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Network analysis of pig movements in Argentina: Identification of key farms in the spread of infectious diseases and their biosecurity levels

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Summary

This study uses network analysis to evaluate how swine movements in Argentina could contribute to disease spread. Movement data for the 2014-2017 period were obtained from Argentina's online livestock traceability registry and categorized as follows: animals of high genetic value sent to other farms, animals to or from markets, animals sent to finisher operations and slaughterhouse. A network analysis was carried out considering the first three movement types. First, descriptive, centrality and cohesion measures were calculated for each movement type and year. Next, to determine if networks had a small-world topology, these were compared with the results from random Erdös–Rényi network simulations. Then, the basic reproductive number (R_0) of the genetic network, the group of farms with higher potential for disease spread standing at the top of the production chain, was calculated to identify farms acting as super-spreaders. Finally, their external biosecurity scores were evaluated. The genetic network in Argentina presented a scale-free and small world topology. Thus, we estimate that disease spread would be fast, preferably to highly connected nodes and with little chances of being contained. Throughout the study, 31 farms were identified as super-spreaders in the genetic network for all years, while other 55 were super-spreaders at least once, from an average of 1613 farms per year. Interestingly, removal of less than 5% of higher degree and betweenness farms resulted in a >90% reduction of R_0 indicating that few farms have a key role in disease spread. When biosecurity scores of the most relevant super-spreaders were examined, it was evident that many were at risk of introducing and disseminating new pathogens across the whole of Argentina's pig production network. These results highlight the usefulness of establishing targeted surveillance and intervention programs, emphasizing the need for better biosecurity scores in Argentinean swine production units, especially in super-spreader farms.

Key words: network analysis, pig movements, basic reproductive number, biosecurity.

1. Introduction

Animal movements are one of the major means for infectious disease transmission in livestock populations (Fritzemeier *et al*., 2000; Mansley *et al*., 2003, Gilbert *et al*., 2005; Kao *et al*., 2006; Fèvre *et al*., 2006; Ortiz-Pelaez *et al*., 2006). Among other factors, the likelihood of introduction of infectious agents in a farm will be a function of the number of movements in a given time span (Enright and Kao, 2016). Similarly, farms with poor biosecurity scores are especially vulnerable to pathogen introduction (Amass et al., 2004; Dewulf and Immerseel, 2018). Once the agent is introduced, disease spread in a country will largely depend on farms contact network (Thakur et al., 2014; VanderWaal et al., 2018) and the biosecurity measures implemented therein (Gibbens *et al*., 2001). Consequently, restriction of animal movements is usually imposed to limit disease spread (Stärk *et al*., 2006; OIE 2011, Salman *et al*., 2013).

Network analysis has been widely used in veterinary epidemiology to assess and describe the spread of infectious diseases based on the interactions among farms or individuals (Keeling and Eames, 2005; Hanneman and Riddle, 2005; Martinez-Lopez *et al*, 2009; Nöremark *et al*, 2011; Dorjee *et al*, 2013; Thakur *et al*, 2014; Lentz *et al*, 2016; Marquetoux *et al*., 2016, Salines *et al*, 2017). Farms that are central in the flow of animal movement´s because of their large number of trading partners have an important role in the spread of diseases (Dubé *et al*., 2009). Therefore, a good understanding of animal movements is necessary to develop rational and targeted interventions to limit disease spread (Nugent and McLeod, 2004*;* Frössling *et al*., 2012). Furthermore, a small fraction of the population might contribute disproportionately to the spread of an infectious disease. Woolhouse *et al.,* (1997) formulated the empirical 80/20 rule according to which 20% of the population contributes to 80% of transmission events. Those individuals in the 20% are called super-spreaders (Keeling and Eames, 2005). The same occurs when transmission is considered not between individuals of a population but between discrete populations in an area, for example, between herds (Woolhouse *et al*., 2005; Volkova *et al*., 2010). Taking this feature into account may be useful for the development of targeted intervention strategies such as the improvement of biosecurity or surveillance measures upon the incursion of an exotic disease in the country (Frössling *et al*., 2012). This is especially relevant for Argentina's pig industry whose steady growth over the past decade partly owes to the country's free status for most major livestock diseases (Monterubbianesi *et al*., 2016, Carpinetti *et al*., 2017; OIE, 2018).

In countries with such competitive advantage, the introduction and potential spread of a new pathogen —particularly one of easy transmission and dissemination— can have catastrophic consequences. Adopting preventive measures against the occurrence and spread of infectious agents along with surveillance systems for early detection of exotic diseases and possible contingency plans is paramount.

Pig farming in Argentina totals to 962,881 commercial productive sows distributed in 16,408 farms. Producers that raise pigs for their own consumption are called non-commercial producers while those selling pigs (to other farms or slaughterhouses) are referred to as commercial producers and are assigned an identification number (called RENSPA) in an electronic registry. Nearly 1,922 commercial pig farms have more than 100 sows, 1,935 have between 50 to 100 sows and 12,325 have between 10 to 50 sows (National Food Safety and Quality Service**,** 2016). Argentina's commercial productive chain is best described as a pyramid structure (Figure_S1_SuppInfo) where officially registered suppliers of animals of high genetic value (gilts, sows or boars) and semen collection centers (boar nucleus) stand at the top. Gilt suppliers serve farrow-to-finish and farrow-to-weaning, and, besides these, there are finishing farms that receive weaners or growers or cull sows (7 kg or more) from different origins and raise them until they reach market weight (ca. 110-120 kg). All commercial farms send animals to slaughterhouses and occasionally they may also send animals to fairs or markets (Iglesias and Ghezan, 2013). The 56.97% (1,095/1,922) of farms are farrow-to-finish, only 1.14% (22/1922) are farrow-to-weaning and there are 41.88% (805/1,922) finishers farms, but there are no farms integrating these two.

At present, in Argentina, all livestock movements are electronically recorded by the National Food Safety and Quality Service (SENASA) using an online integrated information management system for animal health (SIGSA) which centralizes each farm's health information (e.g. animal category, owner, location, commercial inventories, incoming and outgoing animal movements and health record). Each farm is identified with a RENSPA number used to track movements in SIGSA. The only restriction on movements between farms is that of transporting live pigs from Aujeszky's disease-positive farms to negative establishments. However, this program is aimed at farms with more than 100 sows. Thus, compliance with this regulation does not apply to farms with fewer (SENASA, 2009). Despite that, all animal movements must be registered in the electronic system; SIGSA (SENASA, 2017).

The purpose of our study was to characterize the network of commercial pig population movements in Argentina for a better understanding of potential disease spread together with the identification of super-spreader farms for targeted control and surveillance measures. The biosecurity level of those super-spreaders was evaluated in relation to their role in the transmission of diseases through animal movements.

2. Materials and Methods:

2.1. Type of movements.

Taking into account different risk sources for disease transmission posed by different animal categories such as breeders, weaners, etc. (Pileri and Mateu, 2016, Dunowska, 2018), their destination (e.g. movements to other farms *versus* movements to slaughterhouses) (Fèvre *et al*, 2006; Kao *et al*, 2007) and the pig production chain in Argentina, the following movement types were distinguished:

1) **Animals of high genetic value (Genetic network)**: movement of high genetic merit animals (gilts, sows and boars) from an officially registered supplier to a farm whose destination is other farm, for example: a farrow-to-finish or farrow-to-weaning farm, but neither a slaughterhouse, a fair/market nor a finishing farm.

2) **Markets:** movements whose departure or destination holding is a fair/market, regardless of the category of transported animals (sows, boars, gilts, etc.).

3) **Finishers**: Movements whose destination is a finishing farm.

4) **Slaughterhouse**: movements whose destination is a slaughterhouse, registered as such in the National Sanitary Registry of Agricultural Producers (RENSPA).

According to Argentinean regulations, movements between establishments having different RENSPA identification numbers must be recorded, even when involving animals from the same origin (for example between a site 2 and a site 3) (SENASA, 2014). Given the distances between different sites of the same farm, sometimes movements from a nursery to a fattening unit are required to be registered. These movements (2.89%) where the origin and destination were the same farm were excluded from the network, since no mixing with animals from another origin took place and, in practical terms, pigs never abandoned the same farm.

2.2 Data collection

To analyze pig movements from 2014 to 2017, we accessed SIGSA and downloaded the total number of movement control forms (called DT-e) corresponding to this period, their source and target RENSPAs, animal category and number of animals moved (SENASA, 2017).

Pending (procedure initiated, movement not made) or expired animal DT-es (unconfirmed movement at destination unit upon 5 days DT-e was issued) were discarded 1.93% (10,305/534,255). Additionally, 86 registered movements with obvious errors (unlikely number of animals transported in a single truck, etc.) for the 2014-2017 period were discarded. However, this represented a low number of entries (86 out of 523,950 registered movements).

2.3 Network analysis

Directed networks for genetic, market and finishing movements were built for each year (2014-2017). In these unimodal networks, nodes represented either a farm or a market and edges represented the pig movements among them. The slaughter network was excluded because it posed a minor risk for farm-to-farm disease spread.

We calculated different descriptors at network level for each year and movement type such as graph diameter, average path length, reciprocity, clustering coefficient and modularity. Then, we determined the main cohesive blocks and the giant strongly and weakly connected components in each graph. In addition, based on centrality measures at node level, we calculated weighted and unweighted out and in-degree and betweenness, as these values and those previously mentioned usually correlate with the probability of infectious disease introduction or spread and the size of the epidemic (Christley *et al.*, 2005; Kao *et al.*, 2006). The variable to generate the weighted measures was the number of animals involved in each movement. Table_S1_SuppInfo includes the definition of the different network measures used in the analysis. Spearman correlation between the in- and out-degree was also calculated for each year and movement type, in order to assess the relation between the number of contacts in and out of the nodes. Data were analyzed using the *iGraph* package (Csárdi and Nepusz, 2006) within R environment (R development Core Team, 2014).

Degree distribution of the genetic, finisher and market networks in the last year (2017) were analyzed to determine if they fitted a power-law distribution. This allowed for the identification of super-spreaders in those populations, that is, nodes accounting for most of the contacts and therefore making a major contribution to disease spread. In a power-law distribution, it is generally assumed that P(X=x) is proportional to x^{-alpha}, where x is a positive number and α is greater than 1. In many real-world cases, the power-law behavior kicks in only above a threshold value x_{min}. This was done following the guidelines proposed by Clauset *et al.*, 2009. This approach combines maximum-likelihood fitting methods with goodness-of-fit tests on the Kolmogorov-Smirnov statistic and likelihood ratios. The cut-off value (Xmin) and the value of alpha for a given x_{min} were estimated by conducting a hypothesis test to establish whether the observed distribution fitted a power-law. The package used was *powerRlaw* (Colin and Gillespie, 2015) within R environment (R development Core Team, 2014).

Furthermore, average path lengths and clustering coefficients from the observed networks were compared with the confidence interval (percentiles 2.5 and 97.5) for the same descriptors obtained from 10,000 Erdös–Rényi (1960) network simulations. The method simulates a network with random connections whose nodes and edges were of the same size as those in our study. If the clustering coefficients of the random network were smaller than those of the original calculation and the average path lengths were longer, networks were said to satisfy a small-world topology (Newman, 2000; Marquetoux *et al.*, 2016).

2.4. Effect of network properties on the basic reproduction number (R_0)

We followed Volkova *et al.*, 2010 and Woolhouse *et al.*, 2005 to estimate the basic reproduction number (R_0) of the genetic network. This methodology is based on the fact that the heterogeneity in contact patterns enhances the transmission of infectious diseases through the network and estimates R_0 by taking into account the average in- and out-degree and the variance and covariance of the contact rates. The centrality measures used were unweighted in order to explore potential spread of a highly transmissible disease in the network (Volkova *et al*., 2010). To evaluate the impact of targeted interventions on super-spreaders in disease transmission we used the approach proposed by Marquetoux *et al*., 2016. Genetic farms were listed in a descending order according to the total degree and betweenness values. Successive simulations were carried out, removing farms one by one, starting from those with the highest degree values. For each simulation, a ratio between the R_0 of the network after removing one or more farms and the total network's R_0 without farms removed was calculated. Therefore, the ratio represented the fraction of the total R_0 contributed by each farm or group of farms removed. The same procedure was repeated based on betweenness values. Then, farms which contributed to a 90% R_0 reduction value were identified in each network, according to any of the two removal criteria (total degree or betweenness). When this calculation was done for each of the four years studied, it was possible to identify what farms in the genetic network acted as super-spreaders all throughout the study. The calculation was not done for finishers because these farms send animals to slaughterhouses or other finishers and, as result, their incidence in disease spread is much lower.

2.5. Targeted interventions: biosecurity in farms with a dominant role in disease spread

The biosecurity score of those farms that contributed to a 90% of R_0 reduction in the genetic network was extracted from Alarcón *et al*., 2019. In that study, a score named 'risk reduction percentage' was calculated for each genetic farm. Briefly, that was the ratio between the summary of all the biosecurity measures implemented in the farm at that time versus an ideal situation (i.e., the implementation of all different biosecurity measures). Percentage values lower than 95% imply that the adopted biosecurity measures in the farm are not optimal and that there is room for improvement. Further details about the methodology to calculate these scores can be found in Allepuz *et al*., 2018 and Alarcón *et al*., 2019. In our study, the risk reduction percentage score was plotted against the order in which the different nodes were removed in the above-mentioned analysis. Then, for farms identified as super-spreaders for a given year, the number of farms receiving animals from them and the number of farms supplying them with animals were examined, since the risk of infection raises not only with a higher degree (Christley *et al.*, 2005) but also when breeding pigs come from diverse origins (Dewulf and Immerseel, 2018).

3. Results

3.1. General description of pig productive system in Argentina

A yearly description of the number of pigs and movement records in Argentina is described in Figure 1. Between 2014 and 2017, the total number of pigs increased by 8.0% (5,863,281 vs. 6,375,808 in 2014 and 2017), 9.0% (6,375,808 vs. 7,008,726) and 6.9% (7,008,726 vs. 7,525,613) respectively; whereas movements increased by 6.7% (119,265 vs. 127,826), 7.0% (127,826 vs. 137,398) and 1.4% (137,398 vs. 139,375). Throughout, these four years, an average of 6,693,357 animals and 130,966 movements were officially recorded. Among the latter, 83.6% (109,518/130,966) were to slaughterhouses, 3.3% (4338/130,966) were movements of animals coming from genetic establishments, 3.0% (3928/130,966) were movements to finishing holdings, 2.9% (3782/130,966) were movements of piglets among sites of the same farms and 1.2% (1617/130,966) were movements from or to markets. Finally, 5.9% (7784/130,966), average for the four years, of the movements were not classified in any of the networks built because they corresponded to imports (destined to quarantine stations) or exports (animals sent to the border), returns (animals not received at the destination farm) or animals used for research purposes, among other categories.

On average, 5.6 million pigs were slaughtered each year. Of these, 4.9 million came from farrow-to-finish farms and the rest from finishers or genetic farms. From the 110 establishments officially registered as high genetic merit breeder suppliers, 95, 94, 91 and 86 of them moved animals from 2014 to 2017, respectively. These farms contributed to the transportation of animals to 1,546 farms (40,000 gilts, 10,000 sows and 1,500 males) during this period. The discrepancy between the total number of registered genetic farms and those moving animals results from farms being on a temporary cease of operations, change of genetic sources (re-stocking), depopulations, etc.

In the studied period, an average 215 (210 to 219) finishing holdings received animals. Finishers mainly received animals from an average 739 (647 to 783) commercial holdings and only 96 (69 to 134) of the incoming movements were from another finisher farm. Regarding markets, incoming movements were on average 1,543 per year (1,393 to 1,672), but the outgoing movements were only 75 per year (64 to 80), a value that revealed a problem with the official records of the outgoing movements in such markets.

3.2. Networks description of pig movements

Table 1 shows the descriptive and cohesion measures at network level for the year 2017 (other years are shown in Table_S2_SuppInfo). The number of nodes in the genetic network (1444) was higher than in the market (356) and finisher networks (855), whereas density (the fraction of all possible edges realized in the network) was higher in the market (0.011) and finisher networks (0.005) that genetic network (0.002).

As shown by its diameter, the distance between the most separate farms/nodes in the genetic network was six hops, whereas in the market and finisher networks it was only two. The average path length from the different networks ranged from 1.005 (market network) to 1.758 (genetic network) and the clustering coefficient varied from 0 (market network) to 0.071 (genetic).

For the genetic network, the clustering coefficient weighted by the number of moved animals was higher than for the Erdös–Rényi network, 0.0071 in the original vs. percentile (2.5) = 0.001; percentile (97.5) = 0.005 in the random network, but lower for the finisher and market network. In contrast, when the comparison was made using the average path length values of the genetic, finisher and market networks (1.76; 1.12, 1.01), these were shorter than those 2.5 and 97.5 percentiles of the random network (7.86-8.25; 5.11-5.22-4.48-.65). Accordingly, only the genetic network fulfilled the requirements of a small-world topology.

The analysis also revealed the existence of different communities (Table 1, Figure_S2_SuppInfo). Reciprocity was slightly above zero only in the genetic network, indicating a small fraction of bi-directional movements within this population. This last result was also evidenced when we determined the strongly and weakly connected components as well as the modularity from these graphs.

In the present study, the giant strongly connected component (GSCC) comprised almost all the nodes of the genetics network and all the nodes of the market and finishers network (Table 1). This indicated highly unidirectional networks, particularly for the genetic one, which showed the lowest occurrence of reversal links. On the other hand, the weakly giant connected component (GWCC) in the finisher network comprised several components consisting of many nodes of a larger size and higher modularity whereas in the market network values were standard.

Results for degree and betweenness at node level in the network for 2017 (Table 2, Figure_S3_SuppInfo) exhibited a large variation between nodes and highly asymmetrical distributions for each measure. Supplementary Table S3, shows these measures for the rest of the networks (2014-2016). The nodes with the lowest degree had values of 0 or 1, and the maximum of degree values in networks ranged from 299 to 971 in the different years. Unweighted degree ranged from minimums of 1 in the different networks up to maximums of 347 to 971 edges according to network, with a higher preponderance of out edges in the genetic and finisher network compared to markets (Table 2). The Spearman correlation coefficient between the in-degree and the out-degree ranged from -0.2 to -0.7, with clearly no linear relationships. This value was not calculated for the market network because one of the markets concentrated most of the movements, 76.9 % (1,243/1,617), an average for four years. Figure 2 shows the relationship between in-degree and out-degree for the four-year period in the genetic network. Figure_S4_SuppInfo shows a similar graph for the finisher network.

In-degree and out-degree 2017 values at node level were fitted to a power-law distribution model and the tail of the observed distribution satisfied it (exponent alpha values: in-degree/out-degree: genetic network=4.2/1.8, finisher=2.3/2.4, market= 1.6/3.3. X_{min} in-degree/out-degree: genetic network= 9/14, finisher= 31/9, market= 12/10). The goodness-of-fit test via a bootstrapping procedure (Clauset et al, 2009) used for tested the hypothesis of whether the data follows a power-law distribution, performed were unable to reject the null hypothesis (p-values=0.1-0.9) in all cases. Hence, the observed distributions indicated that the power-law model was plausible for all networks.

3.3. Targeted interventions on super-spreaders: carry over effects on potential disease transmission and the relationship with their biosecurity level

The removal of 2.87—4.0% of farms (2014=66/1,637; 2015=51/1,773; 2016=63/1,599 and 2017/1,444=48), out of an average of 1,613/year, from the genetic network allowed for a 90% reduction of the R_0 value in the different years. The set of farms contributing to that 90% were considered as super-spreaders. In total, 86 farms were identified as such in the four-year period studied, 31 of which (2014=31/66 (46.7%), 2015=31/51(60.8%), 2016=31/63 (49.2%) and 2017=31/48 (64.6%)) were super-spreaders every year, 14/86 (16.3%) 3 years, 21/86 (24.4%) 2 years and 20/86 (23.3%) only one. Figure 3 shows R_0 reduction in 2017. In that year, 48 farms were identified as super-spreaders.

To assess the relationship between super-spreader farms biosecurity scores and their contribution to the reduction of R_0, the score for the risk reduction percentage in case of disease introduction was plotted against the order in which farms were removed in the R_0 calculations in 2017 (Figure 4). Interestingly, super-spreaders sent animals to a median of 20 farms with a maximum of 197 destination farms per year, highlighting also a significant difference in the probability of onward transmission among this group (Figure 5). This indicates that the introduction of a transmissible agent in one of those farms would have a huge impact on the spread of infection, as evidenced by the maximum number of infected farms in a possible epidemic in the genetic network, estimated by the Giant Strongly Connected Components, (Table 1).

4. DISCUSSION

This study is the first network analysis of pig movements in Argentina. Data used were downloaded from SENASA's electronic registry and comprised all pig movements from or to commercial holdings in the country, except for a minor proportion of movements destined to a quarantine facility, animals moved for research purposes and undetermined records. Overall, more than 93% of movements were used in the analysis so data is highly representative of Argentina's situation.

Regarding the degree measure, the Spearman correlation coefficients between the in-degree and the out-degree for the genetic and finisher networks were negative, low for the genetic one and negative and high for the other networks. In the case of the genetic network, this indicates that farms would mostly act as spreaders though they can also be recipients of the disease. This is consistent with the swine production structure where gilt producers supply many farms.

In the present case, the genetic network fulfilled all the requirements for being a small-world topology and a scale-free network, in agreement with what other researchers found (Relun *et al*., 2016; Lee *et al*., 2017, Salines *et al*., 2017).

In contrast, the finisher and market networks did not. This apparent contradiction can be explained by the nature of the networks themselves. For finishers, most of the outgoing movements were to slaughterhouses and, in consequence, they were removed from the database (dead-end movement). In the case of the market network, a single market accounted for three quarters of the movements.

The calculation of R_0 and the reduction of this value because of farm removals were only done for the genetic network, since finishers were dead ends regarding transmission. As seen in Figure 3, removal of farms based on degree resulted in a faster decrease of R_0 in agreement with Marquetoux et al., 2016. However, some farms with a very high degree might have a very low betweenness and they would not be recognized as super-spreaders based only on this last node centrality measure. Both measures might be relevant for disease spread, since degree is correlated with the probability of a farm receiving/spreading disease and betweenness with the ability of a farm to link groups of farms. By using both degree and betweenness, a better identification of super-spreaders could be made. For the genetic network, removal of less than 5% of the nodes resulted in a ≥90% reduction of the R_0 indicating the significant role of those farms in disease spread. Moreover, those farms are obvious targets for surveillance, contingency plans and improved biosecurity plans; as the super-spreader biosecurity scores varies between 0.11 to 0.80 (Q1=0.29, Median=0.39, Q3=0.48). Of the total of super-spreader farms identified per year, half of them were the same during the three or four analyzed years. Different reasons can explain this result, for example, some of these farms might have stopped breeding high-genetic merit pigs for commercial purposes to keep them for themselves. We also observed a significant decrease in super-spreader farms during 2017, possibly in association with the economic crisis in the Argentinean pig production sector (El Productor Porcino, 2018), which resulted in the loss of many small and medium-sized pig farms.

The data used in the calculation of the biosecurity score (risk mitigation percentage) were obtained from biosecurity surveys conducted in Argentina by registered veterinarians (Senasa) and a panel of experts held in Argentina, as described in Alarcón *et al.*, 2019. This score presents some limitations, since farmers' answers when being surveyed could be inaccurate. Consequently, 80% of the farmers were contacted by their veterinarians, advisors and laboratories so as to check the data collected. Further details can be found in Allepuz et al., 2018 and Alarcón et al., 2019.

As seen in Figure 4, super-spreaders biosecurity scores in the genetic network can be highly improved. It is important to note that many of those super-spreaders had contact with many different farms. Therefore, if the disease reached those super-spreaders, the epidemic would probably affect most of Argentina's pig production system due to the low biosecurity in most of the commercial pigs' farms of the country (Alarcón *et al*, 2019). Therefore, a targeted plan for motivating all Argentinean farmers, especially super-spreader owners, as regards biosecurity improvement should be a national priority. In addition, targeted surveillance for critical pathogens should focus on those farms. Risk analysis estimating the entry pathways of different pathogens to super-spreaders; as well as an improvement in the biosecurity level of the receiving farms; are also highly needed to reduce the risk of disease spread in the country.

Network analysis has been described as a useful methodology to characterize pigs movements and the impact that the contact structure has on the spread of diseases (Lentz *et al.*, 2016; Schulz *et al.*, 2017; Sterchi *et al.*, 2019) in countries such as Canada (Dorjee *et al.*, 2013; Thakur *et al.*, 2014), the USA (Lee *et al.*, 2017), Germany (Büttner *et al.*, 2015), France (Salines *et al.*, 2017) and Kenya and Uganda (Lichioti *et al.*, 2016). When comparing these studies to our results, we realize that Argentinean networks have a smaller diameter (2-6) than networks in the USA, Canada, France, Germany, Kenya, and Uganda: 9, 3.25, 6 to 20, and 7, respectively. The average path length of Argentina's genetic network is similar to that in France and Canada, but shorter than in the USA, Germany, Kenya and Uganda and the clustering coefficient is similar to that in France but smaller than in the USA and Canada (Lichioti *et al*., 2016, Lee *et al*., 2017, Salines *et al*., 2017). Thus, our networks are smaller yet more rapidly interconnected (1 or 2 movements vs. 3 to 5), despite not being integrated in combined management systems as in leading pig-farming countries. The market network had a higher density than the genetic and finisher network. The data obtained for the latter and degree distribution values in our study were similar to other countries such as Germany and Canada (Thakur et al., 2014).

Following other works' data aggregation methods (Woolhouse *et al*., 2005; Volkova *et al*., 2010; Marquetoux *et al*., 2016), we considered a one-year time span. It could be argued that by using such period we are overestimating the impact of the observed super-spreaders, since most diseases would be detected in the population within less than a year's time of circulation. Other studies analyzed movements monthly or every six months (Lee *et al*., 2017, Salines *et al*., 2017). Yet, as pointed out by Buttner *et al*., 2015, monthly analyses reduce the number of nodes in the network significantly, network fragmentation is higher and indirect contacts are underestimated. Be that as it may, pig movements in Argentina do not show a remarkable seasonal pattern (Dirección Nacional de Producción Ganadera, 2017). Moreover, given the nature of commercial pig production in the country, where practically all farms operate with weekly farrowing batches, the number of movements is distributed evenly throughout the year (an average of 8.3% movements each month with a 0.7% standard deviation). In our opinion, the identification of super-spreaders should not be affected by the time scale chosen.

It is worth noting that outgoing movements from fairs or markets were not being properly recorded by the system, as evidenced by the disproportionately higher number of ingoing movements compared to outgoing. The most likely cause is that outgoing movement DT-e forms were issued, but confirmation of arrival to destination was not registered by the recipient farm. Therefore, the DT-e was considered expired by the system. This emphasizes the need for educating all people involved in the recording of movements and raising awareness on the importance of having accurate data.

As Bigras-Poulin *et al*., 2006, we classified movements following an origin-destination criterion (market, genetic, slaughter) for a better analysis of the different levels in Argentina's pig production pyramid. Within each network (i.e. genetic, finisher and market) all nodes were represented as pertaining to the same class, in order to have unimodal networks for all kind of movements. It is true though that in the market network there are few nodes that do not represent pig farms but markets. Despite that, we did not draw a distinction between nodes because in both cases the number of movements, number of moved animals and origins were similar.

In summary, in this study we identified pig farms with a critical role in disease transmission in Argentina and we examined their biosecurity level. Our findings showed that supers-spreaders were also at risk of introducing diseases due to their limited biosecurity; and although an improvement in the biosecurity of all farms in the country is necessary; are key priority targets for prevention and intervention actions.

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TABLES

Table 1. Network descriptive and cohesion measures according to movement types for 2017.

Networks measures	Genetic	Finisher	Market
Number of nodes	1,444	855	356
Number of edges	3,417	3,238	1,317
Density	0.002	0.005	0.011
Diameter	6	2	2
Average path length	1.758	1.124	1.005
Reciprocity ratio	0.014	0	0
Clustering Coefficient or Transitivity	0.007	0.001	0
Number of cohesive blocks (Communties)	185	105	22
Giant Weakly connected components (GWC)	16	99	16
Giant Strongly connected components (GSC)	1435	855	356
Modularity	0.040	0.663	0.197

Table 2. Summary of distributional aspects (minimum, quartiles, median and maximum) for four main centrality measures (i.e. total, in- and out-degree, and betweenness) at node level for each movement-type of networks. For each column, the value at the right is unweighted and the value after the dash is weighted by the number of animals (year 2017).

	Genetic network					**Finishers network**					**Market network**				
	Min	**Q1**	**Median**	**Q3**	**Max**	**Min**	**Q1**	**Median**	**Q3**	**Max**	**Min**	**Q1**	**Median**	**Q3**	**Max**
Total degree	1/1	1/4	2/12	4/33	347/4719	1/1	1/23	2/71	6/293	386/67200	1/1	1/13	2/40	6/127	971/27268
In degree	0/0	1/3	2/11	3/30	46/2760	0/0	0/0	0/0	1/1	386/67200	0/0	0/0	0/0	0/0	971/27268
Out degree	0/0	0/0	0/0	0/0	330/4029	0/0	1/2	1/30	4/116	110/67200	0/0	1/3	1/25.5	5/100	32/1464
Betweenness	0/0	0/0	0/0	0/0	719/3.5x10^{-4}	0/0	0/0	0/0	0/0	71/9.7x10^{-5}	0/0	0/0	0/0	0/0	2/1.5x10^{-5}/

FIGURE LEGENDS

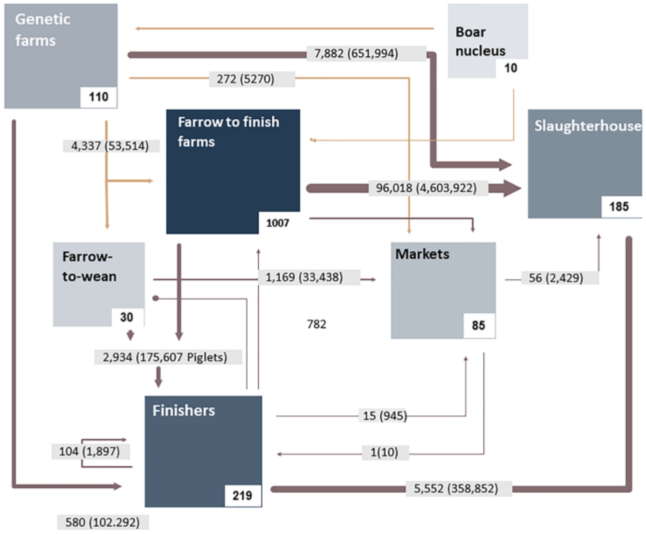
Figure 1. Diagram of commercial pig movements in Argentina, in 2017. Each element of the pig chain (suppliers of animals of high genetic value, farrow-to-finish farms, finishers, etc.) is represented by a shadowed square with an indication of the number of farms or locations (white box). Movements between two elements of the chain are represented by lines. The thickness of the line is proportional to the number of transported animals. For each line, two values are shown: the first indicates the number of movements between two elements of the pig chain (from location *a* to location *b*); the second -between parentheses- indicates the number of transported pigs. Lines with a dot indicate breeders' flow (female or male).

Figure 2. Scatterplot of the unweighted in-degree versus the unweighted out-degree for the genetic network. The year of each network is indicated above the plot. Spearman correlation coefficient (2014 to 2017): -0.07, -0.11, -0.13 and -0.16).

Figure 3. Impact of targeted removal of farms on R_0 value expressed in relative terms (reduced network/full network) based on two potential spread measures: unweighted total degree (blue) and unweighted betweenness (red) in descending order (from higher to lower degree or betweenness) for genetic farms in 2017.

Figure 4. Distribution of farms contributing to a 90% reduction of R_0 in the genetic network. The Y-axis represents the order in which farms in the network were removed, from the first to the one that reached a 90% reduction of the R_0. The X-axis represents the percentage of risk mitigation for introduction of a disease attributable to biosecurity measures.

Figure 5. Aggregated in-degree and out-degree for super-spreaders. Each graph depicts the number of farms sending animals to super-spreaders in a given year (in-degree) and the number of farms that super-spreaders of genetic networks send animals to (out-degree).



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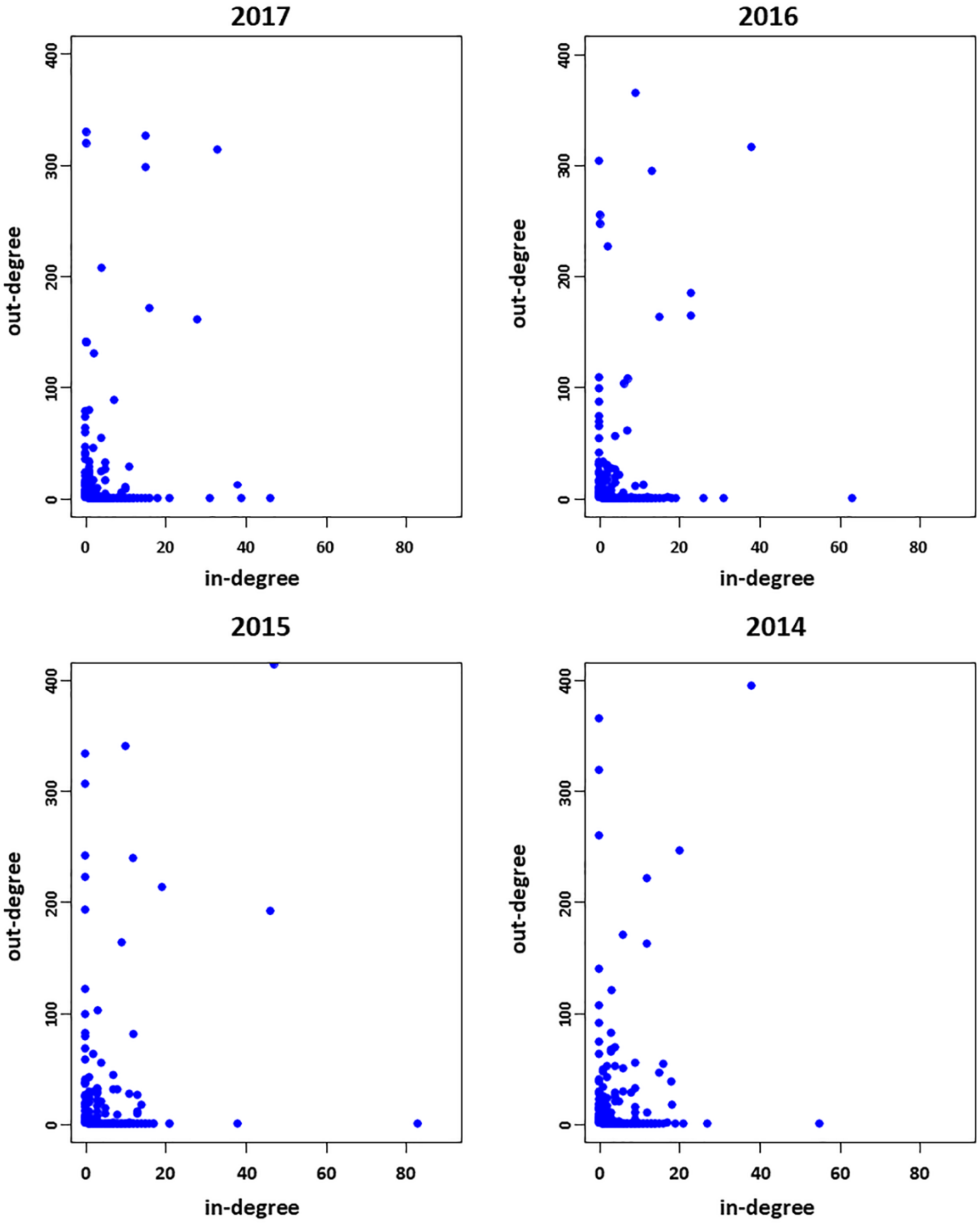

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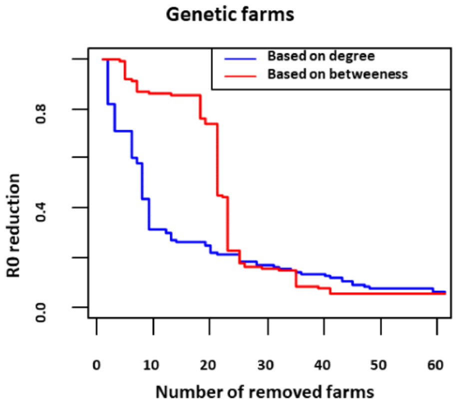

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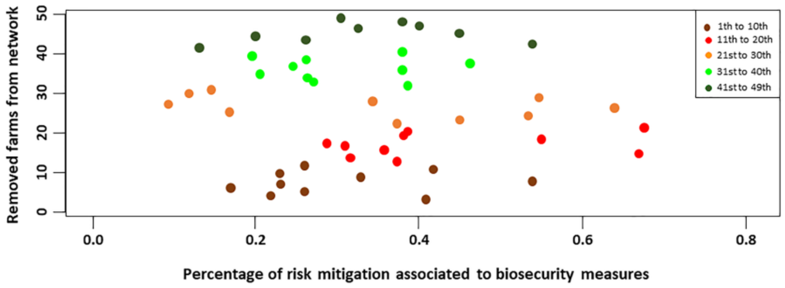

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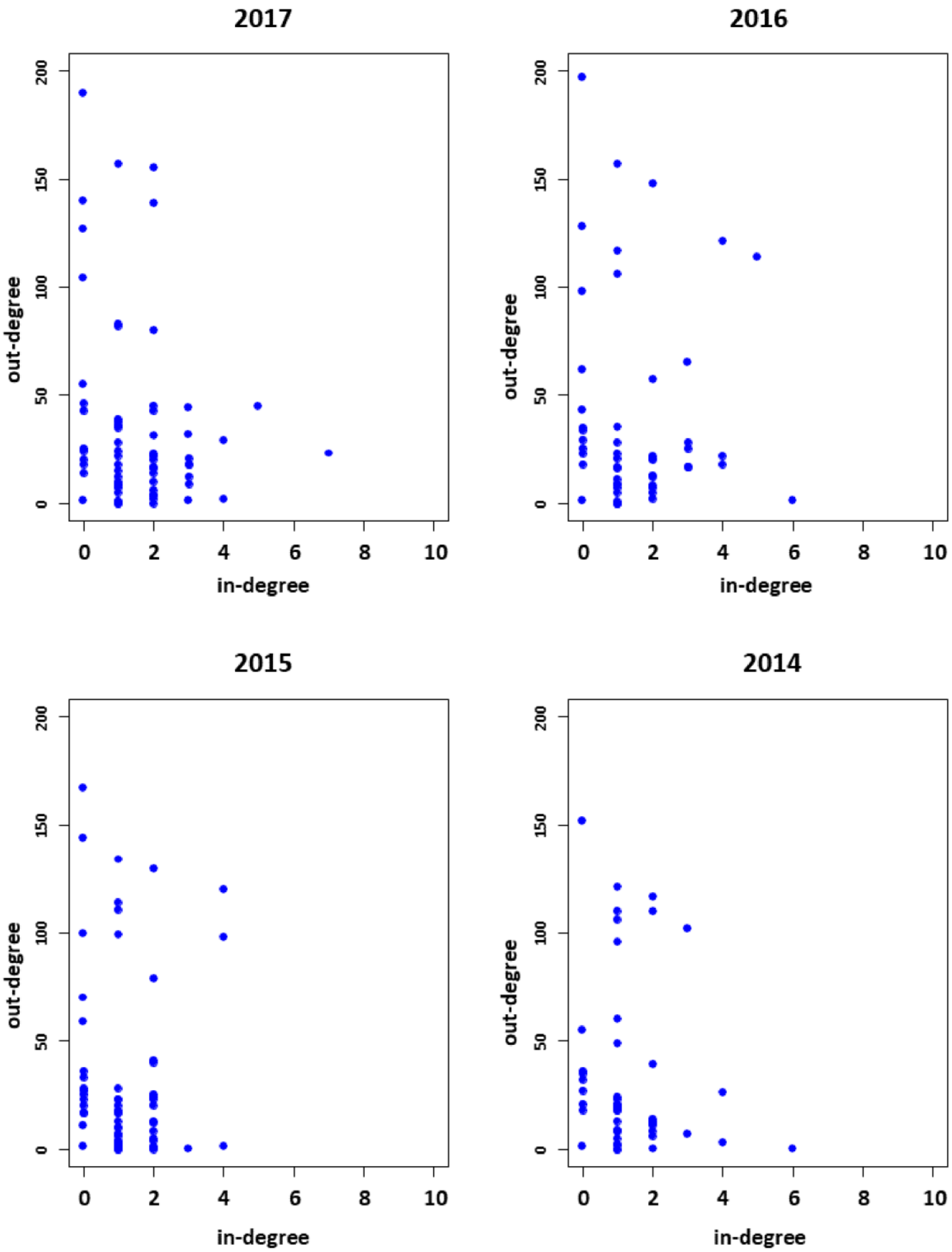

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