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# Unravelling direct and indirect contact patterns between duck farms in France and their association with the 2016–2017 epidemic of Highly Pathogenic Avian Influenza (H5N8)

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## ABSTRACT

Live animal movements generate direct contacts (via the exchange of live animals) and indirect contacts (via the transit of transport vehicles) between farms, which can contribute to the spread of pathogens. However, most analyses focus solely on direct contacts and can therefore underestimate the contribution of live animal movements in the spread of infectious diseases. Here, we used French live duck movement data (2016–2018) from one of the largest transport companies to compare direct and indirect contact patterns between duck farms and evaluate how these patterns were associated with the French 2016–2017 epidemic of highly pathogenic avian influenza H5N8. A total number of 614 farms were included in the study, and two directed networks were generated: the animal introduction network (exchange of live ducks) and the transit network (transit of transport vehicles). Following descriptive analyses, these two networks were scrutinized in relation to farm infection status during the epidemic. Results showed that farms were substantially more connected in the transit network than in the animal introduction network and that the transit of transport vehicles generated more opportunities for transmission than the exchange of live animals. We also showed that animal introduction and transit networks' statistics decreased substantially during the epidemic (January–March 2017) compared to non-epidemic periods (January–March 2016 and January–March 2018). We estimated a probability of 33.3 % that a farm exposed to the infection through either of the two live duck movement networks (*i.e.* that was in direct or indirect contact with a farm that was reported as infected in the following seven days) becomes infected within seven days after the contact. However, we also demonstrated that the level of exposure of farms by these two contact patterns was low, leading only to a handful of transmission events through these routes. As a consequence, we showed that live animal movement patterns are efficient transmission routes for HPAI but have been efficiently reduced to limit the spread during the French 2020–2021 epidemic. These results underpin the relevance of studying indirect contacts resulting from the movement of animals to understand their transmission potential and the importance of accounting for both routes when designing disease control strategies.

## 1. Introduction

In 2016–2017, the emergence and spread of highly pathogenic avian influenza (HPAI) H5N8 in Europe resulted in 1,108 poultry outbreaks distributed in 21 countries (Alarcon et al., 2018). With more than 400 farms affected, France was the hardest-hit country in Europe, due to

extensive farm-to-farm spread (Guinat et al., 2018). Control measures implemented during the epidemic included culling of infected flocks, movement bans from/to suspected farms and implementation of protection and surveillance zones (3 km and 10 km around infected farms, respectively) in accordance to French and EU regulations (DGAL, 2008; The European Commission, 2019). These measures were reinforced on

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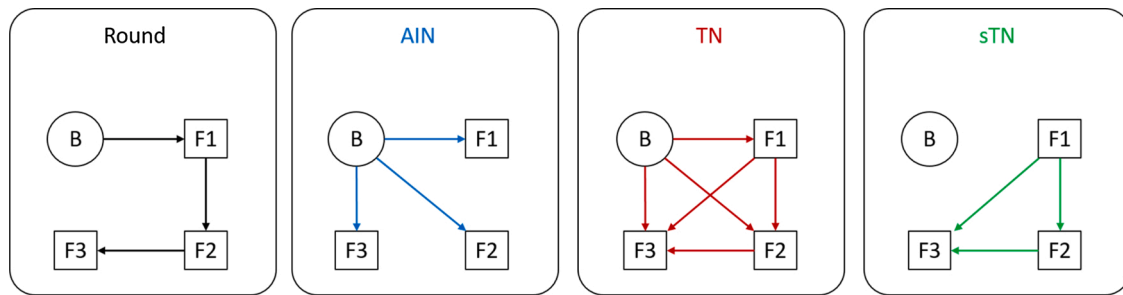
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**Fig. 1.** Illustration of the reconstruction of the different directed networks (AIN: animal introduction network; TN: transit network; sTN: specific transit network) based on a single round. B: breeding farm, FX: fattening farm, with “X” indicating the order in the round (e.g., F1 = first fattening farm visited during the round). The AIN links farms to all those to which it sent live animals; the TN links farms to every single farm located downstream in the round (irrespective of whether there was a live-animal exchange or not); the sTN links farms that did not exchange live-animal but were connected through the transit of transport vehicle.

three occasions with pre-emptive culling of all poultry flocks within 1 km from infected farms and of all duck flocks within 3 km of infected farms (Bronner et al., 2017; DGAL, 2017a, 2017b). This epidemic led to the culling of 6.8 million of birds and induced severe disruptions in the poultry industry, causing important economic losses for local producers and for the whole poultry sector (Guinat et al., 2018). In particular, 81.6 % of H5N8 outbreaks reported in 2016–2017 in France were in farms raising ducks to produce foie gras (hereafter referred to as fattening ducks), mostly located in the southwest region (Guinat et al., 2018). The foie gras sector involves distinct production stages, which may be handled by different farms: rearing (1-day-old ducklings are reared for around three weeks), breeding (1-day to 3-week-old ducks are bred for around 9–12 weeks), and fattening (12-week-old ducks are fattened for around 12 days) (Guinat et al., 2020). Previous studies suggested that trade-related transport of fattening ducks have played a crucial role in the early stages of HPAI H5N8 epidemic (Guinat et al., 2019, 2020).

Network analysis provides a useful analytical framework to study contact patterns between farms generated by animal movements. In addition to the risk posed by movements of potentially infected live animals, contaminated transport vehicles used for these movements can also play a significant role in the transmission process (Lockhart et al., 2010). These contacts are usually defined as indirect, as opposed to exchange of live animal movements which are defined as direct contacts. Investigating these different contacts is key to analyse their respective contribution to a potential spread of pathogens in the duck industry. In recent years, numerous studies have used network analysis to describe potential pathogen spread and inform disease control intervention in various livestock species, including cattle or small ruminants (Kao et al., 2006; Ortiz-Pelaez et al., 2006; Brennan et al., 2008; Dutta et al., 2014; Marquetoux et al., 2016; VanderWaal et al., 2016b; Rossi et al., 2017; Bernini et al., 2019; Büttner and Krieter, 2020), pigs (Bigras-Poulin et al., 2007; Ribbens et al., 2009; Rautureau et al., 2011, 2012; Lentz et al., 2016; Thakur et al., 2016; Salines et al., 2017; Schulz et al., 2017; VanderWaal et al., 2018; Porphyre et al., 2020) and poultry (Soares Magalhães et al., 2010; Kurscheid et al., 2017; Guinat et al., 2020). Most of those studies focused solely on direct contact between farms, but some of them highlighted the potential indirect contact through the transit of contaminated transport vehicles used for the animal movements (Brennan et al., 2008; Ribbens et al., 2009; Thakur et al., 2016; Rossi et al., 2017; Salines et al., 2017; VanderWaal et al., 2018; Bernini et al., 2019; Büttner and Krieter, 2020; Porphyre et al., 2020). Findings suggested that transit of transport vehicles strongly increased the connectivity of farms, and emphasised that focusing only on live animal movements (direct contacts) would likely underestimate the risk of disease transmission.

The objectives of this study were three-fold: (i) to characterise the direct and indirect contact networks resulting from moving fattening ducks between farms in France during a non-epidemic period, (ii) to analyse the impact of the 2016–2017 HPAI H5N8 epidemic on the

topology of these two networks and (iii) to analyse the respective contribution of direct and indirect contact networks in the distribution of HPAI H5N8 outbreaks.

## 2. Materials and methods

### 2.1. Data processing and network building

The recorded movements were collected from one of the most important French private transport companies. It conveys farm animals all over the country and accounted for around 70 % of live-duck movements between farms in southwest France during the study period. The dataset contained records of fattening duck movements operated from January 2016 to December 2018. It included movement characteristics (number of ducks loaded and unloaded and the vehicle identification that performed the movement) and farm details (identification of the sending and receiving farms, geographical location of sending and receiving farms). Movement of ducks from fattening farms to slaughterhouses was not included in the dataset. A single transport vehicle usually loads ducks from one breeding site and unloads them at several different fattening locations visited successively during the same day (DGAL, 2018). Furthermore, French regulations stipulate that transport vehicles have to be cleaned and disinfected at the end of each round. To do so they have to go to specific cleaning and disinfection stations that are distributed all across the region (DGAL, 2018). Therefore, the dataset was reorganised into transport vehicle round records, defined as the loading of ducks on one farm followed by the unloading of ducks on successive farms by a given transport vehicle on a given day. Farm type was determined based on the type of movements they were involved in, *i.e.* breeding (for farms only sending ducks), fattening (for those only receiving ducks) or mixed (for farms sending and receiving ducks during the study period).

A network analysis approach inspired by Salines et al. (2017) was taken to describe these movements. One-mode directed networks were created: farms were considered as nodes, and directional contacts between two nodes were considered as links. Two types of connections were considered, generating two different networks (Fig. 1): (i) the animal introduction network (AIN) where links represented the movements of live animals being exchanged between breeding and fattening farms; (ii) the transit network (TN) where links represented the contacts between farms based on the successive visits of several farms by a transport vehicle during its round. Since the AIN is embedded in the TN, a subnetwork was created that contained only indirect contacts between farms that did not exchange live animals. Hereafter, this subset will be referred to as the “specific transit network” (sTN). Each network was simplified to remove loops and multiple links between farms for the study period.

**Table 1**

Network analysis terminology as used in animal movement networks (Lockhart et al., 2010; Büttner et al., 2013; Dutta et al., 2014; Thakur et al., 2016; Salines et al., 2017; Machado et al., 2020).

Term	Level	Definitions
Betweenness	Farm	The frequency at which a farm is located on the shortest path between any two pairs of farms in the network.
Degree	Farm	The number of unique contacts a farm has (sum of unique in- and out-degrees).
In-degree	Farm	The number of different farms from which a farm receives animals.
Link	Farm	The directed contact between two farms (in our case, the movement of live animals or transit of transport vehicles).
Node	Farm	The epidemiological unit of interest in the network. In our case, a farm that was active during the study period.
Out-degree	Farm	The number of different farms to which a farm sent animals.
Assortativity	Network	The Pearson correlation coefficient between the degrees of linked farms.
Average degree	Network	The mean number of unique contacts a farm has
Average path length	Network	The average number of links along the shortest paths between all possible pairs of farms.
Clustering coefficient	Network	The average proportion of neighbours of a farm that are linked to each other. As a global measure, clustering coefficient quantifies 'cliquishness' within the network.
Density	Network	The proportion of actual links present over all possible links in the network.
Diameter	Network	The number of links in the shortest path between the most distant farms of the network for which a path exists.
Strongly Connected Component (SCC)	Network	The subset of networks involving at least two farms in which every farm can be reached from every other farm via one or several directed paths.

## 2.2. Data analysis

### 2.2.1. Network description

Both networks were described using the farm-to-farm directed networks generated with the movement data for the period from January 2018 to December 2018. This period corresponded to an interepidemic period for which France did not experience any HPAI epidemic (therefore, the networks were not supposed to be altered by any HPAI-related interventions) and for which the data was available. The movement data was aggregated on a yearly basis to compute both farm and network-level descriptive statistics for each network (Table 1). We also investigated if there was an association between farm types, betweenness and in and out-degree for both networks using Kruskal-Wallis and Wilcoxon test. All networks were generated and analysed using the igraph version 1.2.6 (Csardi and Nepusz, 2006) and tidyverse 1.3.0 (Wickham et al., 2019) packages in R version 4.0.2 (R Core Team, 2020).

Next, we assessed the node *in-loyalty* which measures the tendency of a farmer to purchase animals from the same sellers (for the AIN) and of a transport company to do the same rounds (for the TN) between two consecutive quarters in 2018. To do so, the data was aggregated on a quarterly basis to match the duration between the entry of two successive batches of ducks into a breeding farm. More specifically, the node *in-loyalty* index  $\theta$  at time  $t$  measures the fraction of maintained contacts of a farm between periods  $t - 1$  and  $t$ . Therefore, the *in-loyalty* index varies between zero and one, with zero indicating that all connections were different between the periods, and one indicating that all links were maintained. The *in-loyalty* index for farm  $i$  at time  $t$  was calculated as follows:

$$\theta_i^{t-1,t} = \frac{|Y_i^{t-1} \cap Y_i^t|}{|Y_i^{t-1} \cup Y_i^t|} \quad (1)$$

with  $Y_i^t$  being the sets of in-going neighbours for farm  $i$  during the quarter  $t$  (Schulz et al., 2017).

### 2.2.2. Impact of the epidemics and related control measures on the topology of the network

We analysed the impact of the H5N8 epidemic and related control measures on the topology of the two networks (AIN and TN) by comparing the network-level statistics defined in Table 1 as well as the distribution of three farm-level statistics, in- and out-degree and betweenness, during the epidemic (January – March 2017) with those of before the epidemic (January – March 2016) and after the epidemic (January – March 2018). To do so, movement data were aggregated for each these three study periods. Statistical comparisons between the periods and the networks were performed with Wilcoxon tests, using the Bonferroni correction to account for multiple comparisons.

### 2.2.3. Role of direct and indirect contacts in the spread of HPAI H5N8 in France during the 2016–2017 epidemic

We assessed the potential contribution of live animal exchanges in the spread of HPAI H5N8 using a permutation-based approach, referred to as network k-test (VanderWaal et al., 2016a; Guinat et al., 2020), that was applied to the AIN. To assess the contribution of indirect contacts and because the AIN was embedded in the TN, we also applied the k-test to the sTN. The k-test was based upon the calculation of the k-statistic, in our case the number of “infectious” contacts that occurred in the networks. For the AIN, an infectious contact was defined as a live duck movement occurring between two outbreak farms (a breeding and a fattening farms) within  $t$  days before the date of suspicion of the most recent outbreak of the two. Similarly, for the sTN, an infectious contact was defined as a specific indirect contact (through the transit of transport vehicle but without live-animal exchange) occurring between two outbreak farms within  $t$  days before the date of suspicion of the most recent outbreak of the two. Because recent epidemiological findings suggest that duck mortality is likely to increase rapidly after HPAI (H5N8) virus introduction (Vergne et al., 2021), we considered a time-window of  $t = 7$  days, but also tested longer periods of 14 and 21 days, similar to Guinat et al. (2020). The rationale behind the k-test approach was that if the virus spread through the networks, the number of infectious contacts would be significantly greater than expected under the null hypothesis, i.e. if infected farms were randomly distributed in the network. The observed value of the k-statistic was then compared to the distribution of the same statistic obtained by randomly reallocating the date of farms' suspicion date, thus simulating a possible pattern of cases under the null hypothesis of an absence of association between HPAI H5N8 infection status and contacts in the network. The empirical p-value of the k-test was calculated as the proportion of permutations for which the simulated k-statistic was greater than the observed one. We ran the permutation test with 10,000 trials to determine the p-value for the AIN and sTN. Finally, we calculated the risk of transmission by live-bird-movement-related direct (respectively indirect) contact, defined as the ratio of (i) the number of infectious direct (resp. indirect) contacts as defined above to (ii) the overall number of “at-risk” direct (resp. indirect) contacts originating from a farm that was reported in the following seven days and that did not necessarily generate a case in the receiving farm.

## 3. Results

### 3.1. Data description

There were 614 farms identified in the dataset, with 7,447,838 ducks exchanged through 7,371 movements between January 2016 and December 2018. The year 2018 had the highest recorded number of

**Table 2**

Number (and %) of live-duck movements operated between the different farm types in the southwest of France, January 2016 to December 2018.

	2016		2017		2018	
	To fattening	To mixed	To fattening	To mixed	To fattening	To mixed
From breeding	1,445 (60.3)	416 (17.4)	994 (64.8)	218 (14.2)	1,926 (56)	624 (18.1)
From mixed	395 (16.5)	141 (5.9)	225 (14.7)	97 (6.3)	649 (18.9)	241 (7)

**Table 3**

Descriptive indicators of the animal introduction network (AIN) and transit network (TN) in the duck sector, southwest France, 2018.

Indicators	January – December 2018	
	AIN	TN
No. of active nodes	395	395
No. of active links	2,684	3,664
Average degree	13.6	18.6
Average betweenness	4.0e-4	1.9e-03
Average path length	2.6	3.1
Density	0.02	0.03
Diameter	7	9
Clustering coefficient	0.1	0.3
Assortativity	0.09	0.05
Number of strongly connected components (SCCs)	1	4
Size of the largest SCC (proportion of nodes included in the largest SCC)	19 (4.8 %)	152 (38.5 %)

ducks exchanged (3,451,662) and of movements (3,440). The most common farm production type represented in the data was breeding (278), followed by fattening (225), and then mixed (111). The majority of live animal movements occurred from breeding to fattening farms (59.2 %), followed by mixed to fattening (17.2 %), breeding to mixed (17.1 %) and mixed to mixed farms (6.5 %) (Table 2). For that same period, 103 distinct transport vehicles were used to perform these live animal movements. The transport vehicles completed 7,359 rounds, with an average of 2.9 farms per round.

### 3.1.1. Comparison of the animal introduction network (AIN) and the transit network (TN)

In 2018, the AIN and the TN contained 395 active farms (Table 3). All statistics used to compare the two networks suggested that the TN was denser than the AIN, forming larger communities of farms with stronger connectivity. The overall number of links was around 1.4 times higher in the TN than in the AIN (3,664 and 2,684 links, respectively). Over 2018, on average in the TN a farm was in contact with 19 other farms (average degree), while in the AIN, a farm was in contact with 14 other farms. One and four strongly connected component (SCC) were identified in the AIN and the TN, respectively. The largest SCC in the TN included 152 active farms (38 %) which is eight times larger than the size of the only SCC identified in the AIN (19 active farms (4.8 %)), suggesting that the TN was less fragmented than the AIN. Moreover, any two given farms located in the largest SCC were separated on average (average path length) by 3.1 links in the TN versus 2.6 links in the AIN. The TN was 45 % denser than the AIN, with density statistics of 0.03 and 0.02, respectively. Due to TN's components greater size, it also had a longer diameter (1.3 times longer) than the AIN (9 versus 7). The clustering coefficients of the network were two times higher in the TN than in the AIN, suggesting that nodes were more tightly connected in the TN than in the AIN. The assortativity was positive for both networks, indicating that farms were more often linked to farms with similar degrees.

The degree distribution in 2018 for both networks was right-skewed (figure not shown), indicating that the majority of the farms had a low degree. Statistically significant differences of centrality values

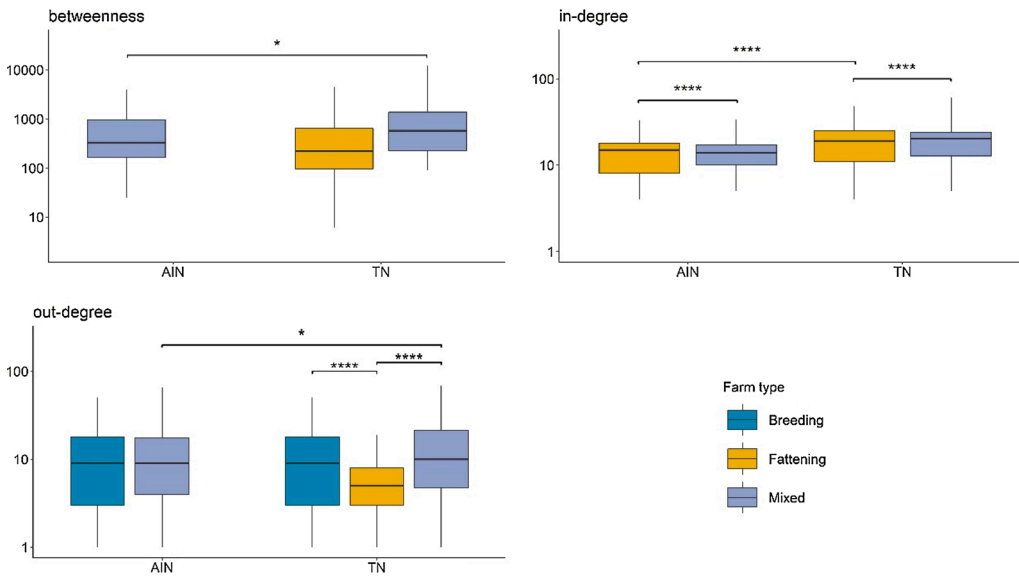
(betweenness, in- and out-degree) were observed between AIN and TN for the different farm types (Fig. 2) with higher values observed in the TN. There were also statistically significant differences of centrality values between farm types for each network (Fig. 2). For in-degree, higher values were observed for fattening as compared to mixed farms in the AIN ( $p < 0.0001$ ) while in the TN, mixed farms had higher values ( $p < 0.0001$ ). Bear in mind that the networks were unidirectional, and as such, the in-degree of breeding farms were equal to zero (Fig. 2) as they did not receive animals from mixed nor from fattening farms. For out-degree, breeding and mixed farms had higher values than fattening farms in the TN ( $p < 0.0001$ ) while no significant difference was observed between mixed and fattening farms. For the TN, no significant difference in the betweenness distribution was observed between fattening and mixed farms (Kruskal-Wallis test:  $p = 0.67$ ).

The distribution of loyalty values computed in both networks showed little variation between quarters (Fig. 3). The average loyalty index was around 15 % in AIN and 16 % in the TN.

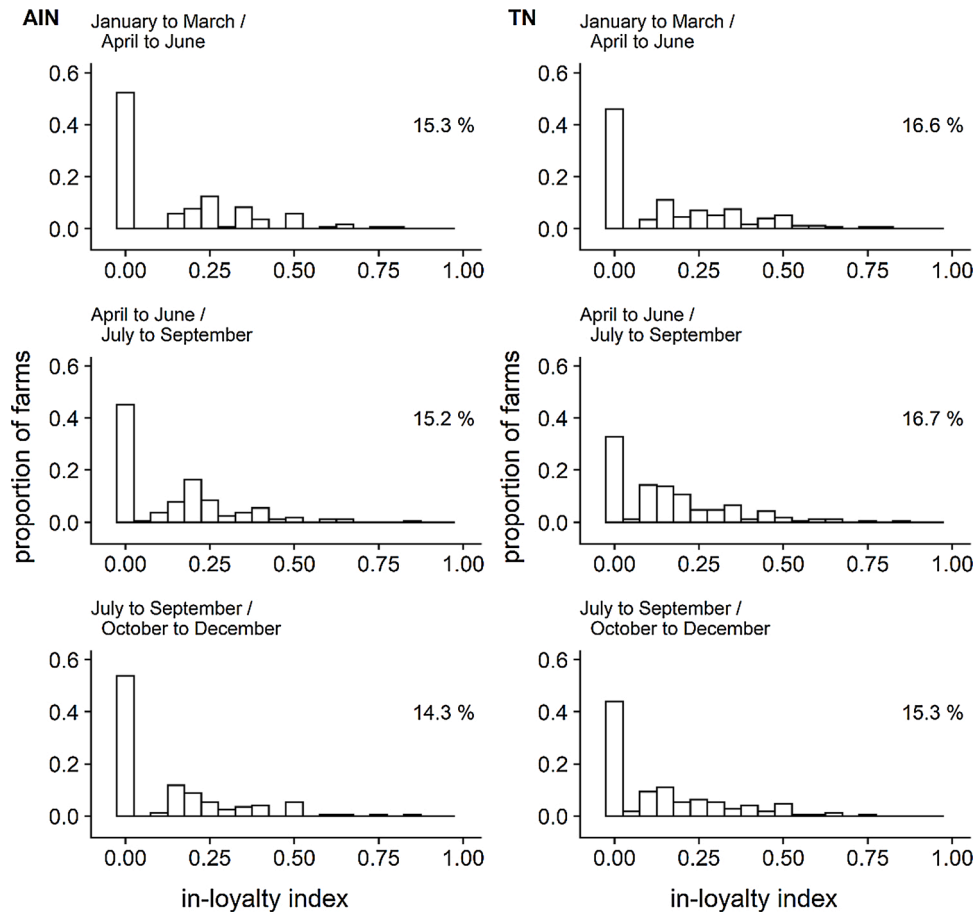
### 3.1.2. Impact of the epidemics and related control measures on the topology of the network

The AIN contained 2.45 times more active nodes (319) during the period before the epidemic (first quarter of 2016) than during the epidemic (130) (Table 4). The number of links in the AIN before the epidemic (808) was 3.7 times higher than during the epidemic (218). On average, a farm exchanged animals with 5.1 different farms before the epidemic, while during the epidemic, this indicator decreased to 3.4 different farms (average degree distribution). The average path length dropped by 43 % during the epidemic from 2.3 to 1, due to a decrease of components size. Indeed, no SCC was detected in the AIN, as each component detected contained less than 1% of active nodes for both periods. The assortativity remained constant (0.2) during both periods. In the AIN, the clustering coefficient decreased from 0.03 to 0 between the period before the epidemic and epidemic period. In the TN, the clustering coefficient remained stable at around 0.16. The size of the largest SCC detected before the epidemic contained 71 active nodes as opposed to two active nodes during the epidemic. After the epidemic (January–March 2018), most network statistics returned to their values close to those before the epidemic. The number of active nodes and links were more than double that of the period during the epidemic. The number of different farms with which a given farm exchanged animals (average degree) was up by 23 % compared to during the epidemic, and the average path length was doubled. In the TN, the size of the largest SCC rose from two during the epidemic to 69 after the epidemic.

Similar to the network statistics, irrespective of the network and the farm type, all centrality measures dropped during the epidemic period and then increased again after, often statistically significantly (Fig. 4). However, in the AIN, the out-degree distributions for breeding and mixed farms did not statistically significantly change between the different periods (Fig. 4). Similarly, in the TN, the out-degree distribution did not drop statistically significantly, except for fattening farms. After the epidemic (January – March 2018), the distributions of the betweenness for all farm types and of the in-degree for mixed farms in the AIN and the TN were not statistically significantly different from the period before the epidemic. Nonetheless, the distributions of the in-degree for fattening farms in the AIN and the TN, despite increasing



**Fig. 2.** Distribution of betweenness, in-degree and out-degree centrality measures in southwest France, 2018, according to different duck farm types, for the Animal Introduction Network (AIN) and Transit Network (TN) using a logarithmic scale. For each comparison, the p-value of the Wilcoxon test is shown to indicate whether the difference observed is significant (\*:  $p \leq 0.05$ , \*\*:  $p \leq 0.01$ , \*\*\*:  $p \leq 0.001$ ; \*\*\*\*:  $p \leq 0.0001$ ). Note that breeding and fattening farms are not represented in the betweenness panel for the AIN since they either send or received animals during a round and thus, there is no transit through them; Breeding farms are not represented in the in-degree panel for the AIN and the TN since they do not receive ducks from other farms; similarly, fattening farms are not represented in the out-degree panel for the AIN since they do not send ducks to other farms.



**Fig. 3.** Node in-loyalty distributions in the animal introduction network (AIN) and transit network (TN) from the duck sector in southwest France in 2018. The average percentage of origins maintained from one period to another is shown in the upper right corner.

**Table 4**

Descriptive indicators of the animal introduction network (AIN) and transit network (TN) of French duck movements for the first quarter (January–March) of 2016, 2017 and 2018 which correspond to the pre-epidemic, epidemic and post-epidemic periods, respectively.

Indicators	AIN			TN		
	2016	2017	2018	2016	2017	2018
No. of active nodes	319	130	310	319	130	310
No. of active links	808	218	676	1055	252	908
Average degree	5.1	3.4	4.4	6.6	3.9	5.9
Average betweenness	10.11	0.02	4.94	260.30	0.99	229.52
Average path length	2.3	1.0	2.0	5.1	1.4	5.0
Density	0.01	0.01	0.01	0.01	0.02	0.01
Diameter	6	2	6	15	4	18
Clustering coefficient	0.03	0	0.02	0.17	0.16	0.16
Assortativity	0.20	0.20	0.05	0.17	0.16	0.16
Number of strongly connected components (SCC)	0	0	1	3	5	3
Size of the largest SCC (proportion of nodes included in the largest SCC)	NA	NA	2 (0.7 %)	71 (22.1 %)	2 (1.5 %)	69 (22.3 %)

again after the epidemic, reached a level that was statistically significantly lower than before the epidemic (Fig. 4).

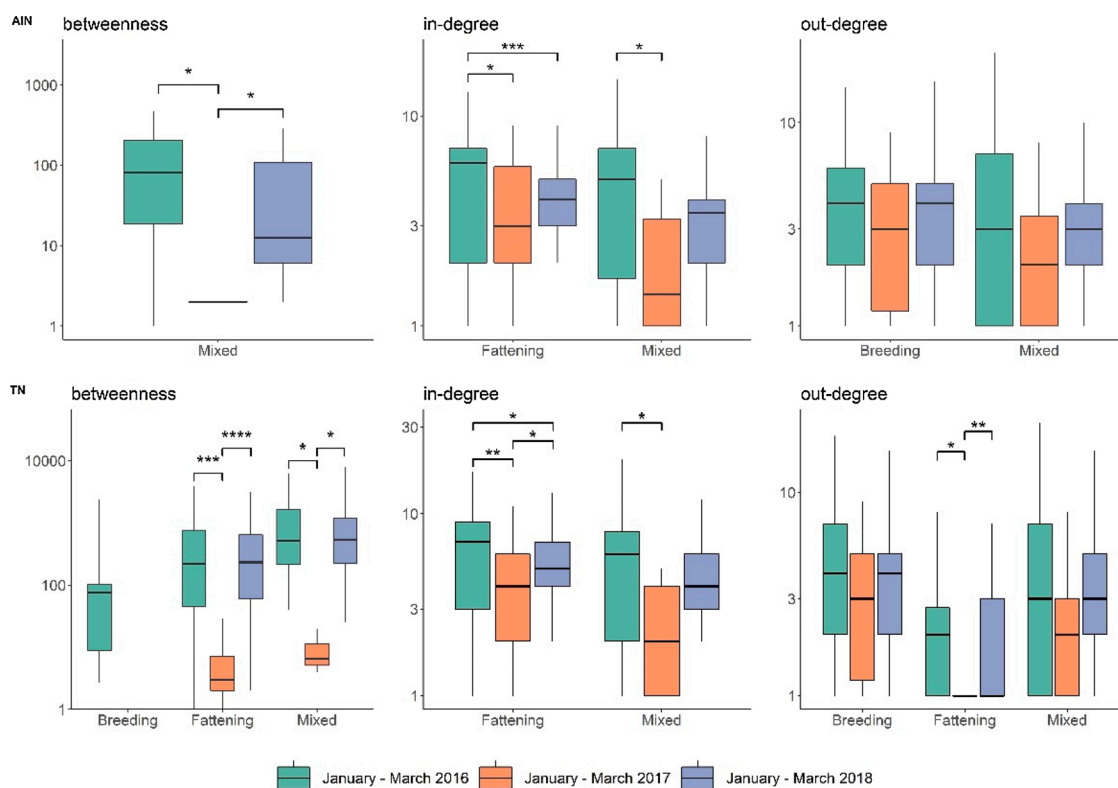
**3.1.3. Role of direct and indirect contacts in the spread of HPAI H5N8 in France during the 2016–2017 epidemic**

Using a time-window of seven days, we identified two infectious contacts in the AIN out of 7,376 movements (0.03 %). It included two movements from one mixed farm to two distinct fattening farms in early December 2016. This number of infectious contacts was found to be statistically significantly higher than what would be expected under the null hypothesis ( $p < 0.0001$ ). Similarly, using the same time-window, one out of 2,763 contacts was considered infectious in the sTN, which was also statistically significantly higher than what would be expected under the null hypothesis ( $p < 0.01$ ). It corresponded to the transit of a

transport vehicle between one fattening and a mixed farm at the end of November 2016. Using the time-window of 14 or 21 days, the number of infectious contacts in each network were still statistically significant greater than what would be observed under the null hypothesis. Finally, the risk of transmission given an at-risk contact was calculated at 33.3 % for both the AIN (2/6) and the sTN (1/3), assuming an at-risk period of seven days prior to the suspicion notification.

**4. Discussion**

Network analysis has been widely used to investigate the implication of network structure in disease spread for various production systems (Rautureau et al., 2011, 2012; Marquetoux et al., 2016; Porphyre et al., 2020). This study showed that duck farms in southwest France are



**Fig. 4.** Centrality indicators for the animal introduction network (AIN) and transit network (TN) in different farm types in the southwest of France before (January – March 2016), during (January – March 2017) and after (January – March 2018) the HPAI H5N8 epidemic using a logarithmic scale for the y-axis. For each comparison, the p-value of the Wilcoxon test is shown to indicate whether the difference observed is significant. Note that breeding and fattening farms are not represented in the betweenness panel for the AIN since they either send or received animals during a round and thus, there is no transit through them; Breeding farms are not represented in the in-degree panel for the AIN and the TN since they do not receive ducks from other farms; similarly, fattening farms are not represented in the out-degree panel for the AIN since they do not send ducks to other farms.

highly connected through the exchange of live birds, which is consistent with a previous analysis (Guinat et al., 2020). Most importantly, it demonstrated that the transport vehicles used to transport live birds were a significant source of inter-farm connectivity through the transit of the same transport vehicles to unload ducks in successive fattening farms. While only one transport company was studied here, this trend is however expected to be the same for other transport companies since the successive unloading of loaded batches of ducks is not specific of a company but is a specificity of the foie gras duck production system. Results showed that the TN connected many more farms than the AIN, as its largest SCC was eight times bigger than the largest SCC in the AIN. These findings are consistent with similar studies focused on transport networks of pig production system (Bigras-Poulin et al., 2007; Thakur et al., 2016; Salines et al., 2017) which is vertically integrated, similar to the foie gras duck production system in France, although the duck production is associated with fewer stages. We need to keep in mind that introducing an infected animal into a farm is expected to be much more effective in spreading a virus than the transit of a contaminated transport vehicle. However, our work highlighted a general need for a deeper knowledge of transmission mediated by fomites, including better ways to properly capture the frequency and probability of contacts due to transport vehicle movements. Consequently, deciphering the contact pattern of these movements could prove essential in constructing fine-tuned epidemiological models, estimating the worst-case scenario in terms of the size of an epidemic (Kao et al., 2006) and bring valuable information for disease management, including contact-tracing and surveillance.

For the French duck industry, our results suggested that mixed farms could be a key production type to consider in order to implement risk-based disease surveillance and to disrupt the contact network between duck farms in case of an epidemic. Indeed, despite their limited number in the dataset, mixed farms appeared more central (higher betweenness and degree values) than specialised breeding or fattening farms, irrespective of the network considered. As such, they present a higher risk to become infected through live-animal movements or the transit of transport vehicles and therefore could be relevant candidates for the implementation of risk-based surveillance approaches. They represent so-called bridges or hubs between different network components, what has been pin-pointed as a potential facilitator of disease spread in the French pig movement network (Rautureau et al., 2011). Therefore, in case of an epidemic, removing these farms through the culling of their flock would decrease theoretically the connection between the network components and limit disease spread through both live-animal movements and the transit of transport vehicles. An alternative to this culling could be to decrease duck farm density by reducing the number of at-risk farms during the high-risk period by forbidding duck placement in these farms and compensating farmers for the production losses. These results also emphasise that strict cleaning and disinfection protocols applied to transport vehicles should be combined with good compliance to external biosecurity measures on farms to limit disease spread. These hypotheses should now be tested by using mechanistic models for simulating disease spread and evaluate targeted control strategies.

Our analysis showed that the live animal movements and the transit of transport vehicles were associated with statistically significantly more infectious contacts than what would be expected if these networks did not contribute to the spread of the virus, suggesting that transmission events were likely to have occurred through these routes. In addition, it was shown that at-risk contacts (direct and indirect) through live-duck movements are relatively efficient at spreading the virus, since around 33 % of them led to an infection event. However, we only identified two and one infectious contacts in the AIN and the sTN, respectively, suggesting that the contribution of direct and indirect contacts to the overall

number of transmission events was likely to be very small. The limited number of infectious contacts associated with the networks is likely to be the result of an effective implementation of movement control. These infectious contacts occurred at the very beginning of the epidemic (end of November 2016 and beginning of December 2016) so it is likely that their only contribution was to allow the epidemic to take-off. Then, following the rapid implementation of movement bans and regulations forbidding successive loadings of ducks during a round, the reinforcement of hygiene measures during transport and the systematic virological screening before animals are moved over long distances (more than 20 km) from breeding to fattening farms in early December have likely contributed to curb successfully the importance of these transmission routes in the subsequent phases of the epidemic.

Our results also demonstrated that node loyalty in both networks was highly volatile. On average, node loyalty from one trimester to the next never exceeded 17 %, indicating future contacts might be almost impossible to predict. Even though the AIN and the TN were profoundly impacted by the epidemic (Fig. 4), it is worth noting that most network characteristics after the epidemic returned to values similar to those from before the epidemic (Table 4). The only exception we noted was for the in-degree of fattening farms which were statistically significantly lower than before the epidemic. These two concurring results suggest that the epidemic led fattening farms to reduce the amount of partnering breeding farms and to be more loyal to them. It must however be acknowledged that network topology in early 2016 may have been partially affected by the HPAI outbreaks which occurred during winter 2015.

A limitation to the results presented here is that the data used were collected from a single transport company. Bias in network-level measures (fragmentation and lack of exhaustivity) can thus exist, resulting in a potential underestimation of farms' true connectivity. However, as previously stated the trend observed with this company is not expected to vary by including the other companies, thus our conclusions regarding the respective contribution of direct and indirect contacts in the H5N8 spread should remain valid. The extension of the analytical framework presented here to a broader dataset consisting of all transport companies would be necessary to gain a comprehensive view of farms' connectivity. However, several challenges subsist to reach this goal, including incompleteness and heterogeneity in data recording for the period of interest. Also, our analyses focused on movements operated between farms and did not consider movements to slaughterhouses, since this data was not available. In addition, although movements from and to slaughterhouses could potentially increase farm connectivity and thus facilitate transmission through indirect contact, this transmission route was deemed unlikely as strict cleaning and disinfection procedures were implemented for all transport vehicles leaving slaughterhouses (DGAL, 2017c).

Finally, it must be acknowledged that only a fraction of contacts which are established between farms were captured in the present study. Previous research (Lockhart et al., 2010) highlighted the variety of contact networks – including feed, live birds, poultry products, and manure and waste litter – co-existing in the poultry sector. While our results bring original insights on the respective contribution of direct and indirect contacts related to duck movements in the spread of H5N8 virus, further work is still needed to explore the role of other activities – including management of manure and waste litter, as well as rendering – in infectious contacts which may contribute to disease spread between farms.

#### Declaration of Competing Interest

The authors report no declarations of interest.



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