Supplementary information

Social network analysis reveals the failure of between-farm movement restrictions to reduce *Salmonella* transmission

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Table S1: Overview of legislative orders and changes in the Danish surveillance and eradication programme for *S.* Dublin in cattle, such as infection categories, movement restrictions and other control measures including Official Veterinary Supervision (OVS) by the veterinary authorities. See description of the testing scheme in the footnote of the Table S1.

Legislative order no.	Effective from date	Levels (L)	Movement restrictions	Other control measures
BEK no. 801 *(updated in BEK no. 974, 413 and 686)*	05/10/2002 *(15/12/2002, 11/06/2003 and 02/08/2003)*	*L1:* Dairy herds: below the two test criteria on Bulk tank milk (BTM) Non-dairy: all of 8 blood samples below 50 ODC%. *L2:* Too high antibody level to be place in *L1*, or recent contact to *L2* or *L3*-properties. *L3:* Bacteria detected by culture upon clinical suspicion. Unknown level: not enough information available to classify.	Locking period for 3 months in *L2* upon purchase or contact with other cattle properties not in *L1*. *L3* only allowed to move cattle to slaughter, not sell for live purpose.	Official Veterinary Supervision (OVS) of all *L3*-properties. Special hygienic slaughter procedures and post-slaughter swabs of carcasses from *L3* for at least 3 months upon detection. Heat treatment of test-positive beef.
BEK no. 112 *(Combined with salmonella legislation for pigs)*	05/03/2005	Same as above.	Same as above, plus duty of disclosure of salmonella status to all who got in contact with the property.	Same as above, plus OVS with special requirements for properties with multiresistant *S.* Typhimurium DT104.
BEK no. 197 *(Combined order for pigs and cattle, Cattle levels*	25/03/2006	*L1* split into: *L1a:* as previous L1 *L1b:* BTM cut-off 40 ODC% allowing collection of 8 blood	Locking period changed to 3 weeks in *L2* upon purchase or contact with	Same as above, plus cattle businesses with multiple properties had to test each property and

explained in 'bilag 18')		samples to reach *L1b* if test-negative (below 50 ODC%). *L2:* too high antibody levels to be placed in *L1*, or *S.* Dublin bacteria detected, but not in *L3*; or recent contact to *L2* or *L3*-properties. *L3:* clinical salmonellosis and *S.* Dublin bacteria detected. When moved from *L3* to *L2*, property locked in *L2* for 6 months. Unknown level for non-dairy herds: not enough information available to classify	other cattle properties not in *L1*. Blood samples from contact animals 3-6 weeks after contact to confirm no spread of infection to move to *L1a*/*L1b*.	the highest risk level assigned to all properties in that business (including 'samdrift').
BEK no. 3 04/01/2010 *(Mainly changes to pig salmonella surveillance)*	14/01/2009	Minor changes.		Some clarifications about special slaughter of cattle and pigs for the abattoirs.
BEK no. 943 26/07/2010	01/08/2010	**Major change:** *L2*-properties 'with signs of spread of *S.* Dublin' introduced for dairy herds with at least one BTM≥40 ODC% without test-negative calves, and for non-dairy herds with at least one blood sample ≥50 ODC%	No movement allowed of animals for live use from OVS-properties (except calves for fattening if receiver has accepted in writing to receive)	OVS introduced on *L2*-properties with signs of spread of *S.* Dublin.
BEK no. 1723 22/12/2010	05/01/2011	*L2R* introduced and added to *L2* to clarify which farms had signs of spread of *S.* Dublin.	Same as above	OVS on *L2R* properties.
BEK no. 143 22/02/2012	25/02/2012	Unknown level added for dairy properties if not enough blood samples		
BEK no. 954 10/07/2013	15/07/2013	**Major change**: Regionalisation introduced. Levels adapted: *L1* (no longer *L1a* and *L1b*) *L2* (no longer *L2* and *L2R*) *L3*	Only movements of bull calves for fattening allowed from Jutland (high-prevalence region) to Islands (low-prevalence region) – unless own or empty farm	*L2*+*L3* mandatory to make agreement with vet to control *S.* Dublin (action plans). Blood samples must be collected in *L2*+*L3* farms from calves to check effect of plan

		No longer unknown levels	property. Animals for shows and shared pastures must have been in *L1* herds for 9 months prior.	every 3 months until in *L1*. Intensified bacteriological sampling when blood sample not negative
BEK no. 886 02/07/2014	15/07/2014	Minor adjustments		Time to action plan ready in new *L2*-farms specified to 3 weeks
BEK no. 351 07/04/2015	10/04/2015 *(for slaughter calves about §18, stk. 3-7, 15/07/2015)*	Minor adjustments		
BEK no. 1192 20/10/2015	26/10/2015	**Major change:** Regions changed in the regionalisation to include areas of Jutland in low-prevalence region Heifer-raising properties required to sample on-farm		Fines to farmer in high-prevalent region if cattle moved illegally from farms in the high-prevalence to the low-prevalence region
BEK no. 537 01/06/2016	01/07/2016	Number of blood samples adjusted to 8 in most cases.	Transported cattle from non-*L1* properties must be picked up last on the transportation route	Fines added to farmer in low-prevalent region if cattle moved illegally from farms in the high-prevalence to the low-prevalence region
BEK no. 1326 29/11/2017	01/01/2018	**Major change:** Regionalisation stopped	Movements restricted from all *L2*-farms No longer allowed to move calves for fattening in other farms from *L2* properties	Animals for slaughter from non-*L1* properties must be picked up last on the route
BEK no. 1687 18/12/2018	01/01/2019	Properties in *L2* for more than 2 years with positive blood sample rounds considered 'special *S.* Dublin risk with imposed veterinary counselling' *L1*-farms that have been in *L2* must test calves free every 3 months for	*L2*-movement restrictions continued Movement between own properties or for export and slaughter still allowed	Properties with 'special *S.* Dublin risk with imposed counselling' must use officially approved *S.* Dublin consultancy veterinarians

		1-2 years (2 years if they move animals out for live purposes)		
BEK no. 1494 13/12/2019	01/01/2020	**Major change:** All *L2* placed under OVS with requirements to make an action plan assisted by the herd health consulting veterinarian within 3 weeks for potential checking by authorities	*L2*-movement restrictions continued Movement between own properties and for export and slaughter still allowed	Veterinary authorities initiated control in few *L2*-farms
BEK no. 1791 02/12/2020	01/01/2021	Minor adjustment with no expected impact on network properties		
BEK no. 1055 31/05/2021	01/07/2021	**Major change:** **Number of levels reduced to two:** *L1* and *L2* with OVS on all *L2*-farms *L1* (test-negative according to criteria; all cattle groups on all properties in the business must be tested negative before the properties can be placed in *L1*); heifer raising facilities must collect 8 blood samples 1-2 per year depending on number of heifer source herds. *L2* (all other cattle herds).	New *L2* based on contacts can be tried/free-tested with herd size dependent blood samples from contact animals 3-6 weeks post-contact.	**Increased sample size and *L2*-farms under OVS:** action plan with vet within 3 weeks *L2* properties visited every 6 months by veterinary authorities for check of action plans and testing Herd-size based sample size of blood samples of calves and heifers mandatory 2-4 times per year until satisfactory to be moved to *L1*
BEK no. 2416 14/12/2021	01/01/2022	Tightened special risk definition: Properties in *L2* for more than 1 year with positive blood sample rounds considered 'special *S.* Dublin risk'		Increasing number of *L2*-farms visited by the veterinary authorities
BEK no. 1493 06/12/2022	01/01/2023	Mainly structural changes to make the legislative order more readable. Minor changes with little expected effect on network properties.		

Official Veterinary Supervision (OVS)

Testing scheme: All dairy herds were tested using bulk tank milk (BTM) samples four times per year, with an indirect O-antigen-based ELISA targeting antibodies directed against serogroup-D *Salmonella* (in Danish cattle, serogroup-D isolates are mainly *S*. serovar Dublin). Dairy herds were placed in *L1* based on two test-criteria: *i*) the average antibody value (called ODC%) measured across the last four BTMs should be below 25 ODC%, and *ii*) the last BTM sample should not have jumped to more than 20 ODC% the average of the previous three BTM-samples. Dairy farmers do not know when or which of the daily/regularly collected BTM samples will be used for the *S*. Dublin ELISA analyses by the laboratory running the milk-quality control scheme for the dairy industry. In non-dairy herds, eight blood samples are tested, and in intensive production farms, at least once per year. The blood samples are typically collected at abattoirs or on-farm when needed. Non-dairy farms were placed in *L1* if none of the last eight blood samples were higher than 50 ODC%. This cut-off was selected to ensure a reasonably high specificity in the herd classification. In addition to the serological testing, detection of *S.* Dublin bacteria by bacteriological culture upon clinical suspicion placed the property under official veterinary supervision (OVS) and in *L3*. Other levels were introduced and removed over the years. The legislative order put in place January 2020 changed the surveillance programme to include two levels: *L1* (test-negative) and *L2* (test-positive and placed under OVS). In *L2*-farms, calves under 6 months old must be tested four times per year to document that mandatory and effective control measures are in place. Once the calves test negative, young stock older than 6 months old must be tested twice per year, until they also test negative, before the farm can be placed in *L1* again (given that the BTM also tests sufficiently low as described above).

Table S2: New group classifications of the *S*. Dublin infection based on the description of the samples and test results, risky contacts, and official veterinary supervision in the surveillance database. Level=L.

Description of the test results	Group Classification
Too high antibody value in milk and blood	B
Detection of *Salmonella* Dublin bacteria	B
Trade and contact (*L1*)	D
Level unknown, no level calculated due to 0 animals on the property	C
Official veterinary supervision due to infection with *Salmonella* Dublin, Special slaughter	B
Lifted official veterinary supervision	B
Risk of infection due to contact with property in *L3*	C
Risk of infection due to purchase from *L3*	B
Salmonella *L1* entered manually (blood)	A
Salmonella *L1* entered manually (milk)	A
Salmonella *L2* entered manually	B
Salmonella *L3* entered manually	B
Probably *Salmonella* Dublin free, based on blood samples	A
Probably *Salmonella* Dublin free, based on bulk tank milk samples	A
Probably infectious, based on blood samples	B
Probably infectious, based on purchase	B
Probably infectious, based on bulk tank milk	B
Infected with *Salmonella* Dublin (without official veterinary supervision). Special slaughter	B
Undetermined until final clarification of "b" sample (bulk tank milk)	C
Undetermined because it has been too long since the last sample	C
Undetermined due to purchase, entry before last sample	A
Undetermined due to lifted *L3*	B
Undetermined due to lifted *L3*, official veterinary supervision	B
Undetermined, awaiting results of new bulk tank milk sample	C
Unknown - Due to missing blood samples	D

Table S3: Summary of the graph-level metrics of cattle movements across years stratified by: **(A)** Non-infected. **(B)** infected farms. **(C)** both infected and non-infected *S.* Dublin farms. Because the network properties were calculated on monthly networks, the values are presented as per-year medians.

A. Non-infected	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020
Number of nodes	4495	4779	4772	4484	4662	4506	4142	4050	3959	3766	3734
Degree	3.223	3.350	3.300	3.309	3.346	3.334	3.316	3.389	3.441	3.485	3.544
In-degree	1.611	1.675	1.650	1.655	1.673	1.667	1.658	1.695	1.720	1.742	1.772
Out-degree	1.611	1.675	1.650	1.655	1.673	1.667	1.658	1.695	1.720	1.742	1.772
Assortativity	-0.093	-0.108	-0.099	-0.106	-0.097	-0.084	-0.073	-0.071	-0.087	-0.094	-0.084
Average Path Length	6.305	6.061	6.223	5.672	5.890	6.555	7.321	7.193	6.959	6.410	6.446
Betweenness	2191.0	2783.0	2617.0	2076.0	2369.0	2441.0	2655.0	2623.0	2562.0	2717.0	2873.0
Closeness	0.334	0.3193	0.3451	0.3402	0.3514	0.3398	0.3628	0.3559	0.3455	0.3289	0.3261
Closeness (In)	0.409	0.3817	0.4009	0.3961	0.4008	0.3895	0.3940	0.3802	0.3703	0.3620	0.3511
Closeness (Out)	0.403	0.3651	0.3845	0.3872	0.3810	0.3755	0.3939	0.3784	0.3708	0.3595	0.3520
Clustering coefficient	0.141	0.1461	0.1534	0.1660	0.1710	0.1545	0.1460	0.1429	0.1495	0.1459	0.1514
Weak component (No. nodes)	1039	1060	1130	1101	1118	1104	1048	1021	945	856	861
Strong component (No. nodes)	1518	1510	1497	1437	1428	1368	1237	1168	1122	1080	1016
Density	0.0003568	0.0003559	0.0003466	0.0003634	0.0003569	0.0003674	0.0003997	0.0004125	0.0004307	0.0004661	0.0004814
Modularity	0.7840	0.7641	0.7742	0.7756	0.7732	0.7773	0.7825	0.7701	0.7762	0.7610	0.7519
B. Infected	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020
Number of nodes	314	316	287	260	223	184	205	181	156	136	79
Degree	2.844	3.003	3.198	3.067	3.419	3.671	3.592	3.656	3.555	3.522	2.916
In-degree	1.422	1.501	1.599	1.533	1.709	1.835	1.796	1.828	1.777	1.761	1.458
Out-degree	1.422	1.501	1.599	1.533	1.709	1.835	1.796	1.828	1.777	1.761	1.458
Assortativity	-0.022	-0.062	-0.076	-0.091	-0.147	-0.222	-0.226	-0.229	-0.266	-0.228	-0.052
Average Path Length	2.520	2.822	3.764	3.863	3.847	3.319	3.446	3.306	2.903	2.713	2.359
Betweenness	7.701	11.059	48.877	43.913	76.28	78.32	100.13	73.93	64.01	51.191	7.926
Closeness	0.5527	0.5277	0.4736	0.5177	0.4485	0.3349	0.3322	0.3437	0.3312	0.3555	0.5507
Closeness (In)	0.5681	0.5346	0.4736	0.5232	0.4495	0.3349	0.3334	0.3437	0.3291	0.3555	0.5589
Closeness (Out)	0.5688	0.5277	0.4736	0.5228	0.4489	0.3349	0.3334	0.3437	0.3291	0.3555	0.5541
Clustering coefficient	0.2682	0.3126	0.2910	0.3069	0.3068	0.3280	0.3653	0.2756	0.2919	0.2550	0.3295

Weak component (No. nodes)	118	110	91	89	59	39	47	35	35	38	31
Strong component (No. nodes)	127	111	93	89	59	40	48	37	36	38	31
Density	0.004701	0.004819	0.005558	0.005957	0.008165	0.010118	0.009185	0.009562	0.011730	0.01258	0.01897
Modularity	0.8754	0.8688	0.8364	0.8437	0.7951	0.7594	0.7615	0.7340	0.7316	0.7333	0.8500
C. Both	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020
Number of nodes	5269	5532	5479	5192	5210	5016	4648	4546	4385	4178	4045
Degree	3.405	3.573	3.632	3.598	3.650	3.604	3.616	3.718	3.731	3.855	3.845
In-degree	1.703	1.787	1.816	1.799	1.825	1.802	1.808	1.859	1.865	1.928	1.922
Out-degree	1.703	1.787	1.816	1.799	1.825	1.802	1.808	1.859	1.865	1.928	1.922
Assortativity	-0.089	-0.108	-0.109	-0.117	-0.121	-0.113	-0.108	-0.111	-0.119	-0.120	-0.103
Average Path Length	6.944	6.002	5.876	5.681	5.647	6.026	6.418	6.424	6.207	5.800	6.007
Betweenness	3900.0	4435.0	4445.0	3929.0	3894.0	3761.0	3869.0	4008.0	3728.0	3548.0	3622.0
Closeness	0.2826	0.2766	0.2759	0.2859	0.2916	0.2996	0.3032	0.2927	0.2891	0.2723	0.2824
Closeness (In)	0.3602	0.3281	0.3204	0.3290	0.3296	0.3345	0.3366	0.3209	0.3157	0.2979	0.3040
Closeness (Out)	0.3507	0.3206	0.3191	0.3191	0.3174	0.3215	0.3281	0.3174	0.3153	0.2998	0.3085
Clustering coefficient	0.1333	0.1465	0.1482	0.1522	0.1625	0.1556	0.1439	0.1336	0.1337	0.1371	0.1447
Weak component (No. nodes)	1046	1058	1029	1022	1036	1035	981	928	877	802	800
Strong component (No. nodes)	1624	1568	1445	1371	1349	1326	1229	1161	1064	1003	945
Density	0.0003245	0.0003252	0.0003354	0.0003472	0.0003494	0.0003600	0.0003862	0.0004041	0.0004249	0.0004584	0.0004784
Modularity	0.7580	0.7352	0.7316	0.7368	0.7339	0.7391	0.7382	0.7190	0.7300	0.7123	0.7120

Table S4: Results of the multiple logistic regression models based on a data of previous month. Association between *S.* Dublin infections and local (radius of 5 km) and trade transmissions in the next month, two, three, four, five, and six months, adjusted for farm size, trade month, production category and total neighborhood (in a radius of 5 km around the infected farm). N.B. local transmission include all cattle farms i.e. also those premises that were not traded with infected and/or non-infected cattle farms.

	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6
(Intercept)	-4.24 ***	-3.58 ***	-3.14 ***	-2.84 ***	-2.61 ***	-2.43 ***
	(0.13)	(0.10)	(0.08)	(0.07)	(0.06)	(0.06)
Local Infection	0.12 *	0.09 *	0.08 *	0.07 *	0.07 *	0.06 *
	(0.06)	(0.04)	(0.04)	(0.03)	(0.03)	(0.03)
Trade Infection	0.57 ***	0.47 ***	0.40 ***	0.37 ***	0.35 ***	0.34 ***
	(0.06)	(0.04)	(0.04)	(0.03)	(0.03)	(0.03)
Dairy	-0.16	-0.08	-0.12	-0.12	-0.12	-0.12 *
	(0.13)	(0.10)	(0.08)	(0.07)	(0.06)	(0.06)
Heifer	-0.31 *	-0.32 **	-0.34 ***	-0.36 ***	-0.35 ***	-0.35 ***
	(0.14)	(0.10)	(0.08)	(0.07)	(0.07)	(0.06)
Small beef	0.21	0.05	-0.06	-0.11	-0.11	-0.11
	(0.17)	(0.13)	(0.11)	(0.09)	(0.08)	(0.08)
Other small	0.80 ***	0.55 ***	0.32 **	0.27 **	0.21 *	0.19 *
	(0.16)	(0.12)	(0.11)	(0.09)	(0.09)	(0.08)

Other large	0.28	0.17	0.08	0.04	0.02	0.01
	(0.14)	(0.11)	(0.09)	(0.08)	(0.07)	(0.07)
Unknown[1]	0.62 ***	0.56 ***	0.49 ***	0.47 ***	0.46 ***	0.45 ***
	(0.14)	(0.10)	(0.09)	(0.08)	(0.07)	(0.06)
Herd size	0.19 ***	0.21 ***	0.22 ***	0.23 ***	0.24 ***	0.24 ***
	(0.02)	(0.02)	(0.01)	(0.01)	(0.01)	(0.01)
Trade Month	0.07 ***	0.12 ***	0.11 ***	0.10 ***	0.07 ***	0.05 ***
	(0.02)	(0.02)	(0.01)	(0.01)	(0.01)	(0.01)
Total neighborhood	0.10 ***	0.10 ***	0.10 ***	0.10 ***	0.10 ***	0.10 ***
	(0.02)	(0.02)	(0.01)	(0.01)	(0.01)	(0.01)
N	135667	135667	135667	135667	135667	135667
AIC	23051.06	37402.49	49244.07	59493.73	68522.71	76565.96
BIC	23168.87	37520.31	49361.88	59611.55	68640.52	76683.78
Pseudo R^2	0.02	0.02	0.02	0.02	0.02	0.03

All continuous predictors are mean-centered and scaled by 1 standard deviation. Significance niveau: *** $p < 0.001$; ** $p < 0.01$; * $p < 0.05$.

[1] Unknown = Production categories are missing for particular months.

Table S5: Results of the multiple logistic regression models based on a data of previous 2 months. Association between *S.* Dublin infections and local (radius of 5 km) and trade transmissions in the next month, two, three, four, five, and six months, adjusted for farm size, trade month, production category and total neighborhood (in a radius of 5 km around the infected farm). N.B. local transmission include all cattle farms i.e. also those premises that were not traded with infected and/or non-infected cattle farms.

	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6
(Intercept)	-3.59 ***	-4.25 ***	-3.14 ***	-2.85 ***	-2.62 ***	-2.44 ***
	(0.10)	(0.13)	(0.08)	(0.07)	(0.06)	(0.06)
Local Infection	0.08	0.10	0.07 *	0.07 *	0.06 *	0.06 *
	(0.04)	(0.06)	(0.04)	(0.03)	(0.03)	(0.03)
Trade Infection	0.48 ***	0.58 ***	0.43 ***	0.40 ***	0.39 ***	0.37 ***
	(0.04)	(0.05)	(0.03)	(0.03)	(0.03)	(0.02)
Dairy	-0.11	-0.19	-0.15	-0.15 *	-0.15 *	-0.15 *
	(0.10)	(0.13)	(0.08)	(0.07)	(0.06)	(0.06)
Heifer	-0.33 **	-0.32 *	-0.36 ***	-0.37 ***	-0.37 ***	-0.36 ***
	(0.10)	(0.14)	(0.08)	(0.07)	(0.07)	(0.06)
Small beef	0.05	0.20	-0.07	-0.12	-0.11	-0.11
	(0.13)	(0.17)	(0.11)	(0.09)	(0.08)	(0.08)
Other small	0.54 ***	0.79 ***	0.32 **	0.26 **	0.21 *	0.18 *
	(0.12)	(0.16)	(0.11)	(0.09)	(0.09)	(0.08)

Other large	0.16	0.26	0.07	0.03	0.01	-0.00
	(0.11)	(0.14)	(0.09)	(0.08)	(0.07)	(0.07)
Unknown[1]	0.56 ***	0.61 ***	0.49 ***	0.46 ***	0.45 ***	0.44 ***
	(0.10)	(0.14)	(0.09)	(0.08)	(0.07)	(0.06)
Herd size	0.20 ***	0.18 ***	0.22 ***	0.22 ***	0.23 ***	0.24 ***
	(0.02)	(0.02)	(0.01)	(0.01)	(0.01)	(0.01)
Trade Month	0.12 ***	0.08 ***	0.11 ***	0.10 ***	0.07 ***	0.05 ***
	(0.02)	(0.02)	(0.01)	(0.01)	(0.01)	(0.01)
Total neighborhood	0.10 ***	0.10 ***	0.10 ***	0.10 ***	0.10 ***	0.10 ***
	(0.02)	(0.02)	(0.01)	(0.01)	(0.01)	(0.01)
N	135667	135667	135667	135667	135667	135667
AIC	37360.86	23022.29	49182.55	59432.25	68444.14	76478.54
BIC	37478.68	23140.10	49300.37	59550.06	68561.96	76596.36
Pseudo R^2	0.02	0.02	0.02	0.03	0.03	0.03

All continuous predictors are mean-centered and scaled by 1 standard deviation. Significance niveau: *** $p < 0.001$; ** $p < 0.01$; * $p < 0.05$.

[1] Unknown = Production categories are missing for particular months.

Table S6: Results of the multiple logistic regression models based on a data of previous 3 months. Association between *S.* Dublin infections and local (radius of 5 km) and trade transmissions in the next month, two, three, four, five, and six months, adjusted for farm size, trade month, production category and total neighborhood (in a radius of 5 km around the infected farm). N.B. local transmission include all cattle farms i.e. also those premises that were not traded with infected and/or non-infected cattle farms.

	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6
(Intercept)	-4.27 ***	-3.60 ***	-3.16 ***	-2.86 ***	-2.64 ***	-2.46 ***
	(0.13)	(0.10)	(0.08)	(0.07)	(0.06)	(0.06)
Local Infection	0.11	0.08	0.07 *	0.08 *	0.08 **	0.08 **
	(0.06)	(0.04)	(0.04)	(0.03)	(0.03)	(0.03)
Trade Infection	0.61 ***	0.54 ***	0.49 ***	0.45 ***	0.43 ***	0.42 ***
	(0.05)	(0.04)	(0.03)	(0.03)	(0.02)	(0.02)
Small beef	0.20	0.05	-0.07	-0.12	-0.11	-0.12
	(0.17)	(0.13)	(0.11)	(0.09)	(0.08)	(0.08)
Dairy	-0.22	-0.14	-0.18 *	-0.18 *	-0.18 **	-0.18 **
	(0.13)	(0.10)	(0.08)	(0.07)	(0.06)	(0.06)
Heifer	-0.34 *	-0.35 ***	-0.37 ***	-0.38 ***	-0.38 ***	-0.38 ***
	(0.14)	(0.10)	(0.08)	(0.07)	(0.07)	(0.06)
Other large	0.24	0.14	0.05	0.02	-0.00	-0.01
	(0.14)	(0.11)	(0.09)	(0.08)	(0.07)	(0.07)

Other small	0.78 ***	0.53 ***	0.31 **	0.26 **	0.20 *	0.18 *
	(0.16)	(0.12)	(0.11)	(0.10)	(0.09)	(0.08)
Unknown1	0.60 ***	0.55 ***	0.48 ***	0.45 ***	0.44 ***	0.43 ***
	(0.14)	(0.10)	(0.09)	(0.08)	(0.07)	(0.06)
Herd size	0.18 ***	0.19 ***	0.21 ***	0.22 ***	0.23 ***	0.23 ***
	(0.02)	(0.02)	(0.01)	(0.01)	(0.01)	(0.01)
Trade Month	0.08 ***	0.12 ***	0.11 ***	0.10 ***	0.07 ***	0.05 ***
	(0.02)	(0.02)	(0.01)	(0.01)	(0.01)	(0.01)
Total neighborhood	0.10 ***	0.09 ***	0.10 ***	0.09 ***	0.09 ***	0.10 ***
	(0.02)	(0.02)	(0.01)	(0.01)	(0.01)	(0.01)
N	135667	135667	135667	135667	135667	135667
AIC	22994.19	37297.48	49107.40	59348.45	68350.29	76374.81
BIC	23112.01	37415.30	49225.22	59466.27	68468.11	76492.63
Pseudo R^2	0.02	0.02	0.03	0.03	0.03	0.03

All continuous predictors are mean-centered and scaled by 1 standard deviation. Significance niveau: *** $p < 0.001$; ** $p < 0.01$; * $p < 0.05$.

[1] Unknown = Production categories are missing for particular months.

Table S7: Results of the multiple logistic regression models based on a data of previous 4 months. Association between *S.* Dublin infections and local (radius of 5 km) and trade transmissions in the next month, two, three, four, five, and six months, adjusted for farm size, trade month, production category and total neighborhood (in a radius of 5 km around the infected farm). N.B. local transmission include all cattle farms i.e. also those premises that were not traded with infected and/or non-infected cattle farms.

	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6
(Intercept)	-4.28 ***	-3.63 ***	-3.18 ***	-2.89 ***	-2.67 ***	-2.49 ***
	(0.13)	(0.10)	(0.08)	(0.07)	(0.06)	(0.06)
Local Infection	0.10	0.09 *	0.10 **	0.10 **	0.10 ***	0.09 ***
	(0.06)	(0.04)	(0.04)	(0.03)	(0.03)	(0.03)
Trade Infection	0.65 ***	0.56 ***	0.51 ***	0.48 ***	0.47 ***	0.45 ***
	(0.05)	(0.03)	(0.03)	(0.03)	(0.02)	(0.02)
Dairy	-0.25	-0.17	-0.20 *	-0.20 **	-0.20 **	-0.20 ***
	(0.13)	(0.10)	(0.08)	(0.07)	(0.06)	(0.06)
Heifer	-0.35 *	-0.36 ***	-0.38 ***	-0.40 ***	-0.39 ***	-0.39 ***
	(0.14)	(0.10)	(0.08)	(0.07)	(0.07)	(0.06)
Small beef	0.20	0.05	-0.07	-0.12	-0.11	-0.12
	(0.17)	(0.13)	(0.11)	(0.09)	(0.08)	(0.08)
Other small	0.78 ***	0.53 ***	0.31 **	0.25 **	0.19 *	0.17 *
	(0.16)	(0.12)	(0.11)	(0.10)	(0.09)	(0.08)

Other large	0.23	0.13	0.04	0.01	-0.02	-0.02
	(0.14)	(0.11)	(0.09)	(0.08)	(0.07)	(0.07)
Unknown[1]	0.59 ***	0.54 ***	0.47 ***	0.44 ***	0.44 ***	0.42 ***
	(0.14)	(0.10)	(0.09)	(0.08)	(0.07)	(0.06)
Herd size	0.17 ***	0.19 ***	0.21 ***	0.22 ***	0.22 ***	0.23 ***
	(0.02)	(0.02)	(0.01)	(0.01)	(0.01)	(0.01)
Trade Month	0.08 ***	0.12 ***	0.11 ***	0.11 ***	0.07 ***	0.05 ***
	(0.02)	(0.02)	(0.01)	(0.01)	(0.01)	(0.01)
Total neighborhood	0.10 ***	0.09 ***	0.09 ***	0.09 ***	0.09 ***	0.09 ***
	(0.02)	(0.02)	(0.01)	(0.01)	(0.01)	(0.01)
N	135667	135667	135667	135667	135667	135667
AIC	22960.97	37258.34	49061.02	59277.21	68265.70	76292.78
BIC	23078.79	37376.15	49178.83	59395.03	68383.52	76410.59
Pseudo R^2	0.02	0.03	0.03	0.03	0.03	0.03

All continuous predictors are mean-centered and scaled by 1 standard deviation. Significance niveau: *** $p < 0.001$; ** $p < 0.01$; * $p < 0.05$.

[1] Unknown = Production categories are missing for particular months.

Figure S1: Map of *S.* Dublin high and low prevalence areas in Denmark. Between both regions (high and low), movement restrictions were implemented (referred to as regionalisation). The map shows the last status of the regionalisation.

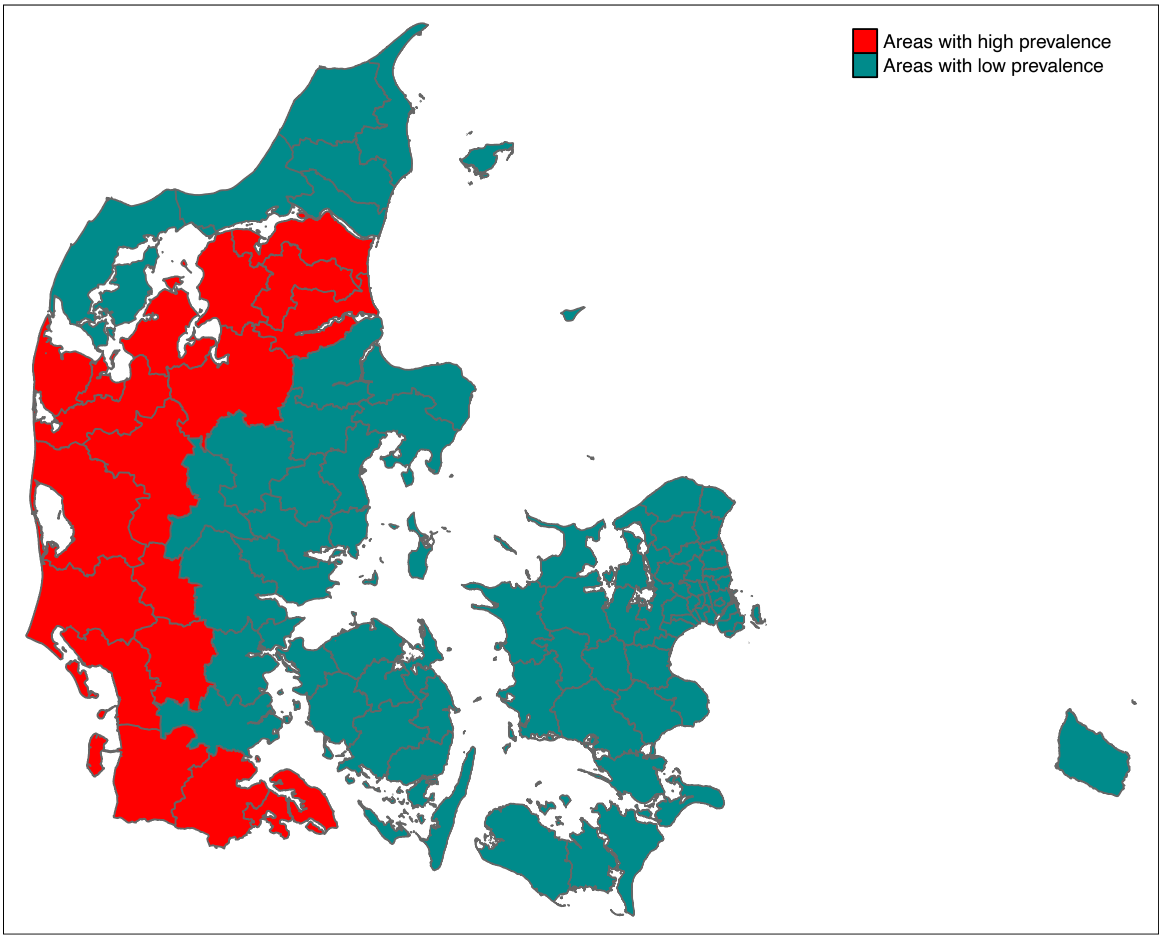


Figure S2: Changes of the production system for three randomly selected holdings according to official records from the Danish holding registry. For example, holding 2 changed its production type from a dairy producer to a slaughterhouse and then to a medical facility, all within one year.

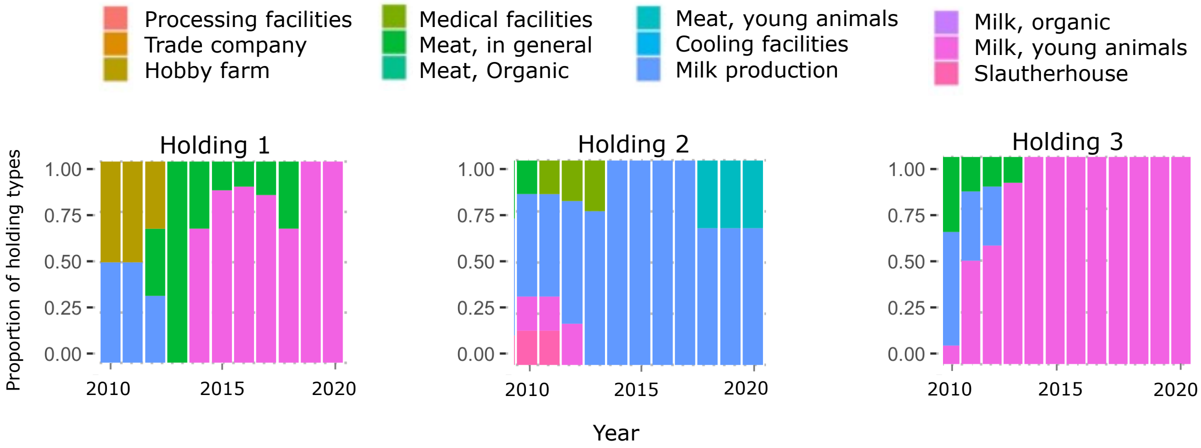


Figure S3: Proportion of movements between different regions and provinces and infection categories over a 11-year period in Denmark. (A) Movements between different regions. (B) Movements between different provinces. (C) Movements of *S.* Dublin -negative farms at the province level. (D) Movements of *S.* Dublin -positive farms at the province level. The colored lines in the circle represent movements assigned to specific regions or provinces and the thickness of the lines represents the proportion of total movements attributable to each movement. Note that the origin and destination were within the same region for a large proportion of cattle movements, ("% within"). The percentage of total movements assigned to regions or provinces is shown in the square brackets along the outer ring. For example, (A) shows that 55% of the total cattle movements originated from Southern Denmark, while 24% were within the same region and 17% were from Southern Denmark to Central Jutland.

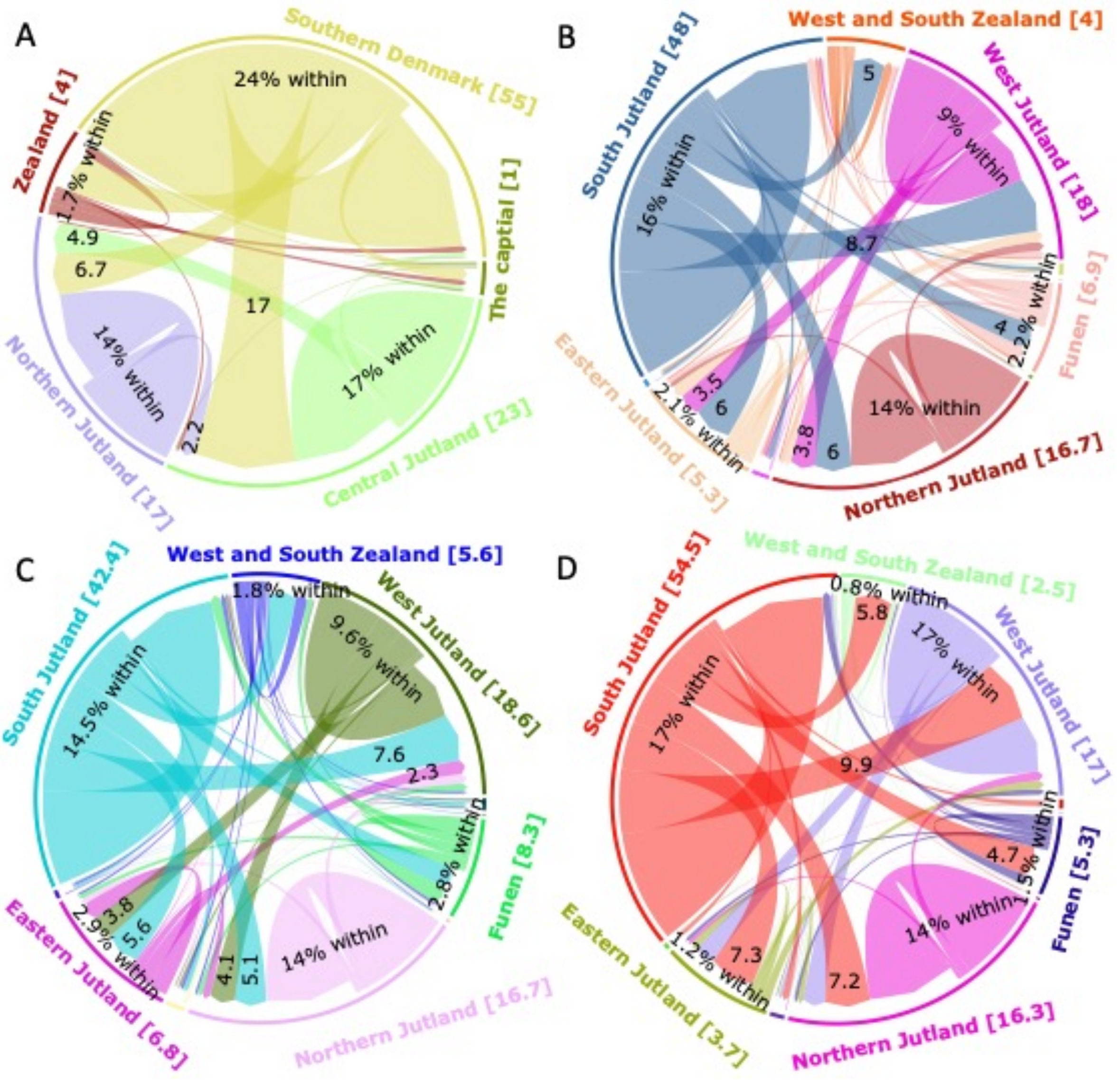


Figure S4: (A) Map of cattle farm locations in Denmark in January 2010 and January 2020. (B) Map of (scrambled) cattle farms (nodes) only with cattle movement records in January 2010 and January 2020. Links between nodes represent the trade movements and their thickness represents the number of cattle traded in January stratified for the year 2010 and 2020. Colours represent infection categories and the size of a point represents the herd size.

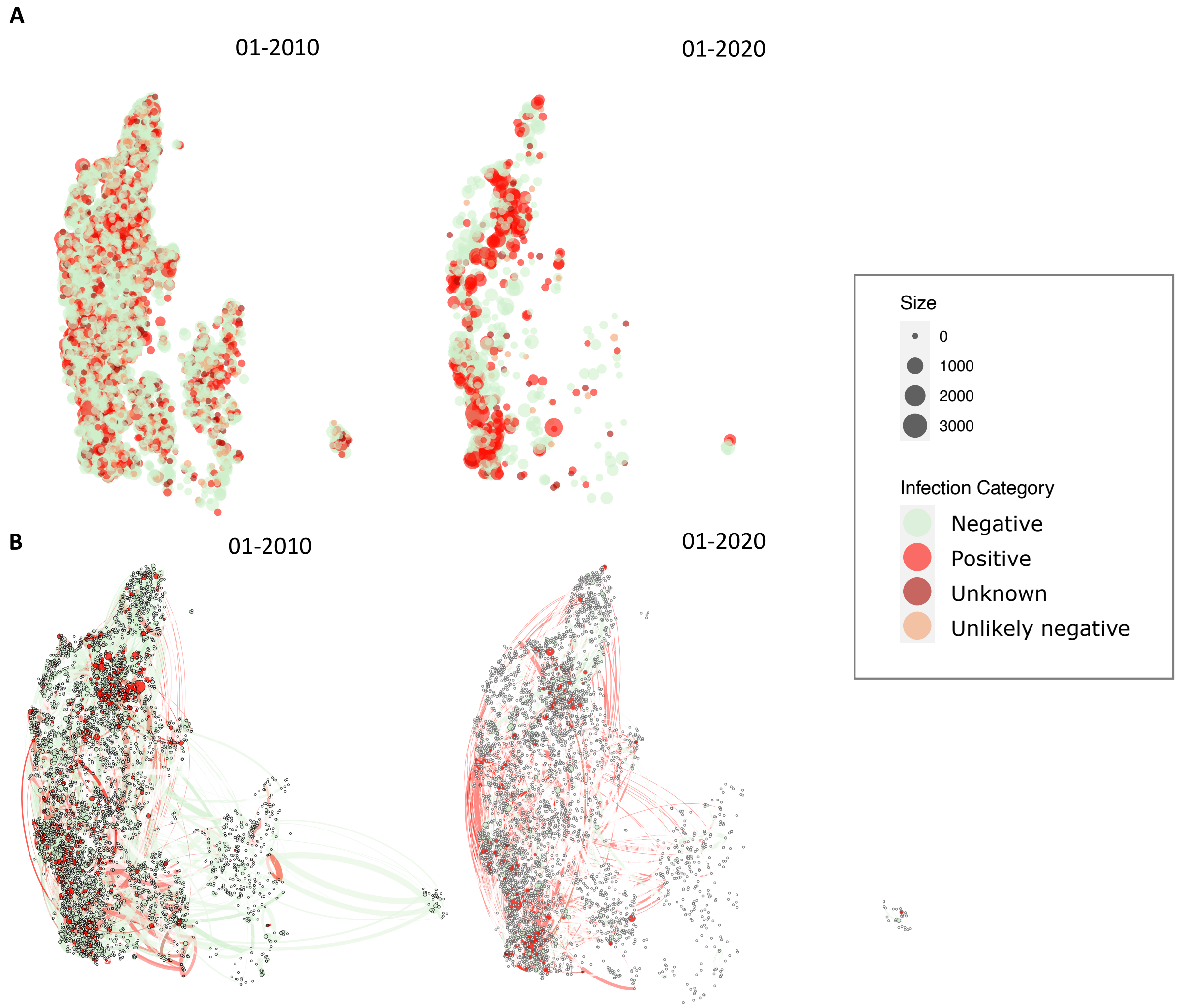


Figure S5: Apparent prevalence of *S*. Dublin in dairy farms over the 11-year period, stratified by Danish regions and aggregated at the national level.

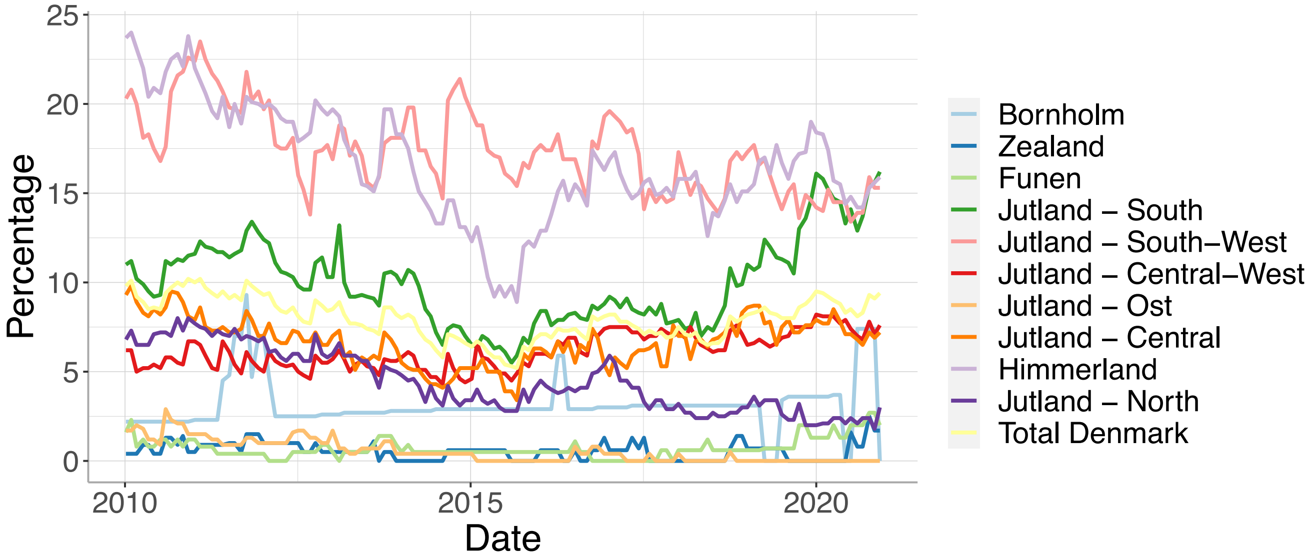


Figure S6: Network properties of non-infected farms and *S.* Dublin infected farms together: (A) Total number of farms that are trading. (B) Average degree. (C) Average path length. (D) Betweenness. (E) Density. (F) Modularity. (G) Component. (H) Closeness.

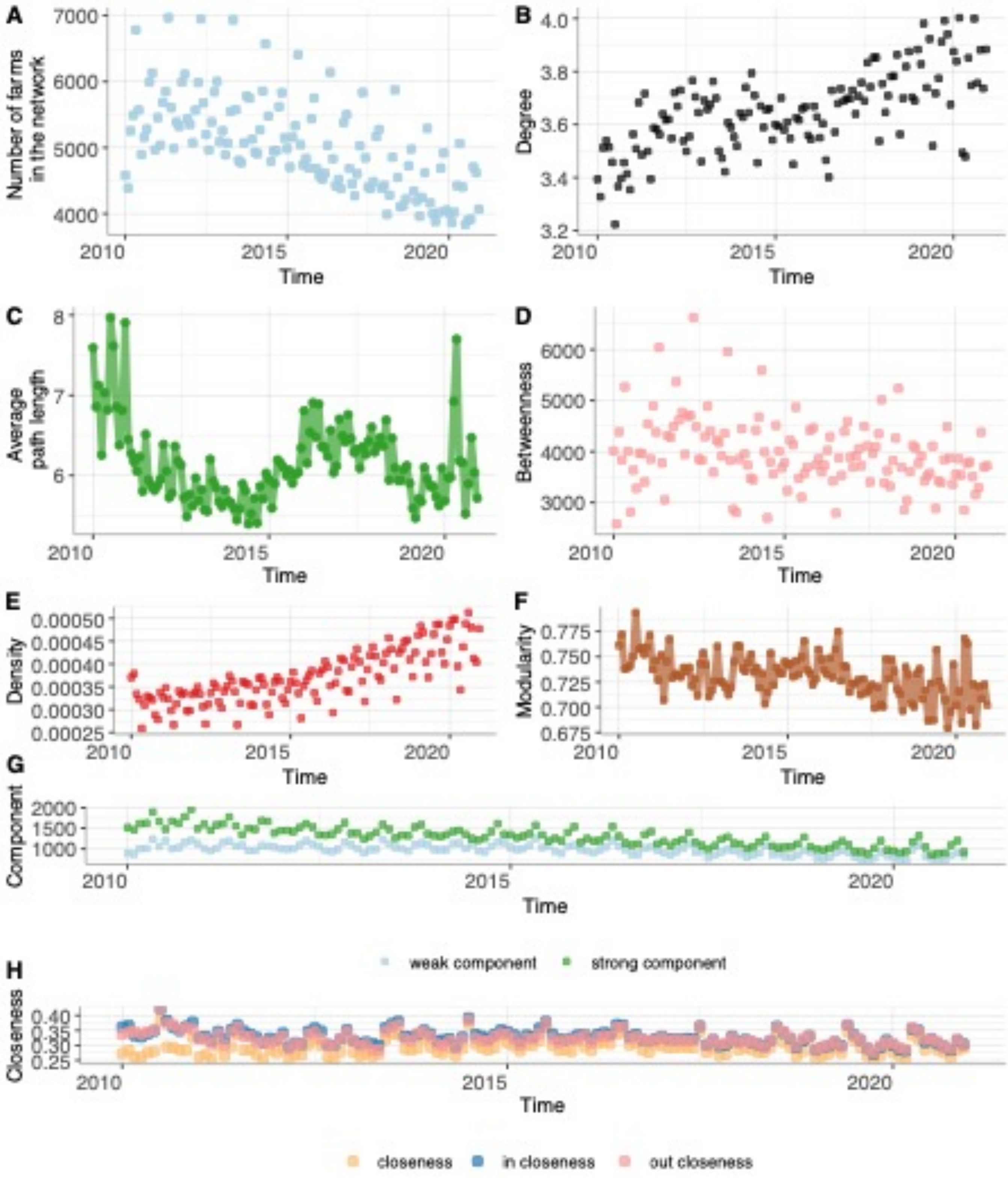
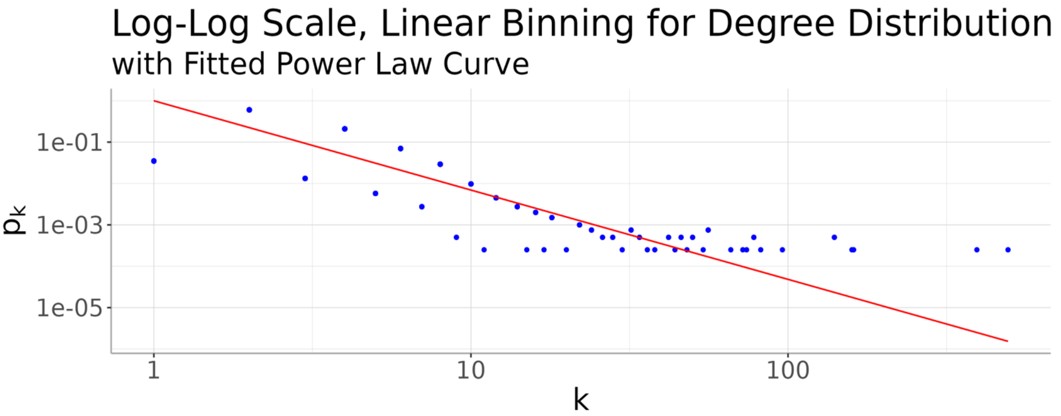


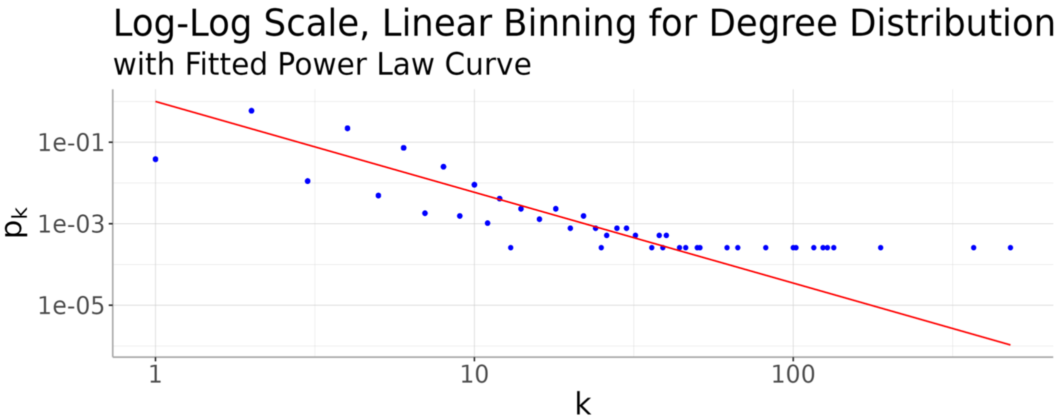
Figure S7: Degree distributions of the Danish cattle trade network for the year 2020 across select months represented on a log-log scale: (A) January, (B) February and (C) March. All other months and years from 2010 to 2020 are available upon request. The degree distribution was fitted by a power law using a maximum likelihood approach. For each month, the exponent of the fitted power law distribution, minimum value from which the power law distribution was fitted, log-likelihood of the fitted parameters, Kolmogorov-Smirnov test statistic, the fitted distribution with the input vector, and the p-value of the Kolmogorov-Smirnov-test are calculated and shown below each plot. The exponents of the fitted power law distributions were very similar across months and years and ranged between 1.9-3.3.

A)


Log-Log Scale, Linear Binning for Degree Distribution
with Fitted Power Law Curve

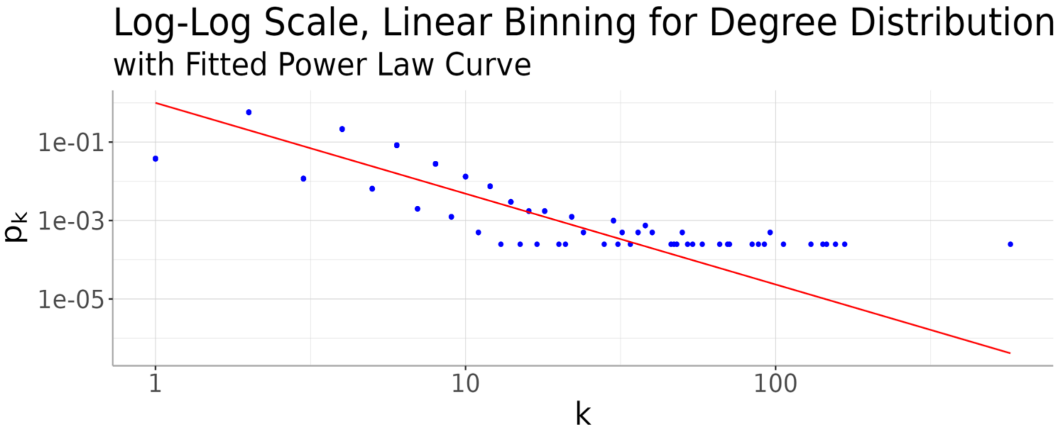
fit_power_law: exponent of the fitted power-law distribution:2.159
minimum value from which the power-law distribution was fitted:14
log-likelihood of the fitted parameters: -311
test statistic of a Kolmogorov-Smirnov test that compares the fitted distribution with the input vector. Smaller scores denote better fit: 0.075
p-value of the Kolmogorov-Smirnov test: 0.8141

B)


Log-Log Scale, Linear Binning for Degree Distribution
with Fitted Power Law Curve

fit_power_law: exponent of the fitted power-law distribution:2.228
minimum value from which the power-law distribution was fitted:16
log-likelihood of the fitted parameters: -256.66
test statistic of a Kolmogorov-Smirnov test that compares the fitted distribution with the input vector. Smaller scores denote better fit: 0.054
p-value of the Kolmogorov-Smirnov test: 0.99574

C)


Log-Log Scale, Linear Binning for Degree Distribution
with Fitted Power Law Curve

fit_power_law: exponent of the fitted power-law distribution:2.315
minimum value from which the power-law distribution was fitted:28
log-likelihood of the fitted parameters: -187.218
test statistic of a Kolmogorov-Smirnov test that compares the fitted distribution with the input vector. Smaller scores denote better fit: 0.076
p-value of the Kolmogorov-Smirnov test: 0.97886

Figure S8: The odds ratio of *S*. Dublin infection due to local (radius of 5 km) and cattle movement transmissions, across months one through six based on data of previous (A) 2-months, (B) 3-months and (C) 4-months. Adjusted for farm size, cattle movement month, production category of farms and total neighbourhood (total number of farms in a radius of 5 km around the infected farm). Note that local transmissions included all premises (i.e., including farms without cattle movements to other premises).