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1 **Network analysis of cattle movements in Ecuador**

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7 **Abstract**

8 We used cattle movement data in Ecuador for 2017 and 2018 to build two types of cattle
9 networks: a network including all cattle movements accounting for a disease of rapid
10 spread like foot and mouth disease and a network including only the cows accounting for
11 brucellosis, a disease of slow evolution occurring mainly in adult females. Parishes (the
12 smallest geographical units) were considered as nodes and cattle movements between
13 parishes as links. Network indicators calculated at the annual and monthly levels were
14 close for both types of networks. For both networks, the largest strong component at the
15 annual level included >90% of nodes and the largest weak component included all nodes
16 indicating a very low fragmentation. A percolation analysis indicated that most of the
17 parishes needed to be removed to eliminate the largest strong components. Based on
18 some network characteristics we established that a highly transmissible disease could
19 spread rapidly and that an infection of slower transmission such as brucellosis could
20 spread within local clusters. These features should be taken into account when
21 considering preventing measures in Ecuador in the case of an emerging disease like foot
22 and mouth disease or control measures for an endemic disease like brucellosis.

23 **Key words:** network analysis; cattle; movements; disease control; Ecuador

24 INTRODUCTION

25 For most infectious diseases of livestock, the infectious agent can be transmitted between
26 farms through local transmission routes such as the direct contact between animals, or
27 through insects, rodents, wind, or alternative hosts (Gilchrist et al., 2007). However,
28 another form of disease propagation can occur between distant farms due to the transport
29 of animals or infected material, causing the diseases to jump between places separated by
30 large areas where the disease is absent and potentially reaching and spreading in remote
31 places (Fèvre et al., 2006; Gilbert et al., 2005; Green et al., 2008).

32 In Ecuador, where cattle are the main domestic species exploited, two diseases of concern
33 are foot and mouth disease (FMD) and bovine brucellosis. FMD is caused by a virus of
34 the genus *Aphthovirus*, *Picornaviridae* family, which is easily contagious and spreads
35 rapidly, leading to a vesicular syndrome mainly in cloven-hoofed animals (OIE, 2021).
36 Until 2015, when Ecuador was declared free from FMD with vaccination by the World
37 Animal Health Organization (OIE), the country had had epidemic waves throughout the
38 mainland territory (PAHO, 2019). The importance of the disease lies in its economic
39 impact, which has been documented by authors in different countries, and which is mainly
40 related to the drop in cattle production, control and eradication costs, as well as limitations
41 in the international trade of cattle and animal products (Thompson et al., 2002). In 2012,
42 the Hemispheric Foot and Mouth Disease Eradication Programme (PHEFA) was
43 launched in South America. The intense vaccination work carried out in Ecuador as part
44 of the program is evidenced by the absence of disease with no FMD transmission detected
45 from 2011 to the present day (PHEFA, 2020).

46 On the other hand, bovine brucellosis, mainly caused by *Brucella abortus*, is a zoonotic
47 disease, which causes economic and public health problems in endemic areas. Brucellosis
48 infection in cows leads to abortion during the last third of gestation (Corbel, 1997;

49 Nicoletti, 1980). In humans, the infection occurs by consuming contaminated,
50 unpasteurized milk or cheese or through the contact with infected animals and aborted
51 fetuses (Borba et al., 2013). The economic impact of the disease is due to abortions in
52 cattle, contamination of milk, infertility, losses due to discarding of highly genetic
53 animals, loss of markets and costs associated with efforts to eliminate the disease (Olsen
54 & Tatum, 2010). In Ecuador, both human and animal cases have been reported (Ron-
55 Román et al., 2014). In cattle, the disease has been described throughout the Ecuadorian
56 territory except in Galapagos Islands (Carbonero et al., 2018, Gioia et al., 2019). A bovine
57 brucellosis control and eradication plan are currently being developed in Ecuador. This
58 plan seeks to implement vaccination, biosafety, and epidemiological surveillance
59 strategies (Agrocalidad, 2008).

60 To strengthen sanitary surveillance and control systems, the
61 World Organization of Animal Health (OIE) has been promoting the implementation of
62 records to identify cattle and their movements between farms (OIE, Chapter 7.3,
63 Terrestrial Code, 2009), which have been implemented in many countries. Computer
64 development has significantly contributed to information management as it facilitates the
65 storage and handling of vast amounts of data.

66 Livestock trading systems can be represented through networks based on a database of
67 animal movements recording their origin and destination. A network is a structure in
68 which holdings are defined as nodes, and the movements of animals between these
69 entities are represented by links, which may be labeled by the date of the movement or
70 the number of displaced animals (Fèvre et al., 2006; Natale et al., 2009). The increasing
71 availability of data and the high coverage of livestock production and trade systems have
72 allowed the analysis of the structure of trade networks through the Social Network
73 Analysis (SNA) methodology based on graph theory (Newman & Park, 2003; Nöremark

74 et al., 2011). In Latin America, as a result of implementing the foot-and-mouth disease
75 (FMD) control and eradication programs, several countries have developed and perfected
76 their inventory records and animal mobility systems, which undoubtedly has contributed
77 to adequate management of the disease (Brito et al., 2017). In Ecuador, the issuance of
78 the Organic Law of Animal Health 2004 (Ley Organica de Sanidad Animal 2004) and
79 the subsequent launch of the Foot-and-Mouth Disease Eradication Program in 2010
80 (Agrocalidad, 2011) gave way to the structuring and improvement of national databases
81 on cattle census and movements. In several Latin American countries, SNA tools were
82 used to describe and analyze the cattle movement networks in Argentina (Aznar et al.,
83 2011), Uruguay (VanderWaal et al., 2016), and Brazil (Júnior et al., 2017). This work
84 have provided information to strengthen epidemiological surveillance in those countries.
85 More generally, the integration of cattle trade data in epidemiological studies and the use
86 of SNA have allowed studying the relationship between animal movements and the
87 spread of infectious diseases of cattle. This was the case for slow-spreading diseases such
88 as bovine tuberculosis in Great Britain (Green et al., 2008) and in France (Bouchez-Zacria
89 et al., 2018; Palisson et al., 2017), or paratuberculosis in dairy cattle in Italy (Rossi et al.,
90 2017). Fast-spreading diseases have also been addressed using SNA, for instance avian
91 influenza in Thailand (Poolkhet et al., 2013) and the relationship between its spread and
92 the movements of backyard birds, or FMD and its potential spread in Peru (Martínez-
93 López et al., 2014).

94 To incorporate livestock trade networks into epidemiological studies, however, it is
95 necessary to first identify the relevant network, which may differ according to the studied
96 disease. Indeed, viral diseases of cattle such as FMD evolve fast in infected hosts of all
97 age categories, and spread within and between farms leading to epizootics. Oppositely,
98 bacterial diseases of cattle such as bovine tuberculosis or bovine brucellosis often evolve

99 slowly in affected hosts, and spread slowly inside and between herds. In the case of bovine
100 brucellosis, infected animals are mostly adult females. Therefore, the relevant network
101 for the study of disease spread is different for FMD (the whole cattle trade network) and
102 for bovine brucellosis (the cow trade network), and these two networks might have
103 different properties.

104 The objectives of this study were to build and compare two distinct networks to address,
105 in Ecuador: i) the spread of an FMD serotype/topotype not included in the current
106 vaccines being used, and ii) bovine brucellosis spread through cow network. Cattle
107 movements were studied at the yearly and monthly scales using data for 2017 and 2018.
108 SNA was implemented to identify network properties that could allow to control an FMD
109 spread or to setup surveillance and control measures for bovine brucellosis.

110 **MATERIALS AND METHODS**

111 **Data**

112 In Ecuador, Agrocalidad is the official institution that has developed two databases in the
113 context of the FMD control program set up in 2010. One database contains information
114 on the cattle inventory by farm collected during the FMD vaccination campaigns carried
115 out every six months throughout the country. This database comprises information on
116 farm location specifying three administrative units (from the smallest to the largest:
117 parish, canton, province), cattle farm type (beef, dairy, mixed) and number of cattle by
118 category (calf, heifer, cow, bull). For this study, we used data for January 2017 and
119 January 2018 to create farm and cattle density maps. The second database gathers all
120 information on cattle movements including the identification numbers of origin and
121 destination holdings, date of movement, geographical origin and destination specifying
122 the three administrative units aforementioned, type of holding at origin (farm or market)
123 type of holding at destination (farm, market, slaughterhouse) and number and category of

124 moved cattle (cows, bulls, steers, calves). Data for movements in 2017 and 2018 were
125 extracted to construct the movement networks.

126 Cleaning of the dataset from the movement database was performed to eliminate
127 duplicated data and to homogenize administrative unit names. For this last operation, we
128 used names approved by the Ecuadorian Institute of Statistics and Census of Ecuador
129 (INEC). As we found inconsistencies on the use of farm identification codes, we decided
130 to aggregate data at the parish level to conduct the analysis. Farm and cattle numbers
131 recorded in the inventory database were aggregated by parish taking farm type into
132 account. All the cleaning and data processing were performed using the R 4.0.3 software
133 (R Core Team, 2020). The resulting dataset was imported into QGIS version 3.10 (Sutton
134 T. 2004) to create farm and cattle density maps. Map layers were obtained from the INEC
135 (<http://www.geoportaligm.gob.ec/>) and the location of markets was provided by
136 Agrocalidad.

137 **Network construction**

138 In this study, the trade of cattle was represented by a network with parishes as nodes and
139 cattle movements between parishes as links. The network was directed because cattle
140 movements occur in just one direction, from nodes at origin to nodes at destination. In
141 previous studies, the possible spread of diseases through fomites had been considered
142 involving slaughterhouses, for example through a network of truck movements (Salines
143 et al., 2017). As in our study only the cattle movements were taken as a potential source
144 of disease spread, movements to the slaughterhouses were not included.

145 To consider disease spread characteristics within the network according to animal
146 category, two distinct networks were constructed: a network including all animal
147 categories and a network with only cows. The “all animal category network” (termed
148 below “global network”) would account for a serotype or toptype not covered by the

149 current FMD vaccine in use in Ecuador that could be transmitted between farms by the
150 trade of cattle, whatever the age or sex of the traded animals. The “only cow network”
151 (termed below “cow network”) would account for diseases that are mainly transmitted
152 between farms by the trade of cows, like bovine brucellosis. These two networks were
153 built by year (2017, 2018) and by month (24 months) yielding a total of 52 networks.

154 **Network description**

155 Several indicators were calculated for each network: the size of the network (number of
156 nodes) and the number of links, the density (total number of links divided by the number
157 of possible connections), the average degree (the degree is the number of parishes that a
158 parish is connected to through cattle movements), the betweenness (frequency with which
159 a node appears on the shortest path between other pair of nodes), the average path length
160 (average number of links along the shortest paths for all possible pairs of network nodes),
161 the diameter (the most extensive shortest path among all the shortest paths in the
162 network), the clustering coefficient measures the extent to which neighbors of a node are
163 also neighbors of each other, the reciprocity (the probability of nodes of being mutually
164 linked) and the assortativity (the tendency of nodes to connect to similar nodes in terms
165 of degree).

166 The Jaccard index (JI), which allows the measurement of the similarity between two data
167 sets, was used to compare the nodes and links included in each network from month to
168 month and from year to year. It takes values between 0 (no elements in common) and 1
169 (the samples are identical). A function to estimate the JI was created using the R 4.0.3
170 software (R Core Team, 2020).

171 The number and size of the strongly (SC) and weakly (WC) connected components were
172 determined for both the global and cow networks at the annual scale. The components
173 are sub-networks where all nodes are connected. They can be interpreted as areas of a

174 network where connectivity is exceptionally high. In SC, all nodes are mutually
175 accessible by directed links, while in WC, all nodes are linked without taking into account
176 the direction of the links (Robinson S.E & Chistley R.M, 2007). Identifying the largest
177 strong or weak components of a network can give an estimation of the maximal size of
178 an epidemic in the case of a disease introduction (Dubé et al., 2008). The closeness
179 centrality (average length of the shortest path between a node and all other nodes) was
180 calculated in the largest SC as it should be computed in connected networks.

181 Likewise, the six largest communities for both the global and cow networks at the annual
182 scale were identified using the Walktrap algorithm and represented on maps.
183 Communities are more densely connected groups within a network with nodes that share
184 common elements (Newman, 2006). In our case, they correspond to the parishes that carry
185 out the most significant commercial exchanges.

186 A network can have scale-free or small-world properties. The scale-free networks are
187 characterized by the presence of hubs, which are responsible for several striking
188 properties for propagation of infections (Meloni et al., 2009). A small-world network
189 represents a situation where most nodes have close neighbors, but a few nodes have very
190 distant neighbors (Watts & Strogatz, 1998). To detect the presence of scale-free and
191 small-world properties in our networks, we plotted their degree distributions on a
192 logarithmic scale, and generated random networks having the same numbers of nodes and
193 links, to compare their clustering coefficient and average path length values with those of
194 our networks.

195 Networks analyses were performed using the Igraph package for R 4.0.3. (Gábor Csárdi
196 & Tamas Nepusz, 2005).

197

198 **Percolation analysis**

199 To evaluate the efficacy of targeted control measures to limit disease spread through a
200 network, a percolation analysis was conducted at the annual scale. The term percolation
201 has been borrowed from the field of physics; in the context of social networks, a
202 percolation analysis is conducted to study the behavior of a graph following the removal
203 of its edges or vertices (Essam, 1980). Percolation analysis allows assessing the most
204 efficient way to disintegrate the largest strong component viewed as an estimate of the
205 maximal size of an epidemic spreading on the network. In our study, two strategies were
206 implemented: i) removing all the parishes where markets were located, and ii) removing
207 nodes with the highest betweenness values iteratively until a largest strong component
208 threshold size representing less than 10% of the total nodes was attained. A specific
209 program was developed to conduct the percolation analysis using the R 4.0.3 software (R
210 Core Team, 2020).

211 **RESULTS**

212 **Cattle inventory dataset description**

213 The numbers of cattle farms recorded for 2017 and 2018 are shown in Table 1. Around
214 70% of the farms were dedicated to mixed production of meat and milk, 17% to milk
215 production, and 13% to meat production. In 2017, the bovine population was slightly
216 higher than in 2018 and the proportion of animals distributed in the different categories
217 of farms followed those of cattle farms.

218 The location of the 63 animal markets recorded in the country is shown in Figure 1.

219 The cattle farm density was higher in the Sierra region, with some parishes recording up
220 to 178 farms per km² (Figure 2a). These high densities corresponded mainly to small
221 holdings. Cattle farm density differed per category with beef and mixed farms mainly
222 concentrated in the Coast and Sierra regions (Figures 2b and 2d), while dairy farm density

223 was higher in the Sierra region (up to 64 farms/km² in 2017) (Figure 2c) The highest farm
224 density was found for mixed farms in a parish located in the center of the Sierra region
225 (109,3 farms/km² in 2017). Farm density was lower in the Amazon region but in some
226 parishes beef and dairy farms were highly concentrated.

227 Density of cattle had a similar geographical trend as farm density for both years (Figure
228 3). The highest density value was recorded for cattle from mixed farms in a parish of the
229 Sierra region in 2017 (652 cattle/ km²).

230 **Cattle trade dataset description**

231 The number of cattle movements and cattle moved were close for both years (Table 2).
232 The number of cow movements and cows moved represented 46% of those for all cattle
233 (441,453 of 952,972 in 2017 and 441,451 of 962,890 in 2018). Seventy percent of the
234 cattle movements originated from farms for both years (675,652 of 952,972 in 2017 and
235 674,668 of 962,890 in 2018), of these approximately 15% (104,622 in 2017 and 106,660
236 in 2018) concerned movements to farms, 53% to markets (353,348 in 2017 and 367,955
237 in 2018) and 32% to slaughterhouses (217,682 in 2017 and 200,053 in 2018). All these
238 proportions were similar for cow movements. The vast majority of movements were
239 carried out between parishes either for all cattle or for cows only (77% in 2017 and 78%
240 in 2017 in both cases). Cattle were moved in small groups of four animals on average
241 (3,855,593 animals moved in 952,972 groups in 2017, and 3,814,917 animals moved in
242 962,890 groups in 2018), the group size being however larger for the between farm
243 movements: 6-7 animals on average (725,026 animals moved in 104,622 groups in 2017,
244 and 676,415 animals moved in 106,660 in 2018). Similar values were obtained for the
245 movements of cows.

246 **Annual network characteristics**

247 *Indicators and components*

248 Out of the 1140 Ecuadorian parishes, 940 and 924 were implicated in cattle and cow trade,
249 respectively; in 2017 and slightly fewer in 2018 (Table 3). The percentage of links in the
250 cow network corresponded to approximately 65% of the global networks links.

251 The global and cow networks showed a very low fragmentation as the largest strong
252 component included >90% of nodes and the largest weak component included all nodes.
253 (Table 3, Figure 4).

254 As expected, density and average degrees were slightly higher for the global network
255 compared to those for the cow network. Overall density values were low meaning cattle
256 movements do not occur between many pairs of parishes. Reciprocity values showed that
257 a little less than a half of parishes to which a given parish sends animals are the same
258 from those from which it receives animals. The degree distribution in a log-log scale did
259 not show a linear shape for any of the networks (S1 Appendix).

260 Clustering coefficient and betweenness values were close for all four networks. The
261 negative assortativity numbers indicated that the networks were disassortative. There was
262 practically no change for the closeness among the annual networks.

263 Degree and betweenness were higher in parishes with animal markets than in parishes
264 without markets (Figure 6).

265 Clustering coefficient values were markedly higher than those of random networks
266 having the same number of nodes and edges (0.04 in both years for the global networks,
267 and 0.03 in 2017 and 0.028 in 2018 for the cow networks). Conversely, average path
268 length values were close to those of the random networks (2.18 in 2017 and 2.12 in 2018
269 for the global networks, and 2.47 in 2017 and 2.39 in 2018 for the cow networks).

270 *Communities*

271 The global networks had a higher number of communities than the cow networks (Table
272 3). The first six largest communities grouped 93% (2017) and 97% (2018) of the parishes
273 in the global networks and 84% (2017) and 91% (2018) in the cow networks. Spatial
274 distribution of the first six communities (S2 Appendix) suggests that the spatial location
275 and extent of the first three communities was close in the global and cow networks for
276 both years.

277 **Monthly network indicators**

278 Monthly indicators showed little variation from month to month for both years (Figure
279 6). Number of nodes, number of links, average degree and reciprocity were lower for
280 cow networks than for global networks while average path length and average
281 betweenness, for most of the months, were higher. Assortativity had negative values
282 and, as for clustering coefficient, there were no remarkable differences for the two types
283 of network.

284 **Node and link trends in time**

285 The Jaccard index for the annual global networks was higher for the nodes (97%) than
286 for the links (40%). The annual cow network JI values were very close: 95% for the
287 nodes and 39% for the links. In other words, practically the same parishes participated in
288 animal trade in both years and only half of the exchanges occurred between the same
289 parishes.

290 For the monthly networks the JI values fluctuated between 83% and 94% for the nodes
291 and between 41% and 46% for the links (S3 Appendix).

292

293 **Percolation analysis**

294 The removal of parishes including markets did not induced break the largest strong
295 component (LSC). For the two types of network, the LSC still represented between 80%
296 in 2017 and 87% in 2018 of the total number of nodes.

297 Results of node removal based on their betweenness are shown in table 4. For the four
298 networks, a high number of nodes needed to be removed to attain the 10% threshold size
299 of the LSC.

300 **DISCUSSION**

301 In this study, a description of Ecuador's cattle inventory was made using the data
302 collected during the FMD vaccination campaigns. Cattle movement records for 2017 and
303 2018 were processed and studied using SNA methodology and network indicators.
304 Networks considering parishes as nodes and cattle movements as links were analyzed at
305 the annual and monthly levels. We analyzed (i) the entire cattle movement database to
306 document network characteristics relevant to the early detection and control of an
307 epidemic disease such as FMD, and (ii) cow movement data, to describe network
308 characteristics relevant to the surveillance and control of an endemic disease primarily
309 affecting adult females, such as bovine brucellosis.

310 Ecuadorian cattle population figures estimated in our study from FMD vaccination
311 campaigns were close for 2017 and 2018, and did not differ from those established in the
312 3rd national livestock census conducted in 2002 (Haro Oñate, 2003). They were also
313 consistent with the results of a study that showed that the cattle population in Ecuador has
314 not experienced changes in the last decade (Sánchez, A. M. et al., 2019). The decrease of
315 cattle population size could be explained by the gradual decline in the red meat

316 consumption, including the tendency to replace beef with other cheaper sources of protein
317 (poultry and pigs).

318 The total number of mixed farms in Ecuador was at least three times higher than beef
319 farms and five times higher than dairy farms, confirming that it is the most general
320 category, as in other countries of South America (FEDEGAN, 2021, MINAGRI, 2017).

321 Mixed production in Ecuador is related to small farms (1 to 20 ha) in which agriculture
322 and dual-purpose livestock are developed with little technology, while specialized meat
323 or milk production almost always corresponds to consolidated businesses (Haro Oñate,
324 2003). As a result, mixed systems mostly resort to self-sufficiency practices, unlike large
325 farms (more than 100 ha) that use technological packages (nutritional, sanitary, and
326 reproductive) and medium-sized farms (20 to 100 ha), which have technical assistance,
327 although to a lesser extent.

328 We found that there was a higher density of farms and animals/km² in the Sierra region
329 and that most of those farms were dairy farms. This finding is in accordance with the
330 results of a study that pointed out that this region has many intensive farms specialized in
331 dairy cattle raising (Requelme & Bonifaz, 2012) The highest density of mixed systems
332 was found on the Coast region. In contrast, the density of farms and animals/km² in the
333 Amazon region was very low as 53% of the land correspond to natural forests and
334 woodlands (Ríos-Núñez & Benítez-Jiménez, 2015).

335 Markets appeared to play a major role in the organization of cattle trade, as half of the
336 movements and moved cattle leaving farms were directed to markets rather than to other
337 farms or to slaughterhouses. As there are not markets in all parishes, this is consistent
338 with the fact that the vast majority of those cattle movements occurred between parishes.
339 Some movements from farm to farm could correspond to a form of seasonal transhumance
340 that still exists in Ecuador among small producers consisting in the temporary use of

341 pastures in the months of drought or shortage of pasture (Stewart et al., 1976). On
342 average, 7 cattle were transported per movement between farms. This figure is lower than
343 the one reported by Aznar et al. (2011) in Argentina, where an average of 32 animals per
344 movement between farms was reported in 2005, which is possibly explained by the size
345 of the farms and the magnitude of the trade.

346 One of our original purposes was to compare network indicators at the holding level and
347 at the parish level. Unfortunately, networks could only reliably be built at the parish level.
348 Networks indicators were very close for global and cow networks at the annual and
349 monthly scales. The degree distribution in a logarithmic scale did not show a linear trend
350 for any of the annual networks, which is a property of scale-free networks. Conversely,
351 the comparison with random networks of the same size (numbers of nodes and links)
352 revealed properties of small-world networks: markedly higher values of the clustering
353 coefficients in our networks than in random networks, whereas the average path lengths
354 were similar.

355 In small-world networks, low average path length values are indicative of a higher
356 propagation speed of a disease (Shirley & Rushton, 2005). This could be the case in
357 Ecuador if a FMD serotype/topotype not covered by the vaccines being currently used
358 were to be introduced. Furthermore, we found that more than 90% of the parishes were
359 included in the largest strong (LSC) and weak (LWC) components.

360 Transmissible cattle diseases such as foot and mouth disease can spread rapidly over
361 practically the whole network (Gábor Csárdi & Tamas Nepusz, 2005), and the size of the
362 largest components of trade networks could be considered helpful for analyzing the
363 maximal extent of an epidemic: Kao et al. (2006) proposed that the size of the LSC is an
364 estimate of the lower bound of the maximum epidemic size, while the size of the LWC is
365 an estimate of its upper bound. However, the size of the LSC might not be the best

366 measure to estimate the maximal size of an epidemic, since there should be a path formed
367 by movements in the network leading back to the farm source of infection, and an
368 epidemic does not follow this rule (Dubé C. et al., 2011). In the same way, the LWC
369 requires that the relationships between nodes are assumed to be reciprocal (Dubé et al.,
370 2009). Moreover, as highlighted by Rautureau et al (2010), when building the networks,
371 movements between pairs of nodes are aggregated and their chronology is not taken into
372 account. In any case, size and geographical extent of largest components represent a
373 structural risk that should be considered when designing measures to mitigate an
374 emerging disease spread.

375 All the built networks were disassortative (negative values) meaning that the parishes had
376 more often links with parishes with a different degree. This finding can be explained by
377 the fact that parishes with markets receive animals from many parishes without markets.
378 Parishes with markets had higher degrees as well as higher betweenness, which are both
379 centrality network indicators, which indicates that the veterinary authorities should
380 improve surveillance of diseases along the market path for the early detection and
381 reporting should outbreak of infectious disease occur within the local livestock sector.
382 Targeting nodes with high centrality values may allow implementing efficient measures
383 of disease control and surveillance. However, neither of the two approaches we
384 implemented to conduct percolation analyses (removal of nodes having higher degrees
385 (parishes with markets) or higher betweenness broke the LSC unless a large proportion
386 of nodes had been removed. This result could be explained by the fact that the networks
387 we studied were not developed from free-scale properties. Indeed, in previous studies,
388 percolation analyses using centrality indicators to remove nodes have been effective when
389 holdings where the nodes and networks were scale-free. This was the case for livestock
390 networks in France (removing 1% or 5% of premises achieved to break the LSC (Dutta

391 et al., 2014; Rautureau et al., 2010), Italy (Bajardi et al., 2011), Germany (Büttner, 2013),
392 and England (Kiss et al., 2006).

393 Finally, besides low average path length values, the higher values of the clustering
394 coefficients we observed in our networks is a property of small-world networks, which
395 implies that an endemic infection such as brucellosis in Ecuador would spread within
396 local clusters. We also found that the first six largest communities were spatially
397 distributed in the same zones for all the annual networks indicating that movements within
398 these regions are more frequent. This finding, as well as high reciprocity values and
399 stability of nodes and links in time, suggest that brucellosis may be spreading locally
400 within those communities through cattle movements and that the transmission could be
401 sustained in time. Unlike Colombia (a neighboring country), where vaccination against
402 brucellosis and the certificate of movement of animals is mandatory throughout its
403 territory (Avila-Granados et al., 2019), these measures have not yet been implemented in
404 Ecuador. The identification of communities may allow the development of control
405 strategies through zoning and compartmentalization by subdividing into sectors where
406 movements are more frequent (OIE, 2019) and could facilitate implementing a brucellosis
407 control program in Ecuador. Some experiences could be implemented in those
408 communities according to their characteristics. For example, it has been possible to face
409 zoonotic and high-priority diseases through the active participation of producers and key
410 decision-making groups (Azhar et al., 2010).

411 Since livestock trade connects practically the whole country and a contagious disease
412 could reach the whole territory, strategies such as compulsory vaccination and movement
413 control of cattle should be implemented as it was the case for FMD. In the case of
414 brucellosis, it should also be considered to include the issuing of vaccination certificates
415 as a requirement for trading cattle.

416 This work has allowed us to understand how two diseases, one of rapid diffusion and the
417 other of slow diffusion, could spread through the movement of cattle on a parish scale in
418 Ecuador. However, we still have to understand if the results we obtained remain valid
419 when the movements are analyzed on a smaller scale, that is, between farms.

420 **CONCLUSIONS**

421 Our analysis showed that cattle movement network in Ecuador using parishes as nodes
422 had properties of small-world networks, both for all cattle and only cows. These
423 properties may allow a fast spread of an epidemic disease such as FMD throughout the
424 country and also favor the local transmission of an endemic disease such as brucellosis.
425 They should be taken into account by the veterinary services when considering preventing
426 measures in the case of an emerging disease or control measures for endemic diseases.

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430

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639 Tables

640 Table 1. Number of cattle and cattle farms recorded in Ecuador in 2017 and 2018

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643 Table 3. Descriptive parameters and indicators for the global and cow networks in
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649 Figure 1. Ecuadorian geographic regions and location for the 63 animal markets present
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660 Figure 6. Monthly network indicators for the global and cow networks in Ecuador in
661 2017 and 2018

662 S1 Appendix. Degree distribution for the global and cow networks in Ecuador in 2017
663 and 2018

664 S2 Appendix. First six largest communities for the global and cow networks in Ecuador
665 in 2017 and 2018

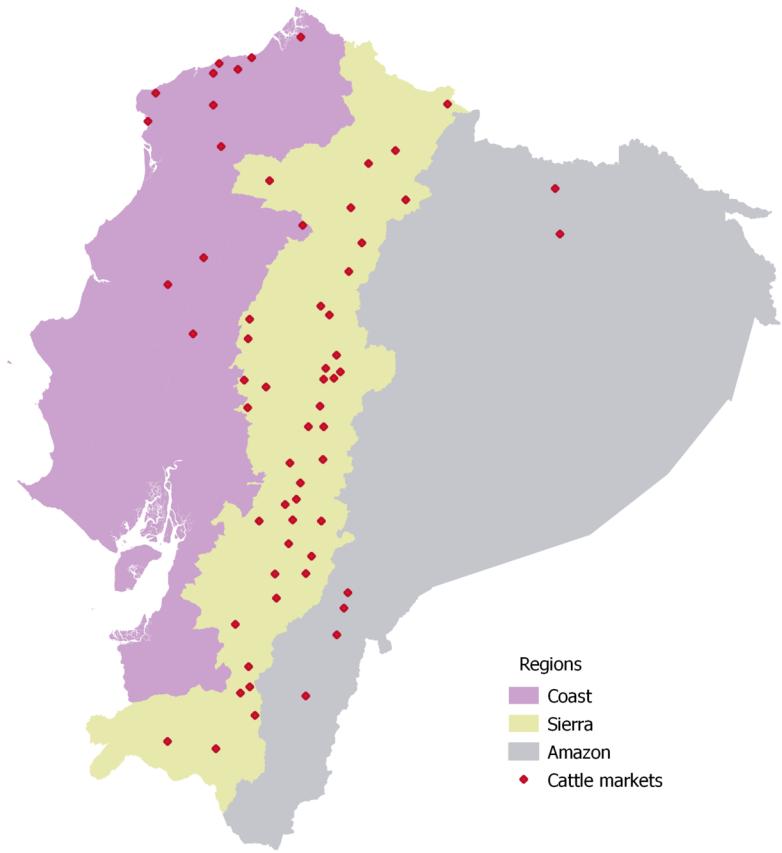
666 S3 Appendix. Jaccard index for the monthly global and cow networks in Ecuador in
667 2017 and 2018

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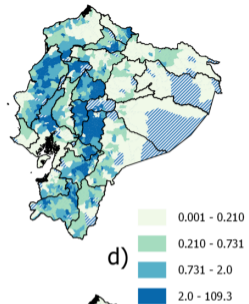
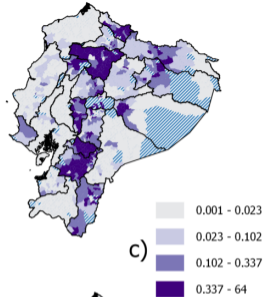
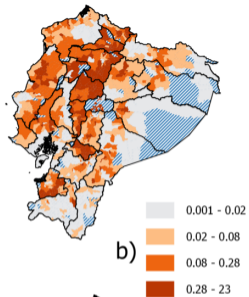
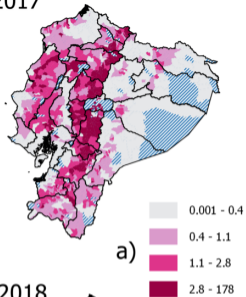
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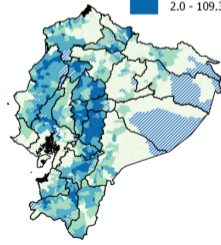
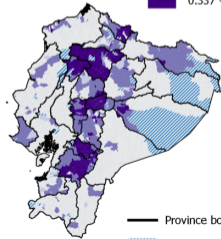
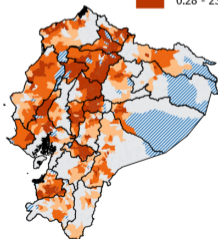
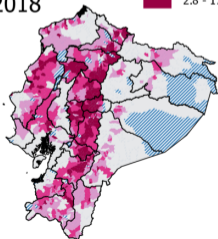
Regions

- Coast
- Sierra
- Amazon
- Cattle markets

2017

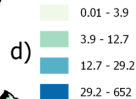
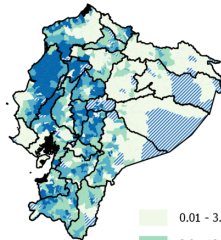
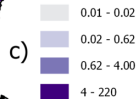
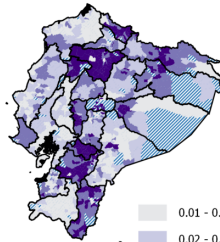
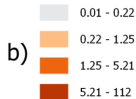
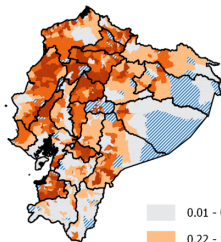
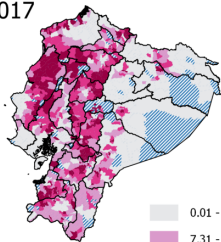


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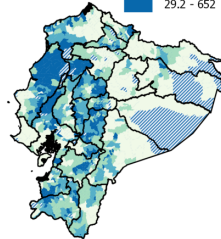
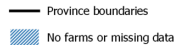
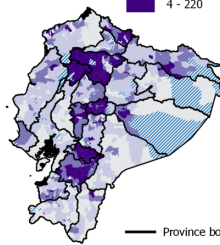
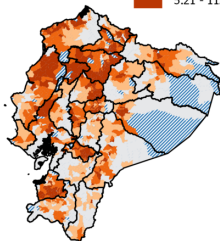
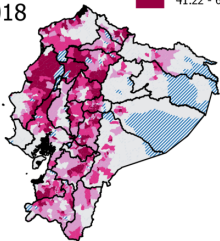


— Province boundaries
No farms or missing data

2017



2018



Largest strong component

Largest weak component

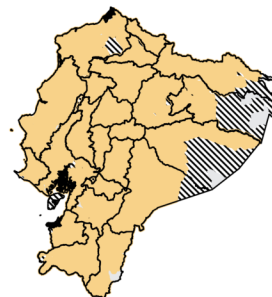
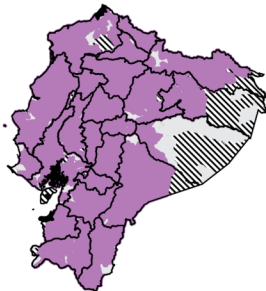
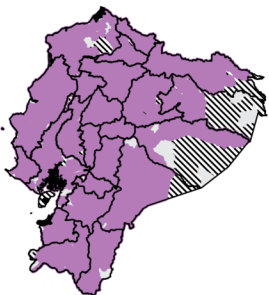
Global network

Cow network

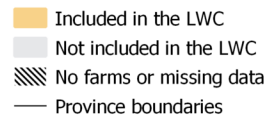
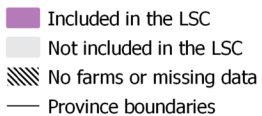
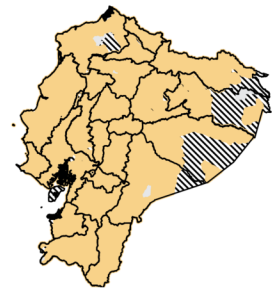
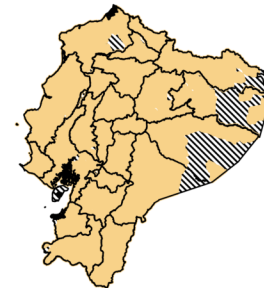
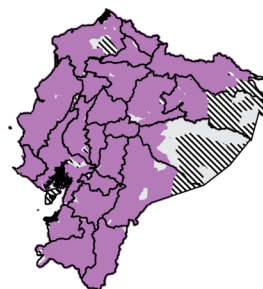
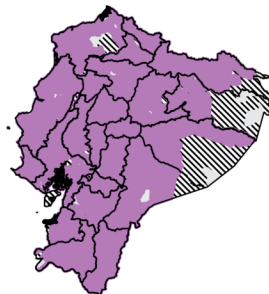
Global network

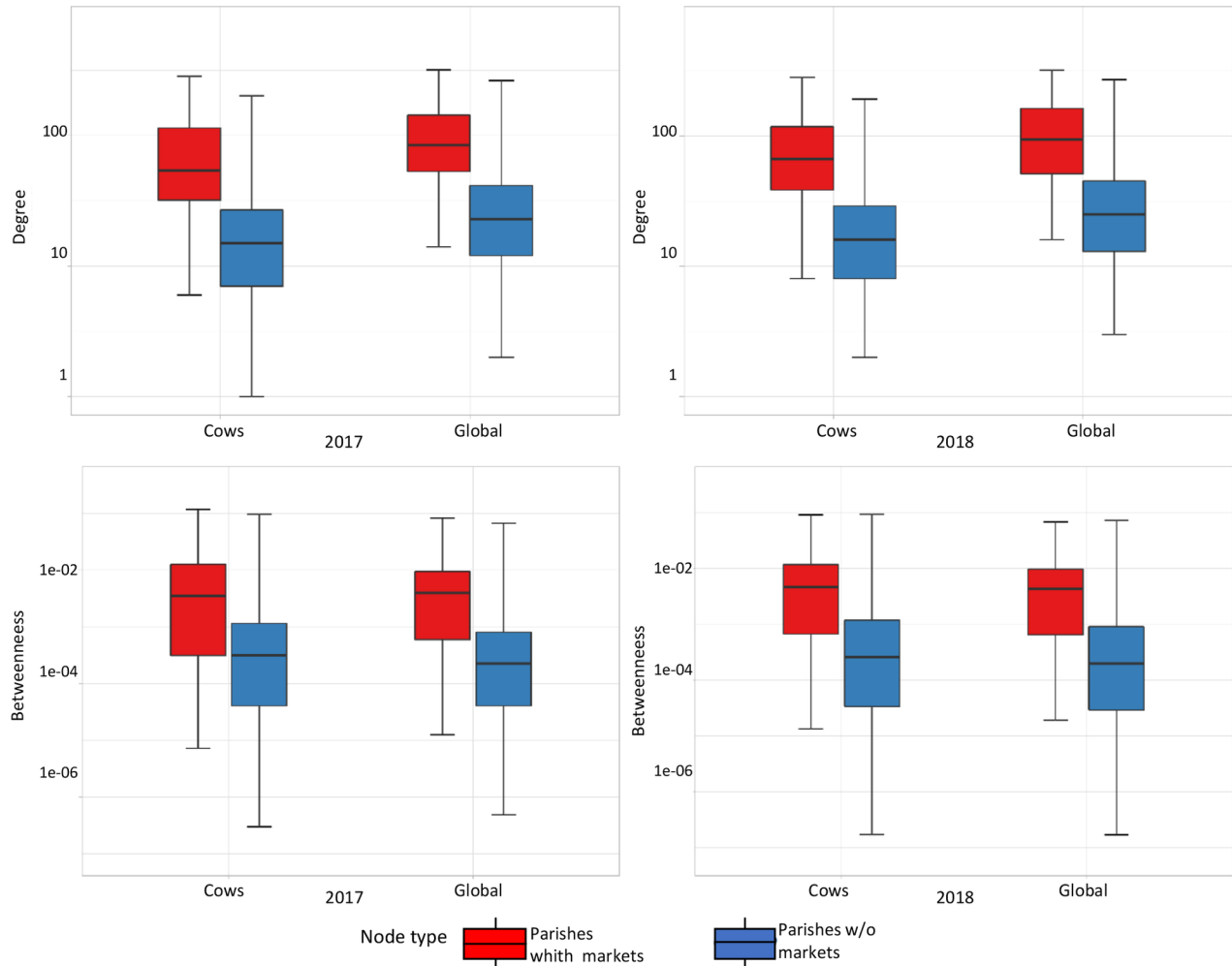
Cow network

2017

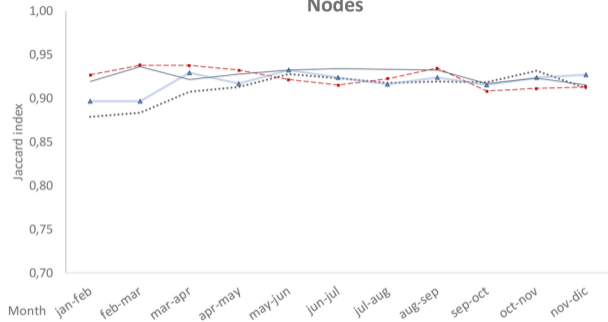


2018

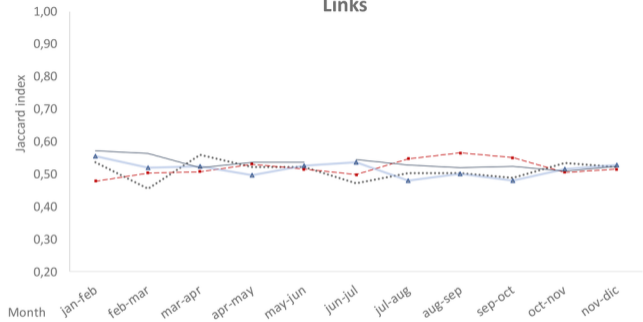




Nodes



Links



..... Global network 2017 - - - Global network 2018
 -▲- Cow network 2017 — Cow network 2018

Table 1. Number of cattle and cattle farms recorded in Ecuador in 2017 and 2018

Category	Cattle farms (% total)		Number of cattle (% total)	
	2017	2018	2017	2018
Dairy	46,645 (17 %)	45,177 (17%)	620,894 (15%)	590,351 (14%)
Beef	33,604 (13%)	33,848 (13%)	546,682 (13%)	591,439 (14%)
Mixed	190,912 (70%)	187,507 (70%)	3,107,915 (72%)	2,994,836 (72%)
Total	271,161	266,532	4,315,229	4,176,626

Table 2. Summary of cattle trade movements within and between parishes for all cattle (including cows) and only cows in Ecuador in 2017 and 2018

Unit	Year	Destination Origin	Number of movements (% within parish)				Number of moved cattle (% within parish)			
			Farm	Market	Slaughterhouse	Total	Farm	Market	Slaughterhouse	Total
All cattle	2017	Farm	104,622 (30%)	353,348 (19%)	217,682 (32%)	675,652 (25%)	725,026 (26%)	1,188,223 (16%)	719,083 (18%)	2,632,332 (19%)
		Market	190,843 (17%)	23,665 (18%)	62,812 (24%)	277,320 (18%)	794,797 (15%)	82,750 (15%)	345,714 (19%)	1,223,261 (16%)
		Total	295,465 (22%)	377,013 (19%)	280,494 (30%)	952,972 (23%)	1,519,823 (21%)	1,270,973 (16%)	1,064,797 (18%)	3,855,593 (19%)
	2018	Farm	106,660 (28%)	367,955 (20%)	200,053 (29%)	674,668 (24%)	676,415 (25%)	1,202,638 (17%)	662,087 (16%)	2,541,140 (19%)
		Market	203,470 (17%)	20,425 (16%)	64,327 (24%)	288,222 (18%)	873,933 (15%)	73,332 (15%)	326,512 (19%)	1,273,777 (16%)
		Total	310,130 (20%)	388,380 (19%)	264,380 (28%)	962,890 (22%)	1,550,348 (19%)	1,275,970 (17%)	988,599 (17%)	3,814,917 (18%)
Cows	2017	Farm	50,579 (32%)	162,881 (18%)	103,071 (33%)	316,531 (25%)	361,250 (29%)	583,219 (15%)	363,459 (20%)	1,307,928 (21%)
		Market	81,998 (16%)	9,820 (14%)	33,104 (24%)	124,992 (18%)	327,193 (15%)	31,189 (11%)	214,000 (22%)	572,382 (17%)
		Total	132,577 (22%)	172,701 (18%)	136,175 (31%)	441,453 (23%)	688,443 (22%)	614,408 (15%)	577,459 (21%)	1,880,310 (20%)
	2018	Farm	49,680 (30%)	169,137 (18%)	93,736 (29%)	312,553 (23%)	311,543 (30%)	589,387 (15%)	319,762 (18%)	1,220,692 (21%)
		Market	85,489 (16%)	9,103 (12%)	34,306 (24%)	128,898 (18%)	353,414 (14%)	30,200 (10%)	204,449 (22%)	588,063 (15%)
		Total	135,169 (21%)	178,240 (18%)	128,042 (28%)	441,451 (22%)	664,957 (22%)	619,587 (15%)	524,211 (21%)	1,808,755 (19%)

Table 3. Descriptive parameters and indicators for the global and cow networks in Ecuador in 2017 and 2018

Year	Global network		Cow network	
	2017	2018	2017	2018
Number of nodes	940	943	924	913
Number of links	17473	19261	11496	12526
Diameter	6	6	8	8
Density	0.02	0.022	0.013	0.015
Average degree	37.2	40.9	24.9	27.4
Reciprocity	0.39	0.39	0.38	0.39
Clustering coefficient	0.24	0.25	0.23	0.24
Average betweenness	0.0018	0.0018	0.0021	0.0021
Average path length	2.76	2.74	3.15	3.07
Assortativity	-0.15	-0.14	-0.17	-0.17
Strong components number	63	3941	90	6059
Largest strong component size (% nodes)	878 (93%)	905 (96%)	835 (90%)	855 (93%)
Average closeness for nodes of the largest strong component	0.37	0.37	0.33	0.33
Weak components number	1	1	1	1
Largest weak component size (% nodes)	940 (100%)	943 (100%)	924 (100%)	913 (100%)
Number of communities	302	253	16	15
Sizes of the first six communities	261 214 170 136 90 44	212 184 161 118 139 139 118 71	226 200 103 99 96 56	224 181 124 108 103 88

Table 4. Percolation results based on the removal of nodes having the highest betweenness centrality, applying a 10% threshold size of the largest strong component for the global and cow networks in Ecuador in 2017 and 2018

Year	Global network		Cow network	
	2017	2018	2017	2018
No initial nodes	940	943	924	913
No removed nodes (% of initial nodes)	263 (64%)	278 (62%)	191 (69%)	208 (69%)
No removed nodes having markets (% of removed nodes / % of nodes with markets)	45 (17% / 71%)	45 (16% / 71%)	42 (22% / 67%)	45 (22% / 71%)