity and effective vehicle disinfection should be ensured, especially in areas where ASFV is circulating among wild boars.

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Transmission Dynamics of African Swine Fever Virus, South Korea, 2019

Appendix

Methods

1. Between-farm vehicle movements

Vehicle movement data were collated from the Korean Animal Health Information System (KAHIS). By law, vehicles used for livestock farming activities, such as veterinary medicine, feed, manure, livestock transport, and used by governmental veterinary services (e.g. for disease surveillance and control), were required to be installed with a GPS device. It was not required for private vehicles due to the personal information protection law. It transmitted a signal to KAHIS when a vehicle was located on the site of a farm registered in the government database. As of 2019, 59,521 vehicles were registered in KAHIS, and, based on results of regular inspections, it could be assumed that the vast majority of vehicles were registered (Yoo, personal communication). In particular, close to 100% of veterinary services vehicles and feed and manure transporters, for which their registration was inspected each time they enter feed or manure disposal plants, were considered to be enrolled.

Vehicle movements between farms were identified in two steps. First, we extracted from KAHIS all vehicle movements made by vehicles that entered IPs during the study period: from 28th August 2019 (20 days before the first IP report) to 16th October 2019 (one week after the last IP report). The definition of the study period was based on the following assumptions. Considering that the number of pigs showing clinical signs indicative of ASF was small, zero to five, at the time of reporting, and that the ASF incubation period in domestic pigs is estimated to be around four to 13 days (I), we assumed that the length of time between infection and reporting was less than 20 days during this epidemic. We also assumed that farms were infectious from the onset of infection, and remained infectious after reporting, until the end of the epidemic, recognizing that vehicles that entered IPs for sample collection, culling and
disinfection could have become contaminated with ASFV from infected pigs and the contaminated environment. Second, from the extracted data, we identified between-farm vehicle movements that could have played a role in the spread of ASFV. We assumed that a vehicle contaminated following the visit of an infected farm was infectious for other farms for a certain time period. Thus, we assumed that a vehicle v could have spread the virus from farm i to farm j if it entered farm j within d days after having visited farm i during the infectious period of that farm. We defined vehicle movements satisfying this condition as ‘potentially contaminating vehicle movements, V’. Such movements were not limited to successive visits. We assumed that vehicle v could infect farm j, regardless of whether it entered other farms during these d days. For example, if contaminated vehicle v entered susceptible farms j and then k within d days after leaving infectious farm i, the vehicles could have infected farm j as well as farm k, with the probability of infecting farm k being independent of whether farm j became infected. ASFV is known to be persistent, with the ability to survive for several weeks in the environment (2). However, considering that vehicles are required by law to be disinfected before entering farms, and were disinfected when entering or exiting a city, town, or village during the epidemic, we assumed that contaminated vehicles could not remain infectious for longer than a week. In the following, we considered different values of d, the number of days during which a contaminated vehicle remained infectious: one, three and six days.

2. Surveillance data on ASF in wild boars and on pig farms

The Ministry of Environment reinforced ASF surveillance in wild boars by providing financial incentives for wild boar hunting, trapping and carcass reporting. All wild boars caught or found dead across the country were tested for ASFV. The Ministry of Environment provided ASFV test results (i.e. positives or negatives) and the spatial coordinates where the tested wild boars were caught or found dead. We assessed whether wild boar cases were spatially clustered using an elliptic version of the spatial scan statistic in SatScan software (https://www.satscan.org). The cluster with the largest maximum likelihood ratio test statistic represented the most likely cluster of ASFV-positive wild boars, and secondary clusters of ASFV-positive wild boars were identified based on the iterative scan statistics (https://www.satscan.org). The statistical significance of detected clusters was assessed by comparing the test statistic of the observed data with those of data randomly generated by 999 Monte Carlo simulations. The p-values were calculated using the default SaTScan option
We set the maximum cluster size to 50% of the population at risk for the following reasons. First, clusters obtained with >50% sizes indicate areas of exceptionally low rates of wild boar cases within the defined cluster, rather than an area of exceptionally high rates of wild boar cases within the cluster (https://www.satscan.org). Thus, 50% is generally recommended as an upper limit (https://www.satscan.org), to consider all possible sizes of clusters below this value. Secondly, restricting cluster sizes below 50% could introduce pre-selection bias in the cluster size unless there was solid epidemiological reason to choose such lower values (https://www.satscan.org).

3. Bayesian modelling approach

We hypothesized that vehicle movements from IPs and ASFV-infected wild boars were the main sources of infection for domestic pig farms. To test this hypothesis, we formulated the force of infection based on four parameters: $P_V$ was the risk of infection resulting from one potentially contaminating vehicle movement, $P_W$ was the daily risk of infection resulting from being located in an ASF-positive wild boar cluster. $P_{B_1}$ and $P_{B_2}$ were the daily risks of infection not captured by $P_V$ and $P_W$. While $P_{B_1}$ represented a background risk for all farms in the country, $P_{B_2}$ represented an additional background risk for farms in the epidemic region.

The force of infection for farm $i$ on day $d$ ($F_{i,d}$) was then modelled as:

$$F_{i,d} = P_V n_{i,d}^V + P_W S_i^W + P_{B_1} + P_{B_2} A_i$$

where $n_{i,d}^V$ was the number of potentially contaminating vehicle movements farm $i$ received on day $d$ and $S_i^W$ and $A_i$ were an indicator variable ($S_i^W = 1$ if farm $i$ was located in the spatial cluster, 0 otherwise, $A_i = 1$ if farm $i$ was located in the epidemic region, 0 otherwise).

Since infection dates were not observed for IPs, we updated infection dates ($I_i$), and therefore the time between infection and reporting ($D_i$), in each iteration by using a data augmentation technique, which has been successfully adopted to infer transmission dynamics from incomplete epidemic data (4). The likelihood of the epidemic data was expressed as follows. As starting values, we randomly selected the time between infection and reporting from a Uniform distribution between 1 and 20 days for each IP, and computed their infection date. For an IP $I$, the time between infection and reporting ($D_i$) and its augmented infection date ($I_i$) were:

$$D_i \sim U(1, 20), D_{set} = \{D_1, ..., D_{14}\}$$
\[ I_i = R_i - D_i, I_{set} = \{I_1, ..., I_{14}\} \]

\( R_i \) was the date at which IP \( i \) reported suspicion of ASFV infection. With \( I_{set} \) as starting values, the probability \( A_i \) that IP \( i \) was not infected between the start of the epidemic and one day before its augmented infection date, \( I_i \), and the probability \( B_i \) that IP \( i \) was infected on day \( I_i \) were expressed as follows:

\[ A_i = e^{\sum_{d=1}^{I_i-1} -F_{i,d}}, B_i = 1 - e^{-F_{i,I_i}} \]

Note that \( n_{i,d}^Y \) and, therefore, \( F_{i,d} \), were updated based on \( I_{set} \). The likelihood \( L_1 \) for the timing of infection of IPs was:

\[ L_1 = \prod_{i \in F_{IP}} A_i B_i f(D_i; \alpha, \beta) \]

\( F_{IP} \) refers to the set of IPs. \( f(D_i; \alpha, \beta) \) was the probability density function of the length of time between infection and reporting in farms. It was expressed as a Gamma distribution, with \( \alpha \) and \( \beta \) as mean and variance. The Gamma distribution was truncated to between 1 and 20, as it was assumed that the time between infection and reporting. For non-IPs, we expressed the probability that farm \( j \) did not become infected during the epidemic (\( C_j \)) and the likelihood for non-IPs (\( L_2 \)) as:

\[ C_j = e^{\sum_{d=1}^{d_{last_j}} -F_{j,d}} \]

\[ L_2 = \prod_{j, j \in F_{IP}} C_j \]

Farms which were depopulated by culling or government purchase were no longer at risk of infection. Thus, for those farms, \( d_{last_i} \) was defined as the date at which farm \( i \) was emptied during the epidemic. For farms that were not subject to those preventive measures, \( d_{last_i} \) was the last date of the study period.

The likelihood of the epidemic data \( L \) was:

\[ L = L_1 L_2 \]
At the first stage of the MH algorithm, new values were proposed for the parameters related to transmission ($P_V$, $P_W$ and $P_B$) and the time between infection and reporting ($\alpha$ and $\beta$). For each parameter $i$, a new value was proposed from the Uniform distribution:

$$\theta_i^{new} \sim U(\theta_i^{old} - \varepsilon_i, \theta_i^{old} + \varepsilon_i)$$

$\theta_i^{new}$ was the proposed value in the current iteration, $\theta_i^{old}$ was the value in the previous iteration, and $\varepsilon_i$ was a scale parameter. We constrained $P_V$, $P_W$, $P_{B_1}$, and $P_{B_2}$ to be between 0 and 1. Therefore, when values outside this range were proposed, they were discarded, and new values were proposed. Then, for the transmission and Gamma distribution parameters, the proposed values were accepted based on the following acceptance ratio:

$$\frac{Posterior(\theta^{new} | Y, D, I)}{Posterior(\theta^{old} | Y, D, I)} \wedge 1$$

$\theta^{new}$ was as a set of proposed values in the current iteration, $\theta^{old}$ was as a set of parameter values in the previous iteration, and $Y$ was the data. If the acceptance ratio was equal to or greater than a random number drawn between 0 and 1, $\theta^{new}$ was accepted. Otherwise, $\theta^{new}$ was discarded, and $\theta^{old}$ was recycled in the next iteration. While the transmission parameters were proposed and accepted (or discarded) separately, the Gamma distribution parameters were proposed and accepted (or discarded) together. Additionally, for effective MCMC mixing, for a set of proposed values $i$, the scale parameter $\varepsilon_i$ was increased or decreased by 20% in every 100th iteration if the acceptance rate fell below 20% or exceeded 30% (Appendix Table 1).

For a given iteration, once parameter values were updated, we also updated the time between infection and reporting (and therefore infection dates) for each IP, one by one, by using an independence MH sampler. For IP $i$, we proposed an integer value randomly drawn from a Uniform distribution between 1 and 20 days as IP $i$’s new value for the time between infection and reporting ($D_i^{new}$).

$$D_i^{new} \sim U(1, 20)$$

$$D_{set}^{new} = D_{set}^{old} - \{D_i^{old}\} + \{D_i^{new}\}$$

We also proposed a new infection date for IP $i$ ($I_i^{new}$) as:
\[ I_{i}^{\text{new}} = R_{i} - D_{i}^{\text{new}} \]

\[ I_{i}^{\text{new}} = I_{i}^{\text{old}} - \{I_{i}^{\text{old}}\} + \{I_{i}^{\text{new}}\} \]

Then, we updated \( n_{i,d}^{R} \) with \( I_{i}^{\text{new}} \) and decided whether to accept \( D_{i}^{\text{new}} \) and \( I_{i}^{\text{new}} \) based on the following acceptance ratio:

\[
\frac{\text{Posterior}(D_{i}^{\text{new}}, I_{i}^{\text{new}} | y, \theta)}{\text{Posterior}(D_{i}^{\text{old}}, I_{i}^{\text{old}} | y, \theta)} \times 1
\]

If the acceptance ratio was equal or greater than a random number drawn between 0 and 1, \( D_{i}^{\text{new}} \) and \( I_{i}^{\text{new}} \) were accepted. Otherwise, \( D_{i}^{\text{old}} \) and \( I_{i}^{\text{old}} \) were recycled in the next iteration.

Weakly informative priors were used for model parameters (Appendix Table 2).

The models were iterated up to the point where convergence was considered to have been achieved based on a visual inspection of MCMC trace plots and Gelman-Rubin convergence diagnostic. The models were run with four chains with different starting values. The first 10,000 iterations were discarded, and the remaining parameter values comprised the posterior distributions. We estimated the posterior predictive distribution of the length of time between infection and reporting through simulations based on the joint posterior distribution of \( \alpha \) and \( \beta \).

We compared models based on their DIC to assess whether the model accounting for both the influence of vehicle movements and wild boars explained the epidemic pattern better than models accounting for the influence of only one of these epidemiological factors, or only the constant background risk (null model). Since infection dates were not observed, the conventional DIC could not be used. A modified version of DIC designed for models with missing data was used instead (3). Since the posterior distribution was right-skewed for some parameters, the posterior median, instead of the posterior mean, was reported and used to compute DIC values (4).

Based on the joint posterior distribution of the parameters, we computed the expected number of secondary farm cases generated by one infected farm through the movement of vehicles, for different values of the average daily numbers of (i) farms visited by a vehicle (\( n_{v \rightarrow f} \)) and (ii) vehicles visiting a farm (\( n_{f \rightarrow v} \)):

\[ n_{v \rightarrow f} n_{f \rightarrow v} C_{v} I_{f} P_{v} \]
was the assumed duration of vehicle infectiousness, \( I_f \) was the average infectious period of a farm, and \( P_v \) was the risk of infection resulting from one potentially contaminating vehicle movement.

Next, we computed \( RR_V \) (or \( RR_W \)), the ratio between the daily probability of a farm becoming infected if it received one potentially contaminating vehicle movement (or if it was located in the spatial cluster of ASFV-positive wild boars) and the daily probability of a farm becoming infected from transmission routes other than vehicle movements and wild boars. With \( P_B = P_{B1} + P_{B2} \):

\[
RR_V = \frac{1 - e^{-(P_V + P_B)}}{1 - e^{-P_B}}
\]

\[
RR_W = \frac{1 - e^{-(P_W + P_B)}}{1 - e^{-P_B}}
\]

We also estimated for individual IPs the force of infection on their estimated dates of infection, and the proportion of ASFV infection attributable to different transmission routes, through simulation. In each iteration, we randomly sampled parameter values \( (P_V, P_W, P_B, \alpha, \beta) \) from the joint posterior distributions. Then, based on the Gamma distribution with the sampled parameters \( \alpha \) and \( \beta \) as mean and variance, we computed the probability that IP \( i \) was infected on day \( d \), \( \delta(i, d) \), and the probability that IP \( j \) was infectious on day \( s \), \( \pi(j, s) \). If vehicle \( v \) left IP \( j \) on day \( s \) and visited IP \( i \) on day \( d \), we computed the force of infection resulting from that vehicle movement \( F_{V,j,s,i,d} \) as follows:

\[
F_{V,j,s,i,d} = \delta(i, d) \pi(j, s) P_V I(s, d)
\]

Where \( I(s, d) \) was equal to 1 if the difference between days \( s \) and \( d \) was lower than or equal to the assumed length of the vehicle infectious period, and 0 if not. \( F_{V,i} \) was then the force of infection resulting from vehicle movements exerted on IP \( i \) when this IP was estimated to have been infected:

\[
F_{V,i} = \sum_{v, j, s, d} F_{V,j,s,i,d}
\]

The force of infection associated with wild boars was \( F_{W,i} = P_W \) if IP \( i \) was located in the cluster, and \( F_{W,i} = 0 \) otherwise. The force of infection associated with the background infection risk was \( F_{B,i} = P_B \). In each iteration (i.e. for each set of parameters sampled from the joint
posterior distribution), we also randomly assigned a source of infection to each IP $i$ by simulating a multinomial trial, with one trial and 3 possible outcomes (i.e. each transmission route) associated with probabilities $F_{V,i}/K$, $F_{W,i}/K$, and $F_{B,i}/K$, with $K = F_{V,i} + F_{W,i} + F_{B,i}$. We repeated this process 30,000 times, and computed the proportion of simulated infections attributed to each route of transmission.

We estimated the weighted number of potentially contaminating vehicle movements between IPs. In each iteration (i.e. a set of parameter values drawn from the joint posterior distribution), we identified all vehicle movements made within the duration of the assumed vehicle infectious period and before entry IPs (i.e., IPs where vehicles moved to) reported a suspicion of ASFV infection. Then, we weighted these vehicle movements by the probability that exit IPs (i.e., IPs that vehicles had visited) were infectious on the day of departure, based on randomly sampled Gamma distribution parameter values. We repeated this process 30,000 times.

Finally, we estimated the force of infection resulting from potentially contaminating vehicle movements for farms associated with such vehicle movements. If vehicle $v$ had visited IP $i$ and day $s$ and farm $i$ on day $d$, we computed the force of infection exerted on farm $j$ resulting from that vehicle movement ($F_{v,j,s,d}$) as follows:

$$F_{v,j,s,i,d} = \pi(j,s)P_Y(s,d)$$

We then computed the overall force of infection exerted on farm $i$ resulting from potentially contaminating vehicle movements ($F_i$) as follows:

$$F_i = \sum_{v,j,s,d} F_{v,j,s,i,d}$$

We compared $F_j$ between farms within and outside affected municipalities.

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**Appendix Table 1.** Initial scale parameter values

| Parameters                              | Initial scale parameter values |
|-----------------------------------------|--------------------------------|
| Force of infection parameters           |                               |
| \(P_V\)                                 | 0.01                           |
| \(P_W\)                                 | 0.001                          |
| \(P_{B_1}\)                             | 0.00001                        |
| \(P_{B_2}\)                             | 0.0001                         |
| Gamma distribution parameters’         |                               |
| \(\alpha\)                              | 3                              |
| \(\beta\)                               | 3                              |

*For effective MCMC mixing, the scale parameters were increased or decreased by 20% in every 100th iteration if the acceptance rate fell below 20% or exceeded 30%.

**Appendix Table 2.** Priors for the transmission and Gamma distribution parameters

| Parameters | Priors                      |
|------------|-----------------------------|
| Transmission parameters | \(P_V\) Uniform (0, 1) \(P_W\) Uniform (0, 1) \(P_{B_1}\) Uniform (0, 1) \(P_{B_2}\) Uniform (0, 1) |
| Gamma distribution parameters’ | \(\alpha\) Uniform (1, 20) \(\beta\) Gamma (mean = 6.5, variance = 2) |

*\(\alpha\) and \(\beta\) were the mean and variance of the Gamma distribution of the time between infection and reporting.

**Appendix Table 3.** The pattern of vehicle movements between pig farms

| Duration of vehicle infectiousness* | No. of vehicles | No. of vehicle movements | Between IPs | IP to non-IPs | No. of non-IPs† |
|------------------------------------|-----------------|--------------------------|-------------|---------------|-----------------|
| One day                            | 122             | 1148                     | 107 (9.3%)  | 1041 (90.7%)  | 182 (2.9%)      |
| Three days                         | 156             | 2824                     | 255 (9.0%)  | 2569 (91.0%)  | 360 (5.7%)      |
| Six days                           | 169             | 4115                     | 355 (8.6%)  | 3760 (91.4%)  | 479 (7.6%)      |

*Vehicle movements were defined as those made between two pig farms within the assumed duration of vehicle infectiousness.
†The number of non-IPs that received at least one vehicle movement among the study population (n=6,340)
Appendix Table 4. The pattern of potentially contaminated vehicle movements between IPs*

| Movement direction                        | No. of potentially contaminated vehicle movements | One day† | Three days† | Six days† |
|------------------------------------------|--------------------------------------------------|----------|-------------|-----------|
| Inside Ganghwa                           | 37 (5)                                           | 63 (5)   | 85 (5)      |
| Outside Ganghwa                          | 10 (5)                                           | 33 (6)   | 46 (7)      |
| From Ganghwa to other municipalities     | 0                                                | 0        | 0           |
| From other municipalities to Ganghwa     | 0                                                | 0        | 0           |
| Total                                    | 47                                               | 96       | 131         |

*Vehicle movements made between IPs up to 20 days before exit IPs (i.e. IPs where vehicles moved from) reported suspicion of infection and before entry IPs (i.e. IPs where vehicles moved to) reported suspicion of infection, with different assumptions on the duration of vehicle infectiousness (i.e. one, three, or six days)
†The assumed duration of vehicle infectiousness
The number in brackets represents the number of IPs involved with given vehicle movements.

Appendix Table 5. Posterior parameter estimates with the three-day assumption on the duration of vehicle infectiousness

| Parameters                                                                 | MCMC output                      |
|---------------------------------------------------------------------------|----------------------------------|
|                                                                           | Median (95% HDI*)                 | G-R†       | DIC‡       |
| Full model                                                                |                                  |           |           |
| Potentially contaminating vehicle movement (𝑃𝑃_𝑉𝑉)                        | 53.9 (7.4-113.4) x10^−4           | 1.00      | 275.8     |
| Wild boar cluster (𝑃𝑃_𝑊𝑊)                                                 | 8.2 (0-19.0) x10^−4               | 1.00      |           |
| Background (country, 𝑃𝑃_𝐵𝐵_1)                                            | 0.03 (0-0.1) x10^−4               | 1.00      |           |
| Background (epidemic region, 𝑃𝑃_𝐵𝐵_2)                                    | 5.4 (1.1-11.2) x10^−4             | 1.00      |           |
| Mean of the Gamma distribution (α)                                        | 3.7 (1.0-8.8)                     | 1.00      |           |
| Variance of the Gamma distribution (β)                                    | 44.6 (5.2-113.5)                  | 1.00      |           |
| 'Vehicle movement' model                                                   |                                  |           |           |
| Potentially contaminating vehicle movement (𝑃𝑃_𝑉𝑉)                        | 50.1 (5.9-110.8) x10^−4           | 1.00      | 277.8     |
| Background (country, 𝑃𝑃_𝐵𝐵_1)                                            | 0.03 (0-0.1) x10^−4               | 1.00      |           |
| Background (epidemic region, 𝑃𝑃_𝐵𝐵_2)                                    | 8.3 (3.5-14.2) x10^−4             | 1.00      |           |
| Mean of the Gamma distribution (α)                                        | 3.8 (1.0-9.1)                     | 1.00      |           |
| Variance of the Gamma distribution (β)                                    | 45.2 (5.5-114.1)                  | 1.00      |           |
| 'ASFV-circulation in wild boars' model                                    |                                  |           |           |
| Wild boar cluster (𝑃𝑃_𝑊𝑊)                                                 | 5.6 (0-16.1) x10^−4               | 1.00      | 285.8     |
| Background (country, 𝑃𝑃_𝐵𝐵_1)                                            | 0.03 (0-0.1) x10^−4               | 1.00      |           |
| Background (epidemic region, 𝑃𝑃_𝐵𝐵_2)                                    | 9.8 (4.4-16.2) x10^−4             | 1.00      |           |
| Mean of the Gamma distribution (α)                                        | 4.7 (1.0-17.9)                    | 1.00      |           |
| Variance of the Gamma distribution (β)                                    | 44.4 (6.1-113.6)                  | 1.00      |           |
| Null Model                                                                |                                  |           |           |
| Background (country, 𝑃𝑃_𝐵𝐵_1)                                            | 0.03 (0-0.1) x10^−4               | 1.00      | 284.6     |
| Background (epidemic region, 𝑃𝑃_𝐵𝐵_2)                                    | 11.5 (6.2-17.7) x10^−4            | 1.00      |           |
| Mean of the Gamma distribution (α)                                        | 4.6 (1.0-17.7)                    | 1.00      |           |
| Variance of the Gamma distribution (β)                                    | 4.5 (6.4-115.0)                   | 1.00      |           |

*Highest density interval
†Gelman-Rubin convergence diagnostic
‡The deviance information criteria. DIC in Celeux, et al. (3) was used.

Appendix Table 6. The probability ratios, based on posterior parameter estimates from the full model

| Probability ratios                                                                 | Median (95% HDI*) |
|-----------------------------------------------------------------------------------|-------------------|
| Duration of vehicle infectiousness: one day                                       |                   |
| Potentially contaminating vehicle movements vs no vehicle movements                | 23.6 (1.5-89.0)   |
| Within vs outside the ASF-positive wild boar cluster                              | 2.5 (1.0-7.7)     |
| Duration of vehicle infectiousness: three days                                    |                   |
| Potentially contaminating vehicle movements vs no vehicle movements                | 11.1 (1.1-39.3)   |
| Within vs outside the ASF-positive wild boar cluster                              | 2.5 (1.0-7.7)     |
| Duration of vehicle infectiousness: six days                                      |                   |
| Potentially contaminating vehicle movements vs no vehicle movements                | 7.5 (1.0-26.1)    |
| Within vs outside the ASF-positive wild boar cluster                              | 2.4 (1.0-7.4)     |

*Highest density interval
### Appendix Table 7. The percentage of simulated infections caused by different transmission routes, based on posterior parameter estimates from the full model

```
| Transmission route | Risk attribution (%) |
|--------------------|----------------------|
| **Duration of vehicle infectiousness: one day** | |
| Potentially contaminating vehicle movement | 37.1 |
| Wild boar cluster | 23.8 |
| Background (country) | 0.3 |
| Background (epidemic region) | 38.9 |
| **Duration of vehicle infectiousness: three days** | |
| Potentially contaminating vehicle movement | 41.2 |
| Wild boar cluster | 24.0 |
| Background (country) | 0.2 |
| Background (epidemic region) | 34.6 |
| **Duration of vehicle infectiousness: six days** | |
| Potentially contaminating vehicle movement | 39.4 |
| Wild boar cluster | 23.2 |
| Background (country) | 0.2 |
| Background (epidemic region) | 37.2 |
```

*The number of vehicle movements was weighted by the probability that exit IPs (i.e. IPs where a vehicle moved from) were already infected on the day of departure, based on the posterior distribution of the length of time between infection and reporting.

### Appendix Table 8. The weighted number of potentially contaminating vehicle movements, based on posterior parameter estimates from the full model*

```
| Movement pattern | Median (95% quantile) |
|------------------|-----------------------|
| **Duration of vehicle infectiousness: one day** | |
| Between IPs | 18.2 (14.4-25.0) |
| IPs to non-IPs | 367.2 (330.9-429.9) |
| **Duration of vehicle infectiousness: three days** | |
| Between IPs | 36.6 (28.6-52.1) |
| IPs to non-IPs | 891.6 (794.9-1,078.0) |
| **Duration of vehicle infectiousness: six days** | |
| Between IPs | 41.2 (31.4-66.8) |
| IPs to non-IPs | 1226.2 (1104.9-1539.7) |
```

*The number of vehicle movements was weighted by the probability that exit IPs (i.e. IPs where a vehicle moved from) were already infected on the day of departure, based on the posterior predictive distribution of the length of time between infection and reporting.

### Appendix Table 9. The weighted number of potentially contaminating vehicle movements between IPs, based on posterior parameter estimates from the full model*

```
| Movement pattern | Median (95% quantile) |
|------------------|-----------------------|
| **Duration of vehicle infectiousness: one day** | |
| Inside wild boar cluster | 0.5 (0.2-0.8) |
| Outside wild boar cluster | 17.7 (14.2-24.2) |
| **Duration of vehicle infectiousness: three days** | |
| Inside wild boar cluster | 2.1 (1.1-3.6) |
| Outside wild boar cluster | 34.5 (27.4-48.6) |
| **Duration of vehicle infectiousness: six days** | |
| Inside wild boar cluster | 2.7 (1.4-5.4) |
| Outside wild boar cluster | 38.5 (29.9-61.3) |
```

*The number of vehicles leaving an IP was weighted by the probability that the IP was already infected on the day of departure, based on the posterior predictive distribution of the length of time between infection and reporting.
Appendix Table 10. Posterior parameter estimates and posterior predictive length of time between infection and reporting, from the full model with different assumptions on the duration of vehicle infectiousness

| Parameters                                                                 | MCMC output                      | G-R† | DIC‡  |
|---------------------------------------------------------------------------|----------------------------------|------|-------|
| Duration of vehicle infectiousness: one day                               |                                   |      |       |
| Potentially contaminating vehicle movement ($P_{PV}$)                     | 121.8 (19.1-260.8) x10^4         | 1.00 | 271.5 |
| Wild boar ($P_{PW}$)                                                      | 8.0 (0-18.9) x10^4               | 1.00 |       |
| Background (country, $P_{B_1}$)                                          | 0.03 (0-0.1) x10^4               | 1.00 |       |
| Background (epidemic region, $P_{B_2}$)                                  | 5.4 (1.0-11.3) x10^4             | 1.00 |       |
| Mean of the Gamma distribution ($\alpha$)                                 | 3.4 (1.0-8.3)                    | 1.00 |       |
| Variance of the Gamma distribution ($\beta$)                              | 47.1 (7.3-118.9)                 | 1.00 |       |
| Length of time between infection and reporting (D)§                        | 4.2 days (1.0-16.0)              |      |       |
| Duration of vehicle infectiousness: six days                              |                                   |      |       |
| Potentially contaminating vehicle movement ($P_{PV}$)                     | 36.6 (3.4-79.3) x10^4            | 1.00 | 280.1 |
| Wild boar ($P_{PW}$)                                                      | 8.0 (0-18.9) x10^4               | 1.00 |       |
| Background (country, $P_{B_1}$)                                          | 0.03 (0-0.1) x10^4               | 1.00 |       |
| Background (epidemic region, $P_{B_2}$)                                  | 5.7 (1.0-11.6) x10^4             | 1.00 |       |
| Mean of the Gamma distribution ($\alpha$)                                 | 3.9 (1.0-9.8)                    | 1.00 |       |
| Variance of the Gamma distribution ($\beta$)                              | 45.7 (6.1-115.0)                 | 1.00 |       |
| Length of time between infection and reporting (D)§                        | 4.5 days (1.0-16.1)              |      |       |

*Highest density interval
†Gelman-Rubin convergence diagnostic
‡The deviance information criteria. DIC in Celeux, et al. (3) was used.
§The distribution was obtained by simulating values from the Gamma distribution, based on randomly sampled gamma distribution parameters ($\alpha$ and $\beta$).

Appendix Figure 1. The distribution of the shortest distance between any two IPs. The shortest distance was computed by using the distm function of the geosphere package in R.3.4.2.
Appendix Figure 2. Histogram of the number of pigs on IPs.

Appendix Figure 3. The number of wild boars that tested positive or negative for ASFV by RT-PCR during the study period. Since the first confirmation of ASFV infection in a domestic pig farm (IP1) on 17th September, ASF surveillance in wild boars has been intensified across the country, resulting in a total of 26 ASFV-positive wild boar out of 1,292 wild boars tested during the study period.
Appendix Figure 4. The distribution of the number of IPs connected through vehicle movements. With (A) one-, (B) three- or (C) six-day assumptions for the duration of vehicle infectiousness, only the movements made up to 20 days before an exit farm (i.e., farms where a vehicle moved from) reported suspicion of ASFV infection and before an entry farm (i.e., farms where a vehicle moved to) reported the suspicion are shown. For each IP (x-axis), a circle (or a triangle) represents the number of other IPs, an IP sent (or received) at least one vehicle movement (y-axis), with different assumptions for vehicle infectiousness.

Appendix Figure 5. The distribution of the distance to the nearest location of an ASFV-positive wild boar from individual IPs. The shortest distance was computed by using the `distm` function of the `geosphere` package in R.3.4.2.
Appendix Figure 6. The vehicle movement pattern and model results. The spatial distribution of IPs, non-IPs, ASFV-positive wild boars, and potentially contaminating vehicle movements between IPs with (A) one- and (B) six-day assumptions for the duration of vehicle infectiousness. Polygons represent municipalities affected by ASFV. Small circles represent IPs, with their numbers representing the order of
reporting dates. Those circles are represented as pie charts, showing the proportion of different transmission routes attributed to the infection of an IP via simulation. Edges represent vehicle movements made between IPs when an exit IP (i.e., where a vehicle moved from) was considered infectious via simulation, and before an entry IP (i.e., where a vehicle moved to) reported suspicion of infection. Edge width is proportional to the sum of the weighted number of such movements; each vehicle movement was weighted by the probability that an exit IP was infectious at the time of departure computed via simulation. Edge arrows represent the direction of vehicle movements. Pig farm density is shown in reddish colors. Green squares represent the location of ASFV-positive wild boars, with greenish ellipses representing their spatial cluster.
Appendix Figure 7. The force of infection on IPs via different transmission results (A) The force of infection exerted on IPs on the estimated dates of infection via different transmission routes. In the boxplots, center lines represent medians, and box limits represent upper and lower quartiles. Upper and lower whiskers extend to the largest and smallest values within 1.5x interquartile ranges, respectively. Points represent outliers. (B) The proportion of simulated infections caused by different transmission routes. 'Baseline background' represents a background risk for all farms in the country, and 'additional background' an additional background risk for farms in the epidemic region. The results are based on the MCMC output from the full model, with the three-day assumption on the duration of vehicle infectiousness.
Appendix Figure 8. The force of infection resulting from potentially contaminating vehicle movements, based on the MCMC output from the full model. The comparison was made between IPs, non-IPs within and outside affected municipalities (Ganghwa island, Gimpo, Paju, and Yeoncheon), among farms visited by vehicles that visited IPs within three days, the assumed length of the vehicle infectious period. The number in each group (in parentheses) corresponds to the number of pig farms visited by vehicles that visited IPs at least once during the study period. In the boxplots, center lines represent medians. Box limits represent upper and lower quartiles. Upper and lower whiskers extend to the largest and smallest values within 1.5x interquartile ranges, respectively.
Appendix Figure 9. The expected number of secondary farm cases (r) caused by one infected farm through the movements of vehicles. r is computed as a function of the average daily number of vehicles visiting a farm (x-axis) and the average daily number of farms visited by a vehicle (y-axis). (a) and (b) are based on the one- and six-day assumptions on the duration of vehicle infectiousness. Different lines represent different thresholds for the proportion of iterations in which r was lower than one (p=1, 0.99, or 0.95). Pale grey lines represent the results when vehicles were assumed to remain infectious for three days after leaving an infected farm.
Appendix Figure 10. The MCMC outputs from the full model testing the contribution of both vehicle movements and wild boars in the spread of ASFV to domestic pig farms, with the three-day assumption on the duration of vehicle infectiousness. (A) The log-likelihood trace plot. Different colors represent chains with different starting values. (B) The posterior distributions of transmission ($P_V$, $P_W$, and $P_B$) and Gamma distribution ($\alpha$ and $\beta$) parameters, and the number of days between infection and reporting ($D$) (in days). The posterior distribution of $D$ was simulated from the Gamma distribution with joint posterior $\alpha$ and $\beta$ values as mean and variance. Thick black horizontal lines represent 95% highest-density intervals (HDIs).
Appendix Figure 11. The daily force of infection for farms exposed to different combinations of the following transmission routes: (i) when visited by a single contaminated vehicle ('Vehicle'), (ii) when located in a spatial cluster of ASFV-positive wild boars ('Wild boar'), and (iii) when exposed to transmission routes other than contaminated livestock vehicles and infected wild boars ('Baseline'). The results are based on the MCMC output from the full model, with the three-day assumption on the duration of vehicle infectiousness.