

1 African Swine Fever spread across Asia, 2018–2019

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3 Running title: ASF spread across Asia, 2018–2019

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9

10 **Abstract**

11 African Swine Fever Virus (ASFV) is a highly contagious pathogen causing disease in pigs, commonly
12 characterised by acute haemorrhagic fever. Prior to August 2018, African Swine Fever (ASF) had not
13 been reported in Asia, but has since spread throughout China, Mongolia, Korea, Vietnam, Laos,
14 Cambodia, Myanmar, the Philippines, Hong Kong, Indonesia, Timor-Leste and Papua New Guinea.
15 Using data collated from reports of confirmed cases, we applied spatio-temporal analysis to describe
16 ASFV spread throughout Asia, from 1 August 2018 (reported start date) to 31 December 2019.
17 Analysis revealed a propagating epidemic of ASFV throughout Asia, with peaks corresponding to
18 increased reports from China, Vietnam and Laos. Two clusters of reported outbreaks were found.
19 During the epidemic, ASFV primarily spread from the North-East to the South-East: a larger,
20 secondary cluster in the North-East represented earlier reports, whilst the smaller, primary cluster in
21 the South-East was characterised by later reports. Significant differences in country-specific
22 epidemics, morbidity, mortality and unit types were discovered, likely attributable to differences in
23 prevention, surveillance and control measures. The initial number of outbreaks and enterprise size
24 are likely predictors of the speed of spread and the effectiveness of ASFV stamping out procedures.
25 Biosecurity methods, wild boar populations and the transportation of pigs and movement of
26 infected fomites are discussed as likely risk factors for facilitating ASFV spread across Asia.

27 **Keywords:** African Swine Fever virus; spatio-temporal analysis; Asia; epidemic; spread

28 Introduction

29 African Swine Fever (ASF) is a highly contagious disease of swine caused by African Swine Fever Virus
30 (ASFV) (Costard et al., 2009; Penrith & Vosloo, 2009; Salguero, 2020; Sánchez–Vizcaíno et al., 2012).
31 The only member of the *Asfarviridae* family and the only known DNA arbovirus, ASFV is a large,
32 double-stranded DNA virus that primarily undergoes cytoplasmic replication (Costard et al., 2009;
33 Dixon et al., 2019; Galindo & Alonso, 2017; Gaudreault et al., 2020; Rojo et al., 1999). African Swine
34 Fever (ASF) is arguably the most important infectious disease prevalent in swine populations and has
35 proved devastating for the pork industry throughout much of the world (Costard et al., 2009; Penrith
36 & Vosloo, 2009; Salguero, 2020; Sánchez–Vizcaíno et al., 2012). For this reason, the World
37 Organisation for Animal Health (OIE) has listed ASF as a notifiable disease.

38 The clinical presentation of ASF varies depending on the route and dose of ASFV infection, the
39 virulence of the strain, as well as host factors. However, it is considered a haemorrhagic disease, and
40 peracute and acute forms of the disease are the most common presentations (Salguero, 2020;
41 Sánchez–Vizcaíno et al., 2012). Peracute ASF is characterised by its rapid clinical progression, with a
42 high fever, lethargy, anorexia and occasionally sudden death occurring without signs (Hess, 1971;
43 Salguero, 2020). Acute ASF is the typical form observed in naïve animals, commonly presenting with
44 respiratory distress and petechial haemorrhages and ecchymoses, together with signs of peracute
45 ASF (Hess, 1971; Salguero, 2020). Subacute and chronic forms – normally associated with infection
46 by a lower virulence strain of ASFV – also occur, but less commonly (Salguero, 2020; Sánchez–
47 Vizcaíno et al., 2012).

48 In wild pig populations, the incubation period has been estimated between 4–19 days, whilst for the
49 acute form in domestic pig populations it is 3–4 days (World Organisation for Animal Health, 2019).
50 This short incubation period together with a short period of latency (~4–15 days) contributes to the
51 rapid spread of ASFV throughout domestic pig herds, possibly even before clinical signs are apparent

52 (de Carvalho Ferreira et al., 2013; Guinat et al., 2016; Pietschmann et al., 2015). Therefore, when
53 infected, domestic pig populations typically display high morbidity and mortality rates (Costard et al.,
54 2013). However, some evidence suggests that in endemic areas, chronic forms have become more
55 common (Costard et al., 2013; Dixon et al., 2019). Wild suids are also an important host to consider
56 in the transmission of ASFV in some regions (Jori & Bastos, 2009; Thomson, 1985; Anderson et al.,
57 1998; Dixon et al., 2019; McVicar et al., 1981), and soft ticks of the genus *Ornithodoros* have been
58 identified as vectors of ASFV (Costard et al., 2013; Jori & Bastos, 2009; Penrith et al., 2019).
59 Therefore, ASFV can be maintained in several different cycles of transmission.

60 ASF was first described in 1921, when it emerged as an acute haemorrhagic fever in domestic pigs in
61 East Africa (Montgomery, 1921). By the 1950s, ASF had been reported from most African countries
62 (De Kock et al., 1940; Thomson, 1985).

63 ASF was first reported in Europe (Portugal) in 1957, likely entering via infected pork products (Bosch
64 et al., 2017; Dixon et al., 2019; Sánchez-Vizcaíno et al., 2015). It spread to other European countries
65 (Belgium, France, Malta, the Netherlands, Italy [Sardinia] and Spain), the Caribbean and South
66 America, where it remained endemic until the mid-1990s (Bosch et al., 2017; Costard et al., 2009;
67 Dixon et al., 2019; Sánchez-Vizcaíno et al., 2015). All of these countries were able to eradicate the
68 disease, except in the case of Sardinia, where ASFV remains endemic (Costard et al., 2013; Dixon et
69 al., 2019).

70 In 2007, ASF was reported in Georgia, where the disease became established within the wild suid
71 populations (Dixon et al., 2019; Rowlands et al., 2008). ASFV spread across the Caucasus and into
72 Russia during 2007 (Cwynar et al., 2019; Dixon et al., 2019; Gogin et al., 2013; Linden et al., 2019;
73 Sánchez-Vizcaíno et al., 2013) and during the subsequent decade further cases were reported from
74 parts of Russia, Ukraine, Belarus and Lithuania (Cwynar et al., 2019; Dixon et al., 2019; Gogin et al.,
75 2013; Linden et al., 2019; Sánchez-Vizcaíno et al., 2013). Between 2014 and 2018, ASF was reported

76 in Belgium, Bulgaria, Czech Republic, Estonia, Hungary, Latvia, Poland and Romania (Cwynar et al.,
77 2019; Dixon et al., 2019; Gogin et al., 2013; Linden et al., 2019; Sánchez-Vizcaíno et al., 2013).

78 The first outbreak of ASF in Asia was reported in August 2018, occurring in North-East China
79 (Shenyang City, Liaoning province) (Dixon et al., 2019; Zhou et al., 2018). As Asia, particularly China,
80 accounts for approximately 50% of the global pig population, this disease has already had a
81 substantial impact on agriculture worldwide, with no prospect of imminent eradication or control
82 (Pitts & Whitnall, 2019).

83 Attempts to develop a vaccine to prevent ASF have not been successful (Costard et al., 2013; Dixon
84 et al., 2019; Gaudreault et al., 2020; Penrith, 2009; Sánchez-Vizcaíno et al., 2012), and there is no
85 recognised treatment, although the use of antivirals has been investigated (Costard et al., 2013;
86 Dixon et al., 2019; Penrith, 2009; Sánchez-Vizcaíno et al., 2012). Therefore, a number of other
87 strategies must be employed to control the spread of disease; primarily relying on biosecurity, early
88 detection and reporting, movement restrictions and zoning, stamping out of affected or potentially
89 exposed animals, and strict biosecurity protocols (Penrith, 2009; Penrith & Vosloo, 2009; Costard et
90 al., 2009; Dixon et al., 2019).

91 This study aimed to describe the spread of ASFV in commercial Asian pig populations between 2018
92 and 2019. Morbidity, mortality and epidemic trends were examined to provide insight into the
93 drivers of the disease and its consequences.

94 **Materials and Methods**

95 *Data Collection and Management*

96 Information on the locations and dates of AFS outbreaks throughout Asia was gathered from the
97 OIE. Immediate Notifications and Follow-up reports were accessed from the Report Archive of the

World Animal Health Information Database (WAHIS) Interface.¹ Reported ASF outbreaks were selected if they were located in an Asian country between 1 August 2018 and 31 December 2019. For each report, the following information was extracted: date of report, outbreak start date and end date (if applicable), location (latitude/longitude and by name), unit type, number of susceptible animals, number of cases, deaths and number of animals killed and disposed of. Reports were only included for domestic pig populations; reports of occurrence in wild boar were excluded. Data were imported into Microsoft Excel 2016 and all reports were combined into a single dataset for further analysis. Error checking was performed by ensuring logical values were recorded for each data point and by random selection of 5% of the data to manually check against the original reports.

Data Analysis

Epidemic curves were developed using RStudio Version 1.2.5033. Weekly incidence of cases was determined and plotted for the outbreak period. Plots were created for all data, both combined and colour-coded by country, as well individually for countries and unit types.

Locations of reported outbreaks (latitude and longitude) were mapped using a shape file of Asia (World Geodetic System 1984) within a geographic information system (ArcGIS v10.5. ESRI, Redlands CA). Reported latitude and longitude values from the collated dataset were used to create points for each report, with only the first occurrence of an outbreak at a specific location included. Based on day of epidemic of report, a colour ramp (epidemic day green to red [day 1 to 507]) was used to visualise epidemic spread of ASFV throughout Asia. In addition, directional ellipses were calculated (1 SD), unweighted and weighted by epidemic day. Utilising SaTScan v9.6, a retrospective space-time analysis was performed to determine the presence of clusters in the dataset, based on cases and number of susceptible animals reported for each outbreak. Identified clusters were interpreted

¹ https://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home

120 based on the ratio of expected to observed cases, and statistical significance was evaluated by log
121 likelihood ratio statistics using a Monte Carlo procedure and 999 iterations.

122 Country data points were assigned to the categories of China, including Hong Kong (hereafter
123 referred to as China), Laos, Vietnam and Other for analysis. Two categories of unit type were
124 created: Backyard and the combination of Farm and Village data points (hereafter referred to as
125 Farm). As there was no standardisation of unit types across countries when providing reports to the
126 OIE, characteristics of the data were investigated to justify the classifications made. The Farm and
127 Village types tended to be larger operations and Backyard types were primarily smaller enterprises.
128 This pattern, together with the infrequent use of both Farm and Village terminology within a single
129 country, justified the assumption that Farm and Village were generally synonymous and therefore
130 comparable statistically.

131 Parameters for further analysis were created in Microsoft Excel 2016. Morbidity (number of cases ÷
132 susceptible animals) and mortality (deaths ÷ susceptible animals) were calculated for each report.
133 Epidemic day was calculated by assigning Day 1 to the first date of the epidemic (1 August 2018) and
134 then each report date was allocated a number relative to this date. Standardised epidemic days for
135 both country and unit type were also calculated. This was performed by assigning Day 1 to the first
136 date of the epidemic for each country or unit type, respectively, and then designating each reported
137 outbreak subsequently an epidemic day number relative to Day 1.

138 A cross-tabulation analysis was performed to determine the proportion of Backyard and Farm unit
139 types for each country. Further analyses were performed for both country and unit type as
140 categorical variables and morbidity, mortality, epidemic day, epidemic day standardised by country
141 and epidemic day standardised by unit type as outcome variables. Kruskal-Wallis one-way analyses
142 of variance with pairwise comparisons (Statistix v8.0. Analytical Software, Tallahassee FL) were used
143 to compare epidemic day, morbidity and mortality between countries and unit types.

144 Results

145 A total of 570 independent reports of African Swine Fever were made throughout Asia in 2018 and
146 2019. These reports involved 3 275 542 susceptible swine, 69 503 cases, 62 067 deaths and 1 902
147 216 pigs which were killed and disposed of. A difference between the unit types affected within
148 countries was noted; China (29%) and Other Countries (25%) had the highest proportion of Backyard
149 type outbreaks, compared to Laos (2%) and Vietnam (0%).

150 The epidemic curve highlights a propagating pattern with three outbreak peaks apparent (Figure 1).
151 Each peak predominantly consists of an increase in case numbers in China, Vietnam and Laos,
152 respectively (Figure 2). The individual epidemic curves of these three countries also display
153 propagating patterns, although the time period of the outbreaks in the epidemic varies between
154 countries (Figure 3). A similar pattern was observed when the epidemic curves were classified by
155 unit type (Figure 4). However, the analysis of epidemic day highlighted variations between these
156 epidemics despite similar patterns. There was a significant difference in epidemics between
157 countries ($P<0.001$). China's epidemic started significantly earlier than all other countries, followed
158 by Vietnam occurring significantly earlier than Laos and Other Countries. The reported Backyard
159 outbreaks also occurred significantly earlier than the Farm outbreaks ($P<0.001$).

160 When analysing epidemic day standardised for country and unit type, a significant difference was
161 found between epidemic day for both unit types ($P=0.009$) and countries ($P<0.001$) (Tables 1 and 2,
162 respectively). The epidemic was significantly longer for reported Farm outbreaks than Backyard.
163 China and Other Countries had significantly longer epidemics than Laos and Vietnam.

164 The spread of ASF outbreaks was primarily confined to mainland Asia, and the majority were located
165 in South-East Asia (Figure 5). The countries from which the highest number of outbreak reports
166 originated were China ($n=163$), Vietnam ($n=186$) and Laos ($n=141$). The direction of spread during

167 the study period was northeast to southwest with a 31–35° rotation. When weighted by epidemic
168 day (1–507), there was a southwest shift as the epidemic progressed (Figure 5).

169 The first report in the epidemic was on 1 August 2018 in the province of Liaoning, located in the
170 northeast of China near the border with the Democratic People's Republic of Korea. The outbreaks
171 spread outward from this source, both south throughout China and west into Mongolia by January
172 2019. By the end of January, the virus had spread far enough south to enter Vietnam. Cambodia
173 reported its first cases in April, whilst in May spread was further reported from Hong Kong and the
174 Democratic People's Republic of Korea. In June, Laos reported its first confirmed outbreak, and by
175 the end of July, so did the Philippines. Further spread into Myanmar occurred in August, whilst the
176 first cases in Indonesia, Timor-Leste and the Republic of Korea were reported in September.
177 Throughout the remainder of 2019, no new countries reported the occurrence of ASF cases. As of 31
178 December 2019, complete resolution of all ASF outbreaks had only been reported by Cambodia,
179 Hong Kong, Mongolia and Myanmar.

180 Two clusters were found when analysing the spatial data (Figure 6). The primary, smaller-sized
181 cluster found in South-East Asia occurred between 22 February and 22 September 2019. Within this
182 cluster there was an observed/expected ratio of cases of 12.87. The larger, secondary cluster was
183 found in North-East Asia and occurred between 14 August and 15 October 2018, with an
184 observed/expected ratio of cases of 6.21.

185 Overall, across all countries, case morbidity was 0.021 and case mortality was 0.019. There was a
186 significant difference in both the morbidity ($P < 0.001$) and mortality ($P < 0.001$) across China, Laos,
187 Vietnam and Other Countries (Table 3). Morbidity was highest in Vietnam, then Laos followed by
188 China and Other Countries. Laos, Vietnam and China all had significantly higher mortality than Other
189 Countries, with Laos also being significantly higher than China. There was also a significant difference

in morbidity and mortality between Backyard and Farm (Table 4). Backyard had a significantly (P=0.002) higher morbidity, whilst Farm had a significantly (P=0.016) higher mortality.

Discussion

This study presents an overview of the early phase of the ASF epidemic that swept across Asia between August 2018 and December 2019. The initial number of outbreaks and the size of the operations affected within each country are likely components that determined both the speed of spread and effectiveness of the stamping out responses employed. Spread of ASFV between neighbouring countries was likely due to local movements (pigs and infected pork products, contaminated fomites, wild boar) combined with ineffective biosecurity (Guinat et al., 2016).

The spread of ASF across Asia has been largely unidirectional. The similar appearance of the epidemics in different countries, despite very different dates of initiation, suggests that outbreaks originated from a single source that then propagated across Asia. Molecular characterisation of the virus in both China and Vietnam has revealed highly homologous strains, which are also largely identical to those characterised from outbreaks in Georgia (2007), Russia (2012), Estonia (2014) and Poland (2015) (Ge et al., 2018; Van Phan Le et al., 2019). Therefore, it is highly likely that the same strain involved in the re-emergence of ASF in Europe was responsible for the new outbreaks throughout Asia.

Several causes of the initial introduction of ASFV in Asia have been postulated including the feeding of contaminated swill, exposure to other ASFV-infected pork products, fomites from infected regions, tick-to-pig transmission and wild-boar transmission (Li & Tian, 2018; Lu et al., 2020; Yu et al., 2015). Asia has more than 50% of the global domestic pig population, therefore it is not unreasonable to assume that some of the spread that has occurred is due to high pig density; also, many herds throughout Asia are small-scale production with poor biosecurity (Food and Agriculture

213 Organisation of the United Nations, 2018; Gulenkin et al., 2011; Lu et al., 2020). In addition, long
214 distance transportation of pigs has historically been very common throughout Asia, which could be
215 an important risk factor for the spread of ASFV (Lu et al., 2020). Free-roaming, infected wild boar
216 might also be a contributing factor (Lu et al., 2020). Several cases of ASF in wild boar in China (2018)
217 and South Korea (2019) were reported to the OIE; however, these cases were excluded from the
218 analysis in the current study.

219 Differences in primary mechanisms of transmission should be considered during initial versus later
220 phases in the epidemic. The earlier, secondary cluster of reports in North-East Asia occurred at a
221 lower density than that of the later, primary cluster in South-East Asia. In the early part of the
222 epidemic, ASFV spread was most likely via transportation of infected stock, products or fomites.
223 However the later, higher density cluster in South-East Asia which consisted of more reports, might
224 have been due to the proximity of swine enterprises and transmission via direct contact, in addition
225 to other risks of spread. The density of pigs stocked in China (~45 pigs/km²) is almost half that of
226 Vietnam (~80 pigs/km²), which suggests much closer geographical contact between pig herds in the
227 South-East versus the North-East of Asia; consequently, this could lead to different primary
228 mechanisms of spread (Food and Agriculture Organisation of the United Nations, 2018).

229 Whilst most reported ASF outbreaks appeared to occur in a progressive and sequential manner
230 without extreme long-distance jumps, there were some reports that do not fit with this pattern.
231 Outbreaks were reported from the Philippines and Indonesia; whilst these are island nations, they
232 are still geographically close to the mainland Asia outbreaks and therefore spread could have
233 occurred by the methods described above. However, the outbreaks in Timor-Leste occurred more
234 than 2000 km from the nearest outbreak of ASF (Lu et al., 2020). Although it is unclear how this
235 occurred, it is concerning because it suggests ASFV can be moved long-distances and possibly spread
236 further outside of Asia to areas free of ASFV, such as Australia and Pacific Island nations.
237 Alternatively, ASFV might have been present throughout Indonesia for some time before it was

238 reported; the high number of outbreaks included in the first Indonesian report supports this
239 suggestion. Nevertheless, being an island does not appear to protect against the introduction of
240 ASFV.

241 To control the spread of ASFV, application of strict biosecurity measures, continued disease
242 surveillance for early recognition and reporting, prohibition of swill feeding, proper disposal of food
243 waste and infected carcasses, stamping out procedures, zoning and movement control are
244 recommended (Food and Agriculture Organisation of the United Nations, 2020; World Organisation
245 for Animal Health, 2018). These control methods have been implemented by all Asian countries
246 where outbreaks occurred, however only Cambodia, Mongolia and Myanmar (and Hong Kong) have
247 been successful at eradicating the disease (no further reports of outbreaks). In these countries, there
248 were comparatively fewer initial outbreaks, likely a contributing factor to control of the outbreaks
249 and prevention of further spread.

250 In Backyard systems estimated morbidity was higher and mortality was lower than that found in
251 Farm systems. Backyard systems have a smaller number of pigs per enterprise and lower biosecurity
252 than farms, allowing for faster spread of ASF throughout the system and hence a higher morbidity. A
253 similar trend was reported in outbreaks in Estonia, 2015–2017 (Nurmoja et al., 2018). However, the
254 smaller number of animals can be monitored more closely for signs of disease, and therefore
255 stamping out protocols are likely to be implemented more quickly, leading to the lower mortality
256 estimated in Backyards. These findings suggest that whilst Backyard enterprises are infected more
257 readily than Farms, outbreaks might be controlled more effectively. This hypothesis is further
258 supported by the shorter epidemic, when standardised by day, observed in Backyard systems.

259 In Laos, Vietnam and China estimated mortality was higher than that of Other Countries. Similar to
260 the Farm enterprise, this is likely due to the scale of production within these countries. China and
261 Vietnam are the largest and sixth largest producers of pork in the world, respectively (Food and

262 Agriculture Organisation of the United Nations, 2018). Consequently, disease surveillance is more
263 challenging and without early detection of disease, stamping out procedures cannot be
264 implemented quickly leading to further disease spread. However, Laos is not a global pork producer
265 and therefore it is unclear why it also experienced increased mortality. Laos' proximity to Vietnam
266 might have influenced its ability to eradicate the disease because of numerous ASFV incursions. In
267 contrast, Other Countries have smaller production and therefore disease surveillance programs
268 might have been more effective, allowing for the early initiation of stamping out protocols, leading
269 to lower mortality. This is supported by the evidence that only countries that had eradicated the
270 disease by the end of 2019 (excluding Hong Kong) were found in the Other Countries category,
271 implying that the eradication protocols implemented were likely more successful.

272 This study was limited by the data each country reported to the OIE. When reporting, the
273 information was not standardised between countries therefore there was a lack of consistency in
274 terminology and method of reporting. Assumptions had to be made when analysing the data; this
275 included the combination of Farm and Village unit types based on general trends in herd size,
276 however the variability in this data made interpretation difficult. Additionally, inferences could only
277 be made on number of reports rather than number of outbreaks, due to differences in the method
278 of reporting multiple outbreaks, with some outbreaks unable to be differentiated from each other.
279 Manual data importation was used to transcribe the reports accessed through WAHIS and despite
280 employing several methods of error checking, some transcription errors might still have occurred.

281 **Conclusion**

282 The characteristics of the epidemic remained largely unchanged across countries and unit types,
283 with the variation that is apparent likely attributable to differences in prevention, surveillance and
284 control measures adopted in each enterprise. Since ASFV has crossed large distances over both land
285 and water this suggests that there is currently no physical barrier to prevent spread. Therefore,

286 countries currently free from ASFV should focus on methods to prevent entry of the virus, including
287 increasing biosecurity surrounding known mechanisms of transmission and improved surveillance.
288 Establishment of a more standardised mechanism of reporting would be beneficial. Additionally,
289 increased accessibility to the data would be advantageous to facilitate data analysis and generate
290 more quickly an understanding of how an epidemic is evolving, thus enabling predictions to be made
291 about further spread, and also to provide information on freedom from disease.

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296 **Conflict of Interest Statement**

297 The author declares that there is no conflict of interest regarding any aspect of this publication.

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301 **Data availability**

302 The data presented in this study is available at <https://doi.org/10.5281/zenodo.4302768>

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415 Figures

416 Figure 1. Distribution, by week, of the number of confirmed reports of African Swine Fever outbreaks
417 diagnosed in Asia 2018-2019. Day 1 = 1 August 2018, Day 507 = 20 December 2019. Data was
418 extracted from the World Organisation for Animal Health (OIE) ([https://www.oie.int/wahis_2/](https://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home)
419 [public/wahid.php/Wahidhome/Home](https://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home)).

420 Figure 2. Distribution, by week and country, of the number of confirmed reports of African Swine
421 Fever outbreaks diagnosed in Asia 2018-2019. Day 1 = 1 August 2018, Day 507 = 20 December 2019.
422 Data was extracted from the World Organisation for Animal Health ([https://www.oie.int/wahis_2/](https://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home)
423 [public/wahid.php/Wahidhome/Home](https://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home)).

424 Figure 3. Distribution, by week, of the number of confirmed reports of African Swine Fever outbreaks
425 diagnosed in China, Vietnam, Laos and Other countries 2018–2019. Day 1 = 1 August 2018, Day 507
426 = 20 December 2019. Data was extracted from the World Organisation for Animal Health ([https://](https://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home)
427 www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home).

428 Figure 4. Distribution, by week, of the number of confirmed reports of African Swine Fever outbreaks
429 diagnosed in Backyard and Farm establishments 2018-2019. Day 1 = 1 August 2018, Day 507 = 20
430 December 2019. Data was extracted from the World Organisation for Animal Health ([https://](https://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home)
431 www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home).

432 Figure 5. Distribution of African Swine Fever outbreak sites in Asia 2018-2019. Sites have been
433 shaded green to red by epidemic day (1 to 507). Day 1 = 1 August 2018, Day 507 = 20 December
434 2019. Directional ellipses (1 SD) are overlaid, both unweighted (light blue) and weighted (dark
435 blue) by epidemic day. Data was extracted from the World Organisation for Animal Health
436 (https://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home).

437 Figure 6. Distribution of African Swine Fever outbreak sites in Asia 2018-2019. Sites have been
438 shaded green to red by epidemic day (1 to 507). Day 1 = 1 August 2018, Day 507 = 20 December
439 2019. Primary (22/02/2019-22/09/2019) and secondary (14/08/2018-15/10/2018) clusters have
440 been overlaid, with observed/expected values being 12.87 and 6.21, respectively. Data was
441 extracted from the World Organisation for Animal Health ([https://www.oie.int/wahis_2/public/](https://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home)
442 [wahid.php/Wahidhome/Home](https://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home)).

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Table 1. Summary statistics of the standardised epidemics (day 1 is assigned to the start date for each group's epidemic) of China, Laos, Vietnam and Other countries, reported to the World Organisation for Animal Health (https://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home). Medians with superscript in common are not significantly different ($p < 0.05$) using a Kruskal-Wallis All-Pairwise Comparisons Test on ranked means.

Parameter	China [†]	Laos	Vietnam	Other [‡]
n	166	141	186	77
Minimum	1	1	1	1
1st Quartile	74	35	42	167
Mean	165	58	63	199
Median	120 ^a	61 ^b	45 ^b	248 ^a
3rd Quartile	254	85	76	261
Maximum	507	123	209	283
Mode	7, 59, 75	61	43	2, 255, 260

[†] China and Hong Kong

[‡] Cambodia, Indonesia, Korea (democratic People's Republic), Korea (Republic of), Mongolia, Myanmar, Philippines, Timor-Leste and Vietnam

Table 2. Summary statistics of the standardised epidemics (day 1 is assigned to the start date for each unit type's epidemic) of Backyard and Farm unit types, reported to the World Organisation for Animal Health (https://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home). Medians with superscript in common are not significantly different ($p < 0.05$) using an independent samples Kruskal-Wallis test on medians.

Parameter	Backyard	Farm [†]
n	64	484
Minimum	1	1
1st Quartile	71	215
Mean	135	262
Median	108 ^b	278 ^a
3rd Quartile	221	366
Maximum	447	484
Mode	132	217

[†] Farm and Village

Table 3. Summary statistics of morbidity and mortality associated with the outbreaks of China, Laos, Vietnam and Other countries, reported to the World Organisation for Animal Health (https://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home). Medians with superscript in common are not significantly different ($p < 0.05$) using a Kruskal-Wallis All-Pairwise Comparisons Test on ranked means.

Parameter		China [†]	Laos	Vietnam	Other [‡]
Morbidity	n	163	139	35	58
	Minimum	0	0.0044	0.1515	0
	1st Quartile	0.0345	0.1532	0.3484	0.0020
	Mean	0.2302	0.3984	0.6652	0.2019
	Median	0.1222 ^c	0.3789 ^b	0.7895 ^a	0.0284 ^c
	3rd Quartile	0.3264	0.6247	1	0.3110
	Maximum	1	1	1	1
Mortality	n	163	139	35	58
	Minimum	0	0.0044	0	0
	1st Quartile	0.0191	0.1532	0.0909	0
	Mean	0.1543	0.3984	0.2213	0.1435
	Median	0.0794 ^b	0.3789 ^a	0.1754 ^{a,b}	0.0008 ^c
	3rd Quartile	0.2059	0.6247	0.2535	0.0803
	Maximum	1	1	1	1

[†] China and Hong Kong

[‡] Cambodia, Indonesia, Korea (democratic People's Republic), Korea (Republic of), Mongolia, Myanmar, Philippines, Timor-Leste and Vietnam

Table 4. Summary statistics of morbidity and mortality associated with the outbreaks of Backyard and Farm unit types, reported to the World Organisation for Animal Health (https://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home). Medians with superscript in common are not significantly different ($p < 0.05$) using an independent samples Kruskal-Wallis test on medians.

Parameter		Backyard	Farm [†]
Morbidity	n	50	326
	Minimum	0.0016	0
	1st Quartile	0.0908	0.0568
	Mean	0.3725	0.3279
	Median	0.2835 ^a	0.2151 ^b
	3rd Quartile	0.5594	0.4932
	Maximum	1	1
Mortality	n	50	326
	Minimum	0	0
	1st Quartile	0.0542	0.0318
	Mean	0.2583	0.2524
	Median	0.1231 ^b	0.1563 ^a
	3rd Quartile	0.3773	0.4034
	Maximum	1	1

[†] Farm and Village