

Risk factors and spatiotemporal analysis of classical swine fever in Ecuador

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1. Abstract

Classical swine fever (CSF) is one of the most important re-emergent swine diseases worldwide. Despite concerted control efforts in the Andean countries, the disease remains endemic in several areas, limiting production and trade opportunities. In this study, we aim to determine herd-level risk factors and spatiotemporal implications associated with CSF. We analysed passive surveillance datasets and vaccination programmes from 2014 to 2020; Then, structured a herd-level case-control study using a multivariable logistic model containing 339 cases, and a spatiotemporal Bayesian model, considering 115 thousand premises, 2.3 million annual vaccine doses and a population of 1.6 million pigs distributed in 1,006 parishes. Our results showed that the risk factors that increased the odds of CSF occurrence were swill feeding (OR 9.28), time of notification (OR 2.18), animal entry in the last 30 days (OR 2.08), lack of CSF vaccination (OR 1.88), age of animals between 3-6 months (OR 1.58) and being in the coastal region (OR 1.87). Spatiotemporal models showed that the vaccination campaign reduced the risk by 33% while temperature increased the risk by 17%. The calculated priority index aims to facilitate the intervention process that should be focused on a couple of provinces, mainly in Morona Santiago and Los Rios as well as in specific parishes around the country. Our findings provide insight and understanding of the risk factors associated with CSF in Ecuador, which stands for the Andean region; even though the results are specific for the implementation of risk-based surveillance for CSF, data and methods could be valuable for the prevention and control of diseases such as African swine fever, or porcine reproductive and respiratory syndrome. In conclusion, the results highlight the complexity of the CSF control programme, the need to inform decision-makers, involve stakeholders and implement better strategies to update continental health policies to eradicate swine diseases.

34 2. Introduction

35 With the growing demand for animal protein in the Andean region, especially pork, diseases such
36 as classical swine fever (CSF) are gaining importance as they are limiting local production and po-
37 tential export opportunities for affected countries. The per capita consumption of pork has in-
38 creased in Ecuador from 7.3 kg in 2010 to 10 kg in 2016 (www.aspe.org.ec). The overall import-
39 ance of pig production is related not only to meat consumption but also to cultural traditions. In An-
40 dean communities, pigs play a central role as a source of protein, festivities and savings (1).

41 Classical swine fever is considered the most relevant re-emerging viral disease of pigs and is
42 caused by a virus belonging to the *Pestivirus* genus within the family *Flaviviridae* (2). The only nat-
43 ural reservoirs are members of the *Suidae* family (domestic and wild pigs). Clinical signs are vari-
44 able and depend on the viral strain, host immune response, age, general health status and con-
45 comitant infections (3).

46 The presentations of the disease include acute, chronic and persistent forms according to their dur-
47 ation rather than their different acute, chronic and persistent manifestations (4,5). Transmission oc-
48 curs mainly by direct contact between infected and susceptible animals via the oronasal route but
49 also indirectly through people, clothes, vehicles, equipment, and ingestion of contaminated and un-
50 dercooked meat as part of swill feeding (6). Outbreaks of CSF usually have dramatic con-
51 sequences when control measures are implemented. These include long quarantine periods,
52 movement restrictions, emergency vaccination, culling of the pig population and major impacts on
53 animal welfare (7,8). For instance, the 1998 epidemic in the Netherlands, had an estimated cost of
54 2.3 billion US dollars and the destruction of 10 million pigs (9). Countries with endemic status are
55 banned from exporting pigs and their products, therefore the impact of the disease on the economy
56 and public health worldwide is enormous. In Ecuador, the economic impact caused annually by
57 CSF was estimated by the NVS to be 6 million US dollars, considering only animal mortality. As
58 many of the involved people are from households with low income, the impact of CSF on particular
59 poor people becomes evident.

60 In South America, the disease is considered endemic in Guyana, Suriname, the North and North-
61 east regions of Brazil and the Andean Community, and these regions struggle to implement suc-
62 cessful control programs (10,11).

63 The national CSF eradication Project in Ecuador was established in 2012 with significant improve-
64 ments against CSF by the National Veterinary Service (NVS). The first national vaccination
65 strategy was gradually initiated in 2014 with a locally produced lapinised Chinese strain vaccine
66 (12). As a result, the highest historical coverage was achieved in 2019 (2.7 million doses) due to a
67 compulsory vaccination campaign, government subsidies and coordination with stakeholders (com-
68 mercial and industrial producers' associations). However, the field response and data analysis ca-
69 pacity of the veterinary service is limited, and in 2020, the disease is still present (<https://>

70 wahis.oie.int). In this regard, the NVS plans to enhance their analysis capacity and apply risk-
71 based surveillance. One of the main challenges in applying risk-based surveillance is to find the
72 factors associated with the occurrence of a given disease; in the case of CSF, the disease and as-
73 sociated risk factors have been well studied for developed countries (13–18). However, in develop-
74 ing countries, where due to very particular production systems, the risk factors may be different,
75 these are yet to be understood. Recently, for some countries in South America such as Colombia
76 (19), Brazil (20), and Peru (21), this issue has been addressed.

77 Despite the importance and need for local CSF risk factors, little is still known about them in
78 Ecuador, generating a lack of knowledge to inform control measures and public policy. This is the
79 first time that official data from the NVS has been analysed to determine risk factors for the period
80 from 2014 to 2020.

81 The objectives of this study were to determine the risk factors associated with the occurrence of
82 CSF and to analyse the spatiotemporal implications in order to identify the regions most at risk.

83 **3. Materials and methods**

84 **3.1 Datasets**

85 Data were collected by the NVS from January 2014 to November 2020 in mainland Ecuador, ex-
86 cluding the Galapagos Islands, as it is a recognised CSF free zone (2). The information was stored
87 in two databases: (1) Ecuador's animal health information system (SIZSE) created to record paper
88 questionnaires for notifiable diseases, suspicious events and laboratory results from passive sur-
89 veillance since 2014 (<https://sistemas.agrocalidad.gob.ec/sizse/>); and (2) the Unified information
90 manager (GUIA) developed by the NVS to manage cadastre, mass vaccination campaign against
91 CSF, and movements since 2016 (<https://guia.agrocalidad.gob.ec/agrodb/ingreso.php>). Shapefiles
92 of administrative units of Ecuador were downloaded from the Institute of Statistics and Census
93 (INEC) (<https://www.ecuadorencifras.gob.ec/division-politico-administrativa/>).

94 All raw data were then imported and processed with R version 4.2.1 (<https://CRAN.R-project.org/>).

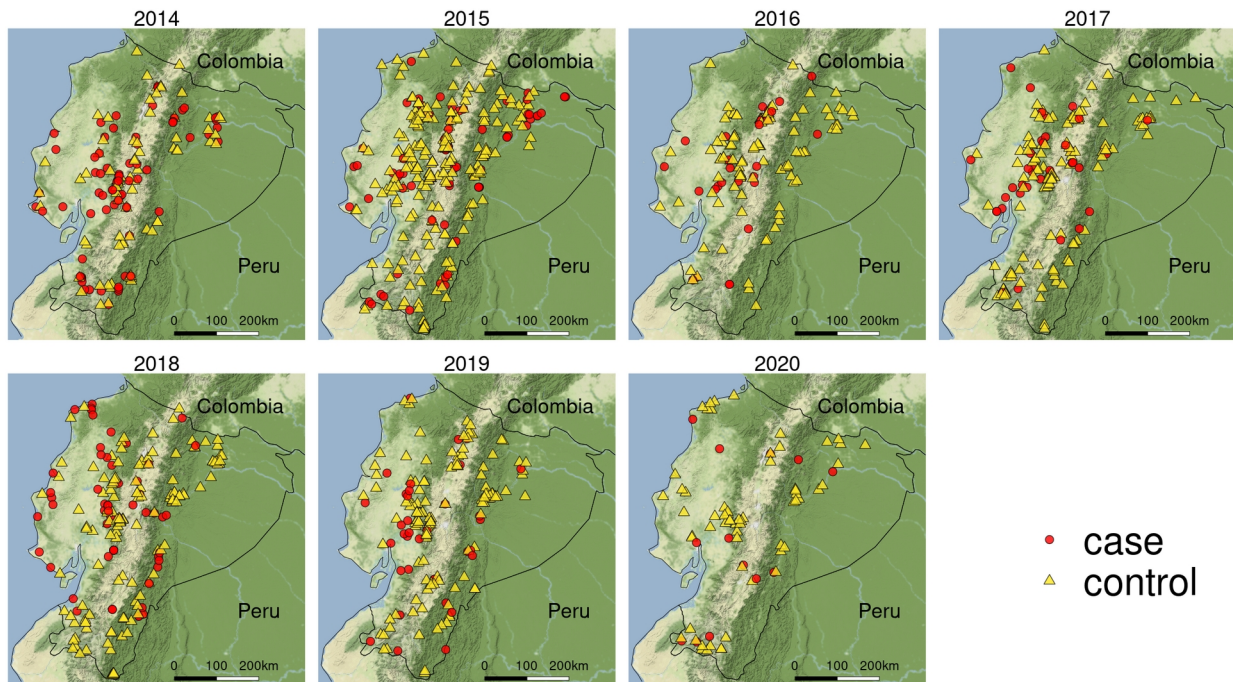
95 **3.2 Factors influencing the risk (variables captured by the surveillance system)**

96 The retrospective analysis used the variables collected historically by the surveillance system. The
97 databases were merged using the individual identification of the owner of the premises.

98 The variables included in the analysis were selected based on published literature, biological
99 plausibility and considering their association with the occurrence of classical swine fever.

100 (14,22,23). Subsequently, they were organised considering risk characteristics according to the
101 RiskSur Surveillance design framework (www.fp7-risksur.eu) (24) and classified into the population
102 level, herd level and animal level.

103 Using the variables included in the passive surveillance system, a case–control study was struc-
104 tured to identify factors associated with CSF occurrence. Herds of pigs with a positive laboratory
105 test for CSF were classified as case herds, and those with a negative result were classified as con-
106 trols (Figure 1).



107
108 Figure 1. Spatial representation of the study area and location of cases and controls of CSF in
109 Ecuador study period 2014–2020.

110 3.3 Questionnaire

111 The surveillance system used a questionnaire designed to obtain information on veterinary health
112 events, including the demographic data of the premises, geographic location, chronology (dates of
113 notification and follow-up), animal species, vaccination declaration, clinical signs, presumptive syn-
114 drome, collection of material, characteristics of samples, laboratory test results, animal population,
115 animal movement and probable origin of the disease.

116 The information was collected by trained NVS veterinarians following the data protection proced-
117 ures of Ecuadorian authorities. The information recorded throughout the country was continually
118 monitored by the national surveillance team (headquarters), who checked the data for complete-
119 ness and errors.

120 Laboratory testing was performed at the National Reference Laboratory (headquarters in *Quito*).
121 Virus detection was carried out by a commercially available antigen ELISA (PrioCheck® CSFV)
122 based on the double antibody sandwich (DAS) principle with a sensitivity of 97% and a specificity
123 of 99% (25) and by qRT–PCR using Roche® reagents (26) with a sensitivity and specificity of ≥
124 95%.

125 3.4 Multivariable logistic analysis

126 All analyses were performed at the herd level and stratified according to CSF status (case or con-
127 trol). Variables were organised by type, continuous variables were transformed into dummies, set-
128 ting their levels according to biological or legal cut-off points. Descriptive statistics assessed the
129 distribution of cases and controls. The dependent variable was the binary variable infected with
130 CSF. The evaluation of individual variables of the Ecuadorian surveillance system was based on
131 the association of each explanatory variable with the binary farm-level outcome, using univariate
132 logistic regression (27). We avoided case–control matching due to the potential of creating selec-
133 tion bias, losing precision, statistical power and not having a prior local analysis of strong well-
134 measured confounding variables (28).

135 A multivariate logistic regression model (Eq. 1) was used to assess the association of explanatory
136 variables with the outcome formulated as follows:

$$137 \quad \log(p(X)/(1-p(X))) = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \dots + \beta_p X_p \quad [1]$$

138 where X_j is the j th predictor variable and β_j is the coefficient estimate for the j th predictor variable.
139 The final model selection used a manual forward stepwise approach (29). We included each vari-
140 able in descending order of statistical significance in the univariate models. Statistically significant
141 variables (chi-square association test < 0.05) were kept in the final model. For each insertion of
142 new variables, we observed the changes in the odds ratio (OR) and the significance of each beta β_i
143 (Wald test) assessing them at each step. Variables were used only if their completeness was \geq
144 0.85. Confounding was assessed using causal diagrams (30,31). Collinearity was analysed using
145 variance inflation factors analysis (32). The goodness of fit of the final model was measured using
146 the conditional R_2 (33) and the Hosmer–Lemeshow goodness of fit test (GOF) ($p > 0.05$) (34).

147 **3.5 Spatiotemporal Bayesian analysis**

148 The analysis used the population and cases restricted to 2017-2020 due to the lack of cadastral
149 and vaccination information prior to the implementation of the increased official vaccination in
150 2017. Data were organised to contain the aggregated annual population over each parish (1040)
151 using time-series missing value imputation (35) for areas without information. Variables were
152 centred and scaled by dividing the centred value by the standard deviation. The variables used to
153 fit the model were the number of CSF vaccine doses applied per km^2 , average temperature (C)
154 and average precipitation (mm), constructing several models. Temperature and precipitation were
155 extracted from (<https://worldclim.com/>) at a spatial resolution of 2.5 arc-minutes ($\sim 5 \text{ Km}^2$).

156 Parish vaccination coverage was adjusted considering the population and the doses applied
157 against CSF, considering 1.55 as the average number of doses a pig receives in a calendar year,
158 according to the average lifespan from birth to slaughter (234 days) (36). We used penalised prior-
159 ity priors model complexity, specified by the divergence between a flexible model and a baseline
160 model; To define the spatial random effect, a neighbourhood matrix from the polygon list was

161 needed, based on regions (parishes), that share two or more boundary points. The spatiotemporal
162 model uses the disease count Y_{ij} observed in area i and time period j , modelled as:

$$163 \quad Y_{ij} \sim Po(E_{ij} \theta_{ij}); i=1, \dots, N; j=t_1, \dots, t_N \quad [2]$$

164 where E_{ij} is the expected number of cases and θ_{ij} is the relative risk, both in the given area (i)
165 and time period (t) (Equation 2). Three sets of components for $\log(\theta_{ij})$ were considered:

$$166 \quad \log(\theta_{ij}) = \alpha + u_i + v_i \quad [3]$$

167 where alpha represents an overall risk in the study region, u_i is the correlated heterogeneity that
168 models the spatial dependence between the relative risks, and v_i is the unstructured exchangeable
169 component that models uncorrelated noise (Equation 3).

$$170 \quad \log(\theta_{ij}) = \alpha_0 + A_i + B_j + C_{ij} + var_1 + var_2 + var \dots n \quad [4]$$

171 where A_i represents the spatial group, B_j is the temporal group, and C_{ij} is the space-time interaction
172 group ($A_i = u_i + v_i$) using the most popular model to spatial disease known as Besag-York-Mollie
173 (BYM) (37), where the clustering component u_i is modelled with the conditional autoregressive dis-
174 tribution (CAR) (38), smoothing the data when two areas share a common boundary given by the
175 neighbourhood matrix ($B_j = \beta t_j$). Using an independent and identically distributed Gaussian random
176 effect (iid). ($C_{ij} = \delta_{it_j}$), where $u_i + v_i$ is an area random effect, βt_j is a linear trend term in time t_j , and
177 δ_{it_j} is an interaction random effect between area and time (Equation 4) (39).

178 To evaluate the models, we used the deviance information criterion (DIC) and the posterior predict-
179 ive p value. To suggest parish in priority of care, we used the *priority index* (PI) which is a risk-
180 based percentage scale that ranks the units of analysis, given by the fitted effects weighted by their
181 probability and a cut-off value (40). The models were implemented using the integrated nested
182 laplace approximation (INLA) (41). We used choropleth maps to represent the spatiotemporal dis-
183 tribution of the population, observed cases, expected cases, infection risk (relative risk) and priority
184 index.

185 All analyses were run in R V4.2.0.

186 **4. Results**

187 **4.1 Descriptive analysis of the variables influencing the risk**

188 The full dataset contained 63 variables, most of which were used for administrative purposes. Fif-
189 teen variables selected for the univariate analysis consisted of 6 dichotomous, 6 nominal and 3
190 continuous variables. They were then classified into the population level ($n=4$), herd level ($n=9$)
191 and animal level ($n=2$). Notification time was transformed into a dummy variable considering a cut

192 point of 7 days (one week). The age of the animals was considered cut-off points of 2 and 6
 193 months due to the official CSF vaccination recommendation: first dose applied after 45 days of age
 194 and revaccination at 180 days of age (Table 1).

Table 1. Description of variables influencing risk and their levels. Data available in Ecuador's CSF surveillance system from 2014 to 2020, levels grouped by risk characterisation.

195

Factors influencing risk	Description of variables captured by the surveillance system	Category
† Control program	Active national control program (vaccination and mobilisation control) on the movement of interview.	Dichotomic ¶
† Natural region	Natural region of the premise according to their location and administrative provincial division.	Amazon, coastal, highlands
† Network community	Community to which the premise belongs according to its parish location (42).	5 communities
† Year	Year of the event.	2014–2020
‡ Animal entry	Reception of pigs within 30 days of onset of clinical signs.	Dichotomic ¶
‡ Notification time	Number of days from onset of clinical signs to notification to the NVS.	0–7, >7
‡ Other species	Existence of species other than swine in the premise.	Dichotomic
‡ Size of the farm	Number of pigs on the premises.	1–25, 26–189, >190,
‡ Swill feeding	Evidence of feeding pigs with swill feed, home-made leftovers.	Dichotomic ¶
‡ Type of farm	Classification of premises according to production category.	Backyard, Family, Commercial, Industrial
‡ CSF vaccination declaration	Owner's declaration of vaccination against CSF in its premise.	Dichotomic ¶
‡ CSF vaccination record	Official record of vaccination against CSF within the last 180 days.	Dichotomic ¶
‡ Who makes the notification	Person who contacted the NVS to make the notification.	Owner, NVS, Sensor
§ Age	Age in months of sampled animals.	1–2, 3–6, >=7
§ Breed	Breed of the animals on the premise.	Landrace (white), Indigenous (black).

Levels of risk characterisation: † Population level, ‡ Herd level, § Animal level. ¶ Dichotomic: 0=No, 1=Yes.

196

197 The average time for official notification to the NVS was more than one week (9.3 days) for cases
 198 and one week (7.0 days) for controls. The median farm size was similar for cases (13.5 pigs) and
 199 controls. The mean age of pigs was similar for cases and controls (~5 months) (Table 2).

Table 2. Descriptive measures of continuous variables from the 2014–2020 CSF risk factor analysis in Ecuador.

	Case herds (n=338)			Control herds (n=916)		
	Mean ± SD	Median(Q2,Q)	Range	Mean ± SD	Median(Q2,Q)	Range
Notification time	9.29 ± 9.13	7 (3–13)	0–70	7.00 ± 13.37	3 (2–7)	0–201
Size of the farm	38.54 ±	13 (6–33)	1–	125.4 ±	13 (6–27)	1–

	101.95		1323	893.54		13,804
Age (months)	5.06 ± 5.54	3 (2–5)	1–48	5.89 ± 7.69	3 (2–5)	1–72

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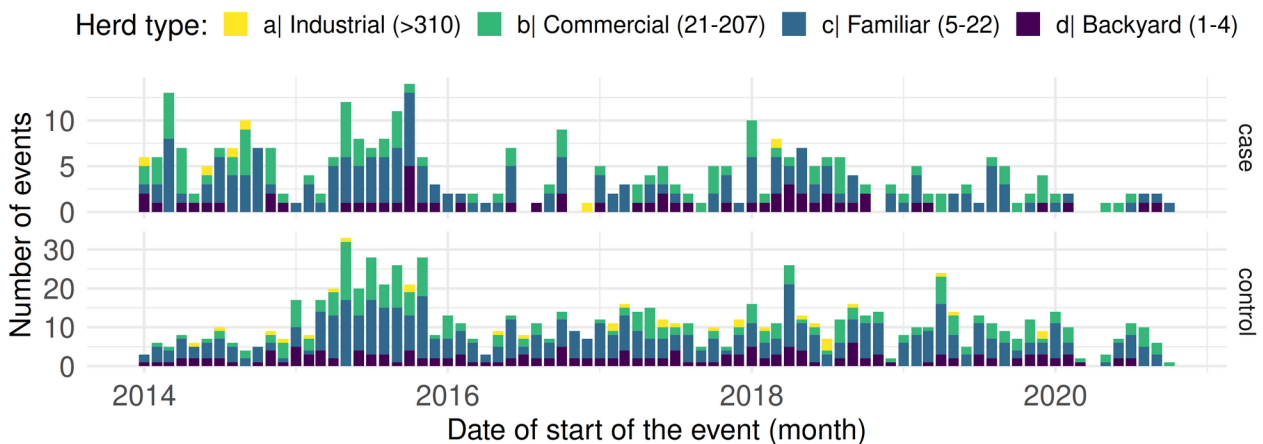
201 Farmer vaccination declaration was higher for case herds (71%) than for control herds (6%). Re-
 202 cording of vaccination (based on official records) was lower (46%) for cases than for controls
 203 (60%). Both cases (96%) and controls (78%) had a high percentage of swill feed use. The entry of
 204 animals within the last 30 days was recorded in 39% of cases and 22% of controls. Only 5% of the
 205 cases and 4% of controls have other species on the property (Table 3).

206 Historical case presentation decreased over the years, with the highest proportion of cases (48%)
 207 occurring between 2014 and 2015 and the lowest (14%) occurring between 2019 and 2020. The
 208 proportion of cases (43%) and controls (45%) was highest in the highlands. More than half of the
 209 case notifications (51%) were reported by the owner, followed by health sensors (42%), which are
 210 volunteers selected by the NVS to enhance the surveillance system directly from the community
 211 across the country. There was a higher proportion of cases (30%) in the third community network,
 212 located in the centre of the country. The highest proportion of cases was in commercial production
 213 (31%) (Table 3).

214 4.2 Description of cases and controls

215 The surveillance database contained 1,254 questionnaires, 338 of which were confirmed CSF
 216 cases. The farm categories were 50.79% family (637), followed by 28.39% commercial (356),
 217 17.98% backyard (224) and 0.03% industrial (37); the distribution of cases and controls over time
 218 is illustrated in Figure 2; The highest case presentation corresponded to October 2015 with 14
 219 monthly cases, followed by March 2014 with 13 cases, and the lowest corresponded to 2020 with ≤
 220 2 monthly cases.

221



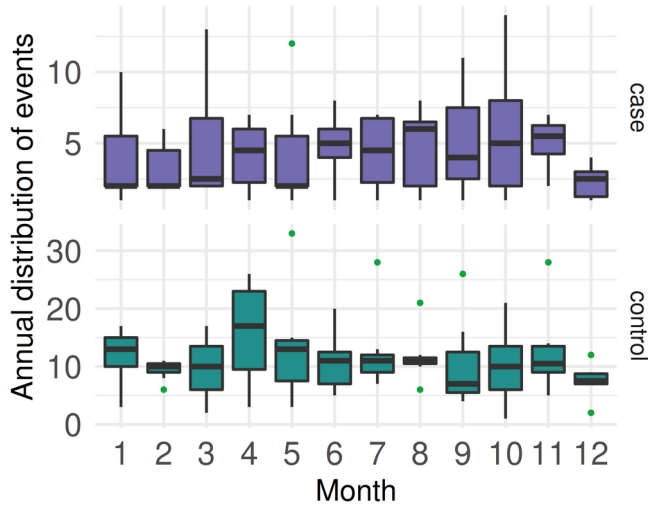
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223

224 Figure 2. Distribution of events (cases and controls) reported between 2014 and 2020 in Ecuador;
 225 bars represent monthly counts, height and colours of bars according to the type of herd (different
 226 scales on the y-axis).

227

228 Distributed by months, the mean number of cases was 4.39 ± 3.09 ; with controls, the mean was
 229 11.31 ± 6.38 . There was a tendency to increase twice a year around April and October (Figure 3).



230

231 Figure 3. Boxplots of monthly distribution of CSF cases and controls from 2014 to 2020 in Ecuador
 232 (different scales on the y-axis).

233 4.3 Multivariable logistic analysis

234 According to the univariable models, twelve out of 15 assessed variables were associated with
 235 CSF ($p < 0.20$). We found a paradoxical fit (Type III error) opposite of the true effect (42), produced
 236 by CSF vaccination declaration; giving an incorrect direction of association and increasing the odds
 237 when the farmer declares vaccination (38.67 OR), instead of the expected protective effect con-
 238 ferred by the vaccine. The natural region showed a higher risk to the coastal region. The univari-
 239 able analysis is presented in Table 3.

240 Table 3. Results of univariable logistic regression analyses, to assess associations of CSF during
 241 2014–2020 in Ecuadorian swine herds. Variables are ordered by their level of significance.

Variable	Category	Tot al	Cases (Percentage)	OR (crude)	CI (95%)	Chi- Square (signif.)
CSF vaccination declaration	No	959	98 (0.1)	1		
	Yes	295	240 (0.81)	38.34	(26.75–54.94)	2.20E-16***
Swill feeding	No	216	13 (0.06)	1		
	Yes	1038	325 (0.31)	7.12	(4.16–13.29)	2.51E-14***
Notification time	7 days	882	191 (0.22)	1		
	>7 days	372	147 (0.4)	2.36	(1.82–3.07)	7.46E-11***
Animal entry (last 30 days)	No	920	207 (0.22)	1		
	Yes	334	131 (0.39)	2.22	(1.7–2.91)	3.65E-09***
CSF vaccination record	Yes	710	157 (0.22)	1		
	No	544	181 (0.33)	1.76	(1.37 – 2.26)	1.01E-05***
Natural Region	Highlands	558	146 (0.26)	1		
	Coastal	311	112 (0.36)	1.59	(1.18-2.14)	**

Year	Amazon	385	80 (0.21)	0.74	(0.54-1.01)	3.37E-05 .
	2019-2020	244	48 (0.2)	1		
	2016-2018	526	129 (0.25)	1.33	(0.90-1.97)	
Age (months)	2014-2015	484	161 (0.33)	2.03	(1.39-3.01)	0.0001***
	1-2	426	93 (0.22)	1		
	3-6	588	186 (0.32)	1.68	(1.25-2.27)	***
Control Program	>=7	248	60 (0.24)	1.14	(0.77-1.68)	0.001
	No	609	190 (0.31)	1		
	Yes	645	148 (0.23)	0.66	(0.51 – 0.84)	0.0009**
Who does the notification	Owner	736	171 (0.23)	1		
	NVS	86	25 (0.29)	1.35	(0.79 – 2.27)	
	Sensor	432	142 (0.33)	1.62	(1.23–2.12)	0.0015***
Size of the farm	>190	53	8 (0.15)	1		
	1-25	910	232 (0.25)	1.92	(0.88 – 4.8)	.
	26-189	293	99 (0.34)	2.86	(1.27-7.31)	0.0028 **
Network Community	1	219	53 (0.24)	1		
	2	157	57 (0.36)	1.78	(1.11–2.87)	*
	3	359	102 (0.28)	1.24	(0.83–1.87)	
	4	184	49 (0.27)	1.14	(0.71–1.83)	
	5	335	77 (0.23)	0.93	(0.62–1.43)	0.027
Breed	Indigenous					
	black	93	20 (0.22)	1		
Other species in the premise	Landrace	970	260 (0.27)	1.33	(0.79–2.36)	0.2680 †
	No	1205	322 (0.27)	1		
Type of farm	Yes	51	17 (0.33)	1.37	(0.76 – 2.49)	0.2900 †
	Industrial	37	6 (0)	1		
Type of farm	Commercial	356	106 (0.08)	2.19	(0.86–6.6)	.
	Family	637	169 (0.13)	1.86	(0.75–5.56)	
	Backyard	224	57 (0.05)	1.76	(0.68–5.53)	0.2699 †

† Indicates an association $p > 0.20$, these variables were excluded in the multivariable models. Signif.: ***

$p < 0.001$, ** $p < 0.01$, * $p < 0.05$, . $P < 0.1$. CI: Confidence interval.

242

243 During the stepwise forward selection of variables we evaluated 8 models; thus, variables that were
 244 not statistically significant ($p > 0.05$), or had an incorrect direction of association (self-declaration of
 245 vaccination) were excluded. Variables that showed a strong association ($p < 0.0001$) in the univari-
 246 able model, maintained their individual and model significance when adjusted in the final multivari-
 247 able model (Table 4).

248 Table 4. Multivariable logistic regression model assessing the associations of variables with the
 249 odds of CSF between 2014 and 2020 in Ecuador.

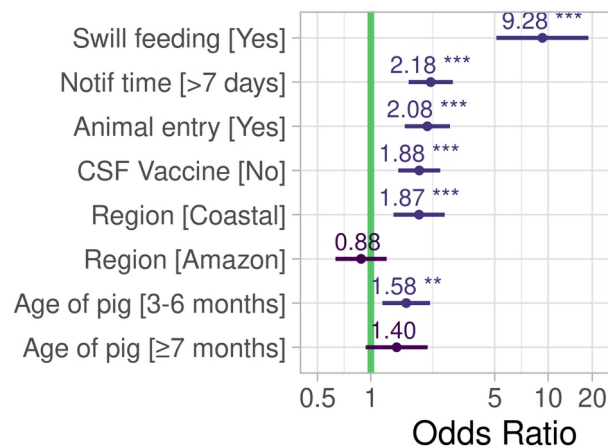
Variable	Category	Estimate	SE	OR (95% CI)	Signif.
Intercept		-4.175	0.356		
‡ Swill feeding	No	-	-	1	
	Yes	2.228	0.305	9.28 (5.30–17.68)	***
‡ Notification time	1–7 days	-	-	1	
	>7 days	0.778	0.147	2.18 (1.63–2.90)	***

‡ Animal entry (last 30 days)	No	-	-	1	
	Yes	0.734	0.149	2.08 (1.55–2.79)	***
‡ Vaccination record CSF	Yes	-	-	1	
	No	0.629	0.139	1.88 (1.43–2.47)	***
† Natural Region	Highlands	-	-	1	
	Coastal	0.627	0.169	1.87 (1.34–2.61)	***
	Amazon	-0.127	0.169	0.88 (0.63–1.23)	
§ Age (months)	1–3	-	-	1	
	3–6	0.460	0.158	1.58 (1.16–2.16)	**
	>= 7	0.340	0.206	1.40 (0.93–2.09)	

Chi-sqrt: 0.0128 *, GOF Hosmer-Lemeshow: 0.788, AUC: 0.746, D2: 0.148, R2: 0.143.
Significance: *** 0.001, ** 0.01. Levels of risk characterisation: † Population level, ‡ Herd level, § Animal level.

250

251 Factors that substantially increased the odds of CSF occurrence at the herd level were swill feed-
252 ing (OR 9.28), notification time (OR 2.18), entry of animals in the last 30 days (OR 2.08) and lack
253 of CSF vaccination (OR 1.88). At the population level: being in a coastal region (OR 1.87) and at
254 the animal level: age of animals between 3–6 months (OR 1.58) (Table 4, Figure 4). The final lo-
255 gistic model presented good fit (GOF=0.79, AUC=0.75). Individual collinearity diagnostics for each
256 variable resulted in individual GVIFs below 1.062. There was no outlier with a significant influence
257 on model fitting, according to the Bonferroni outlier test ($p=0.0072$); also, there was no correlation
258 between residuals.



259

260 Figure 4. Variables associated with the odds of classical swine fever in Ecuador 2014-2020.

261 4.4 Spatiotemporal descriptive analysis

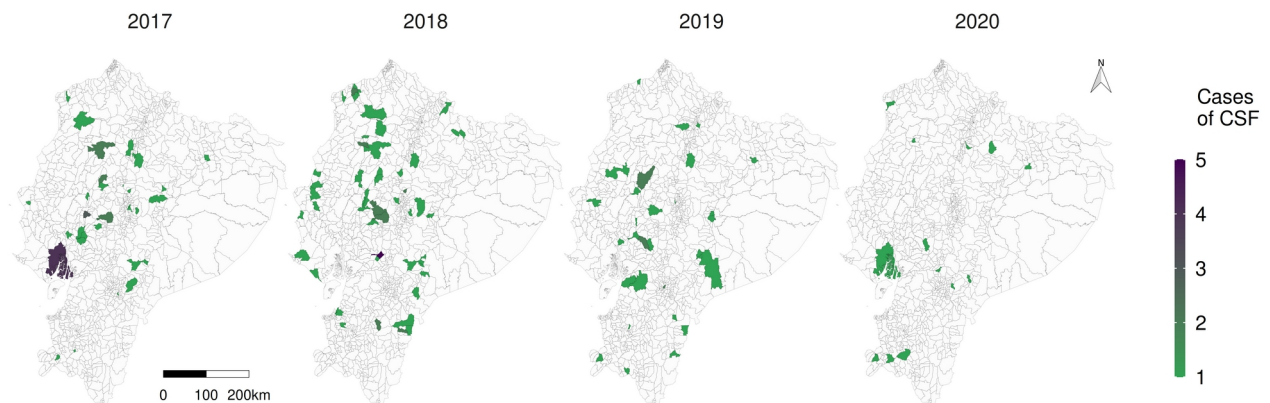
262 The Ecuadorian administrative division has 1,040 parishes; 16 were removed because of being is-
263 lands and 18 were located in the Amazon rainforest with no record of domestic pigs. The length of
264 the neighbouring areas was 4,024 (1,006 for each year), with 271 (6.49%) imputed gaps. When
265 comparing the imputed data with the original dataset, they were not significantly different (t-test:
266 $p=0.55$). The final neighbour list contained 1,006 parishes with an average of 5.71 parish neigh-
267 bours. The average parish area was 198.03 ± 249.48 km², with a range from 2.23 to 2,429.64 km².
268 The annual average of registered premises was 115,411.8, housing an average of 1,633,922 pigs.

269 The annual average of CSF vaccine doses between 2017 and 2019 was 2,375,290, expressed as
 270 vaccine doses per square kilometre from 15.7 in 2017 to 23.0 in 2020; the highest average vaccin-
 271 ation coverage was 81% in 2019, and the lowest was 60% in 2017. The number of applied doses
 272 increased from 1.8 millions in 2017 to 2.4 millions in 2020. The annual average of premises
 273 was 115,411 (Table 5).

Table. 5 Centrality measures of model variables (fixed effects) aggregated by parish distribution in Ecuador.

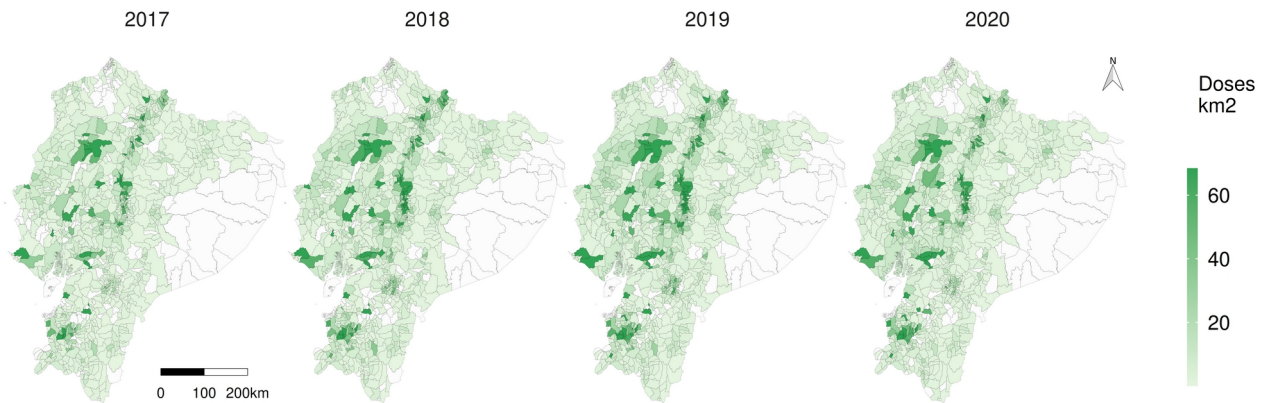
Variable	2017		2018		2019		2020	
	Average	Median (max)	Average	Median (max)	Average	Median (max)	Average	Median (max)
Doses CSF/km ²	15.74	2.31 (976.5)	23.78	4.15 (1057.6)	27.63	5.08 (1,282)	23.0	4.2 (1,477.3)
Population of pigs	1,671.3	284 (224,448)	1,948.7	391 (256,107)	2,030.4	447 (254,042)	1,867.1	434.5 (227,186)
Vaccine coverage %	60	64 (129)	71	80 (108)	81	100 (105)	70	73 (103)

274
 275 What stands out in figure 5 is the decline of the number of observed cases, corresponding to 39 in
 276 2017, 60 in 2018, 33 in 2019 and 13 in 2020; it is possible to observe a significant reduction in the
 277 number of cases specially in the highlands over the years.



278
 Figure 5. Representation of the number of observed CSF cases (number of positive premises) in Ecuador grouped by parish from 2017 to 2020.

279 Figure 6 reveals that there was a marked higher density on the number of doses of CSF applied by
 280 square kilometre in the western centre (Santo Domingo), the north (Carchi), west south (El Oro)
 281 and the central highlands (Cotopaxi, Chimborazo), this general pattern repeated over the years,
 282 however there were 105, 78, 52 and 62 parishes without vaccination coverage in 2017, 2018, 2019
 283 and 2020 (white on Figure 6).



284

Figure 6. Classical swine fever vaccination density per square kilometre in Ecuador. Polygons of the parishes on the map. White parish without applied doses.

285 Temperature and precipitation in Ecuador are modulated by the Andes mountains, warmer temper-
 286 atures on the Amazon and Coastal regions and cooler temperatures on the highlands. There is a
 287 range difference of 11 °C in the Coastal, 20.5 °C in the Highlands and 18.9 °C in the Amazon.
 288 Precipitation on the Amazon is almost 3 times higher than the highlands and two times compared
 289 with the Coastal (Table 6).

Table 6. Descriptive measures of covariants spatiotemporal model in Ecuador.

Covariate	Coastal	Highlands	Amazon
	Mean ± SD (range)	Mean ± SD (range)	Mean ± SD (range)
Doses vac. Km ²	18.93 ± 69.83 (0–636.9)	19 ± 61.01 (0–976.5)	1.77 ± 2.99 (0–15.26)
Temperature	24.36 ± 1.63 (15–26)	14.26 ± 4.43 (4.6–25.1)	20.60 ± 4.19 (6.8–25.7)
Precipitation	1362.24 ± 712.20 (122–3253)	1012.89 ± 434.16 (432–3824)	2718.53 ± 957.47 (722–4482)

290 4.5 Spatiotemporal Relative Risk

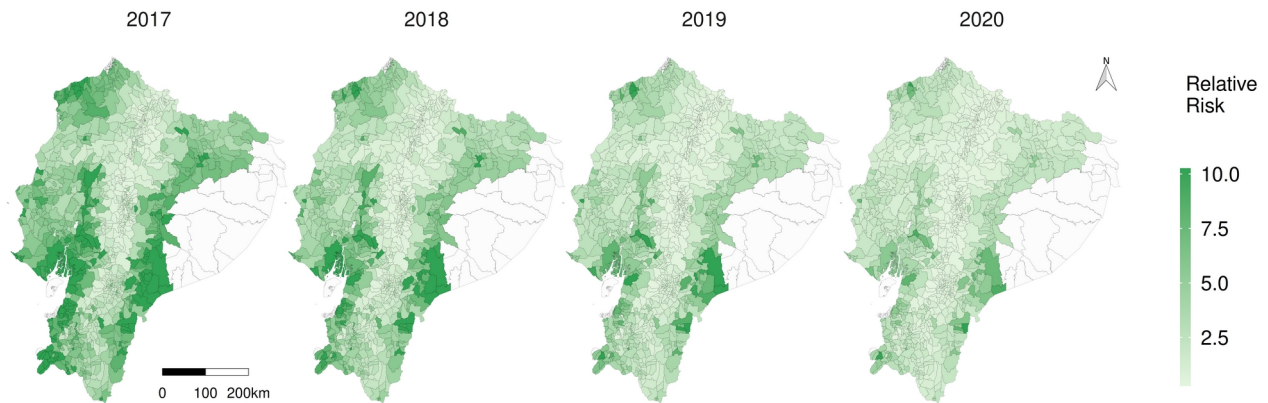
291 The annual average relative risk dropped from 4.01 in 2017 to 1.30 in 2020. Regarding the doses
 292 of vaccine applied per km², they behaved as an expected protective factor, which means that an
 293 increase in one SD in the doses applied per kilometre decreased the risk by 33%. Temperature
 294 was a risk factor, considering that an increase in one SD in temperature degree increased the risk
 295 by 16.7%. Precipitation had no effect: RR=1.00 (1.00–1.001) (Table 7), and the spatial distribution
 296 of risk is shown in Figure 8.

Table 7. Summary statistics of the effect of covariates on the estimated risk (RR) of CSF in a spatiotemporal Bayesian model.

Covariate	Univariate			Multivariate			Relative risk	
	Mean	0.95 % CI	DIC	Mean	(0.95 % CI)	DIC	RR	(0.95 % CI)
Intercept	–	–	–	-2.26	(-3.30 – -1.31)	1140	–	–
Time (years)	–	–	–	-0.36	(-0.51 – -0.21)	–	0.70	(0.60 – 0.81)
Doses by Km2	-0.309	(-0.68 – 0.02)	1188	-0.41	(-0.77 – -0.09)	–	0.67	(0.46 – 0.91)
Temperature	0.158	(0.11 – 0.21)	1142	0.15	(0.11 – 0.20)	–	1.17	(1.12 – 1.22)
Precipitation	0.001	(0.00 – 0.001)	1156	–	–	–	–	–

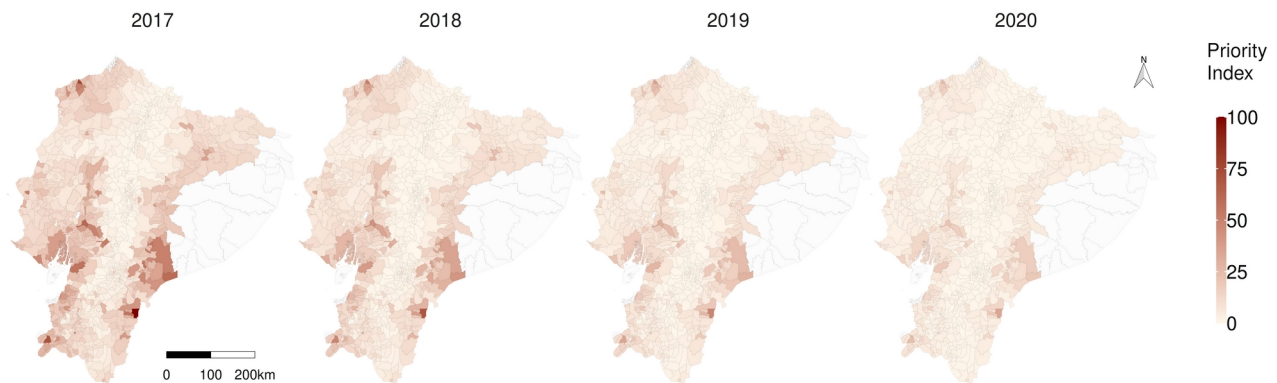
297 The proportion of variance explained by each component was 57% for the random effect (iid), a
298 major contributor to the explained variance, and 43% for the spatiotemporal (besag). The DIC
299 mean deviance was 1,140 and the effective number of parameters was 136.7.

300 Hot spots of increased risk were spatially identified on the map, in the coastal southwestern and
301 also the southeastern Amazon, reducing the risk over the years (Figure 7).



302
303 Figure 7. Spatiotemporal representation of the relative risk (RR) of CSF in Ecuador.

304 According to the priority index (PI), prime concern parishes are located in the eastern Amazon as
305 *Tundayme*, followed by *Tachina* in the northwestern and *Paletilla* in the southern zone (Figure 8).
306 The provinces with higher risk, considering the average RR per province in the year 2020, were
307 Morona Santiago (3.68), Los Rios (3.12) and Santa Elena, (3.07).



308
309 Figure 8. Spatiotemporal representation of the priority index (PI) to fight classical swine fever in
310 Ecuador.

311 5. Discussion

312 When countries mount resource-intensive control strategies for high-impact disease as CSF but fail
313 to reach the goal of control and elimination, a deeper analysis of the disease dynamics and the im-
314 plemented control interventions is needed to identify strategic intervention points. Despite the fact
315 that in general terms many CSF risk factors are known, their relevance in the specific setting of a
316 pig sector and the respective control program is ideally assessed using all available data.

317 Swill feeding is one of the main risk factors for CSF transmission; it is common and rooted in the
318 cultural tradition of backyard producers (43); therefore, it is very likely to be a key disease driver of
319 the disease in endemic areas of Andean countries. The Agricultural Health Law of 2019 (44), es-
320 tablished best practices for animal feed, but lacked specific regulations on swill. Consideration
321 needs to be given to promoting risk-reducing practices such as heat treatment (45) and stricter reg-
322 ulations that prohibit the use of animal protein as a feed source for pigs.

323 Vaccination misreporting could be related to the producer's lack of knowledge regarding veterinary
324 treatments linked with injections (vaccination, iron supplementation in piglets, deworming or other).
325 Fear associated with owners' legal responsibilities and misunderstandings during the interviews
326 may also lead to misreporting (46). In Indonesia, vaccination against CSF resulted in an increased
327 risk of CSF due to inaccurate vaccination claims (23); considering these facts, reporting behaviour
328 could be further analysed as an early target of the surveillance programme (47); suggesting that
329 communication and health education activities might be advisable to improve producers' under-
330 standing of animal disease prevention and control practices.

331 Our findings on increased risk at the age of 3-6 months could be related to the fact that young an-
332 imals might be more likely to be exposed to CSFV because this is the age at which they are nor-
333 mally marketed. The age with increased risk for CSF also reflects a complicated age from the im-
334 munological perspective. Maternal immunity fades out after three months (48), and animals not
335 vaccinated become susceptible just as animals vaccinated too early where maternal antibodies in-
336 terfere with the vaccination. Nowadays, the established recommendation for piglets in Ecuador is a
337 primary vaccination at relatively early 45 days and revaccination every 6 months. This practice
338 might have to reassess once targeted sero-surveillance studies to clarify the effects of vaccination
339 ages and herd immune status.

340 Maternal-derived antibody (MDA) interference is the most common factor affecting the induction of
341 protective immunity against CSFV; in Thailand the vaccination program has been implemented for
342 decades without achieving eradication (49). In addition, emergency vaccination protocols imple-
343 mented in very young piglets, especially during an outbreak, could be further analysed. It would be
344 necessary to evaluate diagnostic tools (rapid test) (50) that could detect non clinical, persistent
345 CSF forms in the field, as well as apply vaccination serological monitoring tools (51).

346 Cases occurred on farms that recorded vaccination, this could be related to illegal movements of
347 unvaccinated animals (52); and, they could also be a result of vaccination failures due to poor
348 handling and malpractice as evidenced in Colombia (4,19). The risk associated with temperature in
349 the spatiotemporal analysis, could be related to vaccination failures, as the vaccine cold-chain in
350 regions such as the Amazon and the Coastal with average temperatures above 20 degrees
351 Celsius, which corroborates that vaccination strategies alone are not sufficient to eradicate the dis-

352 ease (53,54); possible antigenic alteration due to vaccination pressure and their effects on disease
353 epidemiology could also be further analysed (55,56).

354 The identified individual parish risk could help identify neglected territories; as in many developing
355 countries with limited resources for disease control, prioritisation is often done on the basis of his-
356 toric surveillance information; therefore, reduced surveillance sensitivity may leave areas of high
357 risk unnoticed. Our model included all parishes and considered the influence of their neighbours to
358 improve the predictions (57). Concepts such as spatial RR or excess risk might be difficult to inter-
359 pret outside the scientific community, but the priority index (PI) could facilitate understanding and
360 communication of which parishes should be prioritised.

361 The identification of the risk factors should respond to the initial demand of the NVS and contribute
362 to the implementation of a risk-based surveillance strategy for CSF. As risk factors are specific for
363 each disease new studies could be implemented using depurated data and methodology for preval-
364 ent diseases where symptomatology could be confused with CSF such as the porcine reproductive
365 and respiratory syndrome (58,59), also prepare the surveillance system for re-emerging diseases
366 such as African swine fever, currently detected in Central America (60,61).

367 In total, the results indicate once again the complexity a CSF control program is facing, particularly
368 if the pig sector is diverse and comprises a large share of farms falling under the subsistence or
369 backyard category. Here, NVS faces risky production methods combined with reduced knowledge
370 on disease prevention and compliance with sanitary regulations.

371 **Conflict of interest**

372 The authors declare no conflicts of interest.

373 **Author contributions**

374 A. Acosta, F. Ferreira and K. Depner conceived the study; C. Imbacuan and L. Burbano coordin-
375 ated the data collection; K. Dietze, G. Osowski and A. Acosta curated the data and wrote the ma-
376 nuscript; O. Baquero participated in the spatiotemporal analysis; A. Acosta conducted data pro-
377 cessing and coding; All authors discussed the results and critically reviewed the final manuscript.

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382

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388 **Data availability statement**

389 The surveillance data contain private information of each Ecuadorian pig farmer and therefore can-
390 not be made available due to legal restrictions.

391 **Ethics statement**

392 The authors confirm that the ethical policies of the journal, as noted on the journal's author
393 guidelines page, have been adhered to. No ethical approval was needed as this work did not in-
394 volve animal sampling or questionnaire data collection by the researchers.

395 **References**

1. Benitez W, Sanchez MD. Los cerdos locales en los sistemas tradicionales de producción [Internet]. 1st ed. Estudio FAO producción y sanidad animal 148. Roma: Organización de las Naciones Unidas para la Agricultura y la Alimentación; 2001. 208 p. Available from: https://www.google.com.br/books/edition/Los_cerdos_locales_en_los_sistemas_tradi/Cpq4orS80rsC?hl=pt-BR&gbpv=1&dq=Los+cerdos+locales+en+los+sistemas+tradicionales+de+producci%C3%B3n&printsec=frontcover
2. Ganges L, Crooke HR, Bohórquez JA, Postel A, Sakoda Y, Becher P, et al. Classical swine fever virus: the past, present and future. *Virus Research*. 2020 Nov 1;289:198151.
3. OIE. Terrestrial Manual Online Access [Internet]. OIE - World Organisation for Animal Health. 2020 [cited 2020 Dec 14]. Available from: <https://www.oie.int/en/what-we-do/standards/codes-and-manuals/terrestrial-manual-online-access/>
4. Coronado L, Bohórquez JA, Muñoz-González S, Perez LJ, Rosell R, Fonseca O, et al. Investigation of chronic and persistent classical swine fever infections under field conditions and their impact on vaccine efficacy. *BMC Veterinary Research*. 2019 Jul 15;15(1):247.
5. Depner K, Le Potier MF, Dietze K. Classic Swine Fever. In: *Veterinary Vaccines* [Internet]. John Wiley & Sons, Ltd; 2021 [cited 2021 Nov 12]. p. 327–34. Available from: <https://onlinelibrary.wiley.com/doi/abs/10.1002/9781119506287.ch24>
6. Bronsvort BM de C, Alban L, Greiner M. Quantitative assessment of the likelihood of the introduction of classical swine fever virus into the Danish swine population. *Preventive Veterinary Medicine*. 2008;85(3/4):226–40.
7. Backer JA, Hagenaars TJ, van Roermund HJW, de Jong MCM. Modelling the effectiveness and risks of vaccination strategies to control classical swine fever epidemics. *Journal of the Royal Society, Interface*. 2009 Oct;6(39):849–61.
8. Terpstra C. The 1997/1998 epizootic of swine fever in the Netherlands: control strategies under a non-vaccination regimen. *Veterinary Microbiology*. 2000 Nov;77(1–2):3–15.

9. Beltran-Alcrudo D, Falco JR, Raizman E, Dietze K. Transboundary spread of pig diseases: the role of international trade and travel. *BMC Veterinary Research*. 2019 Dec;15(1):64–64.
10. Araínga M, Hisanaga T, Hills K, Handel K, Rivera H, Pasick J. Phylogenetic Analysis of Classical Swine Fever Virus Isolates from Peru. *Transboundary and Emerging Diseases*. 2010;57(4):262–70.
11. Ferrer E, Fonseca O, Percedo M, Abeledo M. La Peste porcina clásica en las américas y el caribe. Actualidad y perspectivas de control y erradicación. *Revista de Salud Animal*. 2010;32(1):11–21.
12. Santafe-Huera VN, Barrera-Valle MI, Barrionuevo-Samaniego MY, Sotomayor-Ramos WR, Garrido-Haro AD, Acosta-Batallas AJ, et al. Assessment of the Ecuadorian ECJB 2000 isolate of classical swine fever virus as challenge strain. *Revista de Salud Animal [Internet]*. 2019 Aug;41. Available from: http://scielo.sld.cu/scielo.php?script=sci_arttext&pid=S0253-570X2019000200001&nrm=iso
13. Blome S, Staubach C, Henke J, Carlson J, Beer M. Classical swine fever—an updated review. *Viruses*. 2017;9(4):1–24.
14. Elbers AR, Stegeman JA, de Jong MC. Factors associated with the introduction of classical swine fever virus into pig herds in the central area of the 1997/98 epidemic in The Netherlands. *The Veterinary record*. 2001 Sep;149(13):377–82.
15. Fritzemeier J. Epidemiology of classical swine fever in Germany in the 1990s. [doi.org](https://doi.org/10.1016/S0950-2688(00)01901-1). 2000 Nov;(1–2):29–41.
16. Mintiens K, Laevens H, Dewulf J, Boelaert F, Verloo D, Koenen F. Risk analysis of the spread of classical swine fever virus through ‘neighbourhood infections’ for different regions in Belgium. *Preventive veterinary medicine*. 2003 Jul;60(1):27–36.
17. Ribbens1 S, Dewule J, Koenen2 F, Laevens3 H, De Kruie A. Transmission of classical swine fever. A review. *Veterinary Quarterly*. 2004;26(4):146–55.
18. Van Oirschot JT. Vaccinology of classical swine fever: From lab to field. *Veterinary Microbiology*. 2003 Nov;96(4):367–84.
19. Pineda P, Deluque A, Peña M, Diaz OL, Allepuz A, Casal J. Descriptive epidemiology of classical swine fever outbreaks in the period 2013-2018 in Colombia. *PLOS ONE*. 2020 Jun 17;15(6):e0234490.
20. de Oliveira LG, Gatto IRH, Mechler-Dreibi ML, Almeida HMS, Sonálio K, Storino GY. Achievements and Challenges of Classical Swine Fever Eradication in Brazil. *Viruses*. 2020 Nov;12(11):1327.
21. Gomez-Vazquez JP, Quevedo-Valle M, Flores U, Portilla Jarufe K, Martinez-Lopez B. Evaluation of the impact of live pig trade network, vaccination coverage and socio-economic factors in the classical swine fever eradication program in Peru. *Preventive Veterinary Medicine*. 2019 Jan;162:29–37.
22. Martínez-López B, Alexandrov T, Mur L, Sánchez-Vizcaíno F, Sánchez-Vizcaíno JM. Evaluation of the spatial patterns and risk factors, including backyard pigs, for classical swine fever occurrence in Bulgaria using a Bayesian model. *Geospat Health*. 2014 May 1;8(2):489.

23. Sawford K, Geong M, Bulu PM, Drayton E, Mahardika GNK, Leslie EEC, et al. An investigation of classical swine fever virus seroprevalence and risk factors in pigs in East Nusa Tenggara, eastern Indonesia. *Preventive Veterinary Medicine*. 2015 May;119(3–4):190–202.
24. Peyre M, Hoinville L, Njoroge J, Cameron A, Traon D, Goutard F, et al. The RISKSUR EVA tool (Survtool): A tool for the integrated evaluation of animal health surveillance systems. *Preventive Veterinary Medicine*. 2019 Dec 1;173:104777.
25. Wensvoort G, Terpstra C, Boonstra J, Bloemraad M, Van Zaane D. Production of monoclonal antibodies against swine fever virus and their use in laboratory diagnosis. *Veterinary Microbiology*. 1986 Jul 1;12(2):101–8.
26. Hoffmann B, Depner K, Beer M. Method of Detection of Classical Swine Fever [Internet]. 2006 [cited 2021 Aug 10]. Available from: <https://patentscope.wipo.int/search/en/detail.jsf?docId=WO2006086377>
27. Thrusfield Michael, Christley R. *Veterinary Epidemiology*. Wiley [Internet]. 2018. 864 p. Available from: <https://www.wiley.com/en-br/Veterinary+Epidemiology,+4th+Edition-p-9781118280287>
28. Mansournia MA, Jewell NP, Greenland S. Case–control matching: effects, misconceptions, and recommendations. *Eur J Epidemiol*. 2018 Jan 1;33(1):5–14.
29. Sauerbrei W, Perperoglou A, Schmid M, Abrahamowicz M, Becher H, Binder H, et al. State of the art in selection of variables and functional forms in multivariable analysis—outstanding issues. *Diagnostic and Prognostic Research*. 2020 Apr 2;4(1):3.
30. Greenland S, Pearl J, Robins JM. Causal Diagrams for Epidemiologic Research. *Epidemiology*. 1999;10(1):37–48.
31. Hernán MA, Hernández-Díaz S, Werler MM, Mitchell AA. Causal Knowledge as a Prerequisite for Confounding Evaluation: An Application to Birth Defects Epidemiology. *American Journal of Epidemiology*. 2002 Jan 15;155(2):176–84.
32. Fox J, Monette G. Generalized Collinearity Diagnostics. *Journal of the American Statistical Association*. 1992;87(417):178–83.
33. Dohoo IR, Martin SW, Stryhn H. *Veterinary Epidemiologic Research* [Internet]. VER, Incorporated; 2009. Available from: <https://books.google.com.br/books?id=snlqQwAACAAJ>
34. Hosmer D, Lemeshow S. Assessing the Fit of the Model. In: *Applied Logistic Regression* [Internet]. John Wiley & Sons, Ltd; 2000. p. 143–202. Available from: <https://onlinelibrary.wiley.com/doi/abs/10.1002/0471722146.ch5>
35. Moritz S, Bartz-Beielstein T. imputeTS: Time Series Missing Value Imputation in R. 2017;9:12.
36. Acosta A, Cardenas NC, Imbacuan C, Lentz HHK, Dietze K, Amaku M, et al. Modelling control strategies against classical swine fever: Influence of traders and markets using static and temporal networks in Ecuador. *Preventive Veterinary Medicine*. 2022 Aug 1;205:105683.
37. Besag J, York J, Mollie A. Bayesian image restoration, with two applications in spatial statistics. *Ann Inst Stat Math*. 1991 Mar;43(1):1–20.
38. Bernardinelli L, Clayton D, Pascutto C, Montomoli C, Ghislandi M, Songini M. Bayesian analysis of space–time variation in disease risk. *Statistics in Medicine*. 1995;14(21–22):2433–43.

39. Lawson A. Bayesian Disease Mapping: Hierarchical Modeling in Spatial Epidemiology [Internet]. 3rd ed. 2009 [cited 2021 Mar 30]. Available from: <https://sil0.pub/bayesian-disease-mapping-hierarchical-modeling-in-spatial-epidemiology.html>
40. Baquero OS, Machado G. Spatiotemporal dynamics and risk factors for human Leptospirosis in Brazil. *Scientific Reports*. 2018 Oct 11;8(1):15170.
41. Rue H, Martino S, Chopin N. Approximate Bayesian inference for latent Gaussian models by using integrated nested Laplace approximations. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*. 2009;71(2):319–92.
42. Peduzzi P, Concato J, Kemper E, Holford TR, Feinstein AR. A simulation study of the number of events per variable in logistic regression analysis. *Journal of Clinical Epidemiology*. 1996 Dec 1;49(12):1373–9.
43. Valverde Lucio A, Gonzalez-Martínez A, Alcívar Cobeña JL, Rodero Serrano E. Characterization and Typology of Backyard Small Pig Farms in Jipijapa, Ecuador. *Animals*. 2021 Jun;11(6):1728.
44. Official Registry. Law of agricultural health [Internet]. Oct 29, 2019 p. 92. Available from: http://www.epmrq.gob.ec/images/servicios/Reglamento_LOSA.pdf
45. Albernaz-Gonçalves R, Olmos G, Hötzel MJ. My pigs are ok, why change? – animal welfare accounts of pig farmers. *Animal*. 2021 Mar 1;15(3):100154.
46. Gates MC, Earl L, Enticott G. Factors influencing the performance of voluntary farmer disease reporting in passive surveillance systems: A scoping review. *Preventive Veterinary Medicine*. 2021 Nov 1;196:105487.
47. Pfeiffer C, Stevenson M, Firestone S, Larsen J, Campbell A. Using farmer observations for animal health syndromic surveillance: Participation and performance of an online enhanced passive surveillance system. *Preventive Veterinary Medicine*. 2021 Mar 1;188:105262.
48. Suradhat S, Damrongwatanapokin S. The influence of maternal immunity on the efficacy of a classical swine fever vaccine against classical swine fever virus, genogroup 2.2, infection. *Veterinary Microbiology*. 2003 Mar 20;92(1):187–94.
49. Suradhat S, Damrongwatanapokin S, Thanawongnuwech R. Factors critical for successful vaccination against classical swine fever in endemic areas. *Veterinary Microbiology*. 2007 Jan;119(1):1–9.
50. Wu K, Zhang Y, Zeng S, Liu X, Li Y, Li X, et al. Development and Application of RAA Nucleic Acid Test Strip Assay and Double RAA Gel Electrophoresis Detection Methods for ASFV and CSFV. *Frontiers in Molecular Biosciences* [Internet]. 2022 [cited 2022 Aug 18];8. Available from: <https://www.frontiersin.org/articles/10.3389/fmolb.2021.811824>
51. Bai Y, Jia R, Wei Q, Wang L, Sun Y, Li Y, et al. Development and application of a high-sensitivity immunochromatographic test strip for detecting classical swine fever virus antibodies. *Transboundary and Emerging Diseases*. 2022;69(4):e788–98.
52. Acosta AJ, Cespedes N, Pisuna LM, Galvis JO, Vinueza RL, Vasquez KS, et al. Network analysis of pig movements in Ecuador: Strengthening surveillance of classical swine fever. *Transboundary and Emerging Diseases* [Internet]. 2022 [cited 2022 Jun 23];n/a(n/a). Available from: <https://onlinelibrary.wiley.com/doi/abs/10.1111/tbed.14640>

53. Ganges L, Núñez JI, Sobrino F, Borrego B, Fernández-Borges N, Frías-Lepoureau MT, et al. Recent advances in the development of recombinant vaccines against classical swine fever virus: Cellular responses also play a role in protection. *The Veterinary Journal*. 2008 Aug 1;177(2):169–77.
54. Muñoz-González S, Ruggli N, Rosell R, Pérez LJ, Frías-Leuporeau MT, Fraile L, et al. Postnatal persistent infection with classical Swine Fever virus and its immunological implications. *PloS one*. 2015;10(5):e0125692–e0125692.
55. Ji W, Niu DD, Si HL, Ding NZ, He CQ. Vaccination influences the evolution of classical swine fever virus. *Infection, Genetics and Evolution* [Internet]. 2014; Available from: <https://www.sciencedirect.com/science/article/pii/S1567134814001300?via%3Dihub>
56. Nguyen NH, Nguyen PBT, Nguyen TQ, Do DT, Nguyen MDT, Nguyen MN. Genotypic diversity of CSFV field strains: A silent risk reduces vaccination efficacy of CSFV vaccines in Vietnam. *Virology*. 2022 Jun 1;571:39–45.
57. Stojanović O, Leugering J, Pipa G, Ghozzi S, Ullrich A. A Bayesian Monte Carlo approach for predicting the spread of infectious diseases. *PLOS ONE*. 2019 Dec 18;14(12):e0225838.
58. Arruda AG, Vilalta C, Perez A, Morrison R. Land altitude, slope, and coverage as risk factors for Porcine Reproductive and Respiratory Syndrome (PRRS) outbreaks in the United States. *PLOS ONE*. 2017 Apr 17;12(4):e0172638.
59. Sanhueza JM, Stevenson MA, Vilalta C, Kikuti M, Corzo CA. Spatial relative risk and factors associated with porcine reproductive and respiratory syndrome outbreaks in United States breeding herds. *Prev Vet Med*. 2020 Oct;183:105128.
60. Gonzales W, Moreno C, Duran U, Henao N, Bencosme M, Lora P, et al. African swine fever in the Dominican Republic. *Transboundary and Emerging Diseases*. 2021;68(6):3018–9.
61. Jurado C, Paternoster G, Martínez-López B, Burton K, Mur L. Could African swine fever and classical swine fever viruses enter into the United States via swine products carried in air passengers' luggage? *Transboundary and Emerging Diseases*. 2019;66(1):166–80.