A new method for estimating transmission rates of mastitis-causing pathogens

**General information**

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A strain-, cow-, and herd-specific bio-economic simulation model of intramammary infections in dairy cattle herds

Intramammary infections (IMI) in dairy cattle lead to economic losses for farmers, both through reduced milk production and disease control measures. We present the first strain-, cow- and herd-specific bio-economic simulation model of intramammary infections in a dairy cattle herd. The model can be used to investigate the cost-effectiveness of different prevention and control strategies against IMI. The objective of this study was to describe a transmission framework, which simulates spread of IMI causing pathogens through different transmission modes. These include the traditional contagious and environmental spread and a new opportunistic transmission mode. In addition, the within-herd transmission dynamics of IMI causing pathogens were studied. Sensitivity analysis was conducted to investigate the influence of input parameters on model predictions. The results show that the model is able to represent various within-herd levels of IMI prevalence, depending on the simulated pathogens and their parameter settings. The parameters can be adjusted to include different combinations of IMI causing pathogens at different prevalence levels, representing herd-specific situations. The model is most sensitive to varying the transmission rate parameters and the strain-specific recovery rates from IMI. It can be used for investigating both short term operational and long term strategic decisions for the prevention and control of IMI in dairy cattle herds.

**General information**

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Epidemiology and genetic characterization of Peste des petits ruminants virus in Bangladesh

Peste des petits ruminants (PPR) is an acute, highly contagious disease responsible for high morbidity and mortality rates in susceptible sheep and goats. Adequate knowledge of the diversity of circulating strains of PPR virus will help livestock authorities choose appropriate vaccines. The objective of this study was to describe the epidemiology of PPR and characterize the strains circulating in Bangladesh. Veterinarians enrolled goats showing signs consistent with PPR, including diarrhoea, fever and respiratory distress, from three veterinary hospitals. Post-treatment follow up was carried out to ascertain health outcomes of the goats. Faecal and throat swab samples were collected from the goats and tested for PPRV RNA using real-time reverse transcription polymerase chain reaction (rRT-PCR). Nucleotide sequence-based phylogenetic analyses of two structural genes, the nucleocapsid (N gene), and the haemagglutinin (H gene) were studied to determine the genetic variations of PPRV strains. Of the 539 goats enrolled, 38% (203/539) had detectable RNA for PPRV. We were able to follow up with 91% (184/203) of the PPRV infected goats; 44% of them died. PPRV was more frequently identified in the summer (45%) than in the rainy season (29%) (Odds ratio = 1.9, 95% confidence interval: 1.3–3.1). Bangladeshi strains were phylogenetically similar to the lineage IV PPRV strains; showing particularly strong affiliation with Tibetan and Indian strains. PPR is a common viral infection of the goats in Bangladesh, with a high case-fatality rate. This study confirms the circulation of lineage IV PPRV in the country with unique amino acid substitutions in N and H proteins and provides baseline data for vaccine development and implementation.
median sensitivity for the BRSV multiplex and the BRSV ELISA was 94.4 [89.8–98.7 95% Posterior Credibility Interval (PCI)] and 99.8 [98.7–100 95% PCI], respectively. The median specificity for the BRSV multiplex was 90.6 [85.5–94.4 95% PCI], but only 57.4 [50.5–64.4 95% PCI] for the BRSV ELISA. However, increasing the cut-off of the BRSV ELISA increased specificity without compromising sensitivity. For the BCV multiplex we found that by using only one of the three antigens included in the test, the specificity increased, without concurrent loss in sensitivity. At the recommended cut-off this resulted in a sensitivity of 99.9 [99.3–100 95% PCI] and specificity of 93.7 [88.8–97.8 95% PCI] for the multiplex and a sensitivity of 99.5 [98.1–100 95% PCI] and a specificity of 99.6 [97.6–100 95% PCI] for the BCV ELISA.
Latent class analysis of real time qPCR and bacteriological culturing for the diagnosis of Streptococcus agalactiae in cow composite milk samples

Streptococcus agalactiae (S. agalactiae) has re-emerged as a mastitis pathogen among Norwegian dairy cows. The Norwegian cattle health services recommend that infected herds implement measures to eradicate S. agalactiae, this includes a screening of milk samples from all lactating cows. The performance of the qPCR-test currently in use for this purpose has not been evaluated under field conditions. The objective of this study was to estimate the sensitivity and specificity of the real-time qPCR assay in use in Norway (Mastitis 4 qPCR, DNA Diagnostics A/S, Risskov, Denmark) and compare it to conventional bacteriological culturing for detection of S. agalactiae in milk samples. Because none of these tests are considered a perfect reference test, the evaluation was performed using latent class models in a Bayesian analysis. Aseptically collected cow-composite milk samples from 578 cows belonging to 6 herds were cultured and tested by qPCR. While 37 (6.4%) samples were positive for S. agalactiae by bacteriological culture, 66 (11.4%) samples were positive by qPCR. The within-herd prevalence in the six herds, as estimated by the latent class models ranged from 7.7 to 50.8%. At the recommended cut-off (cycle threshold 37), the sensitivity of the qPCR was significantly higher at 95.3 (95% posterior probability interval [PPI] [84.2; 99.6]) than that of bacteriological culture at 58.2 (95% PPI [43.8; 74.4]). However, bacterial culture had a higher specificity of 99.7 (95% PPI [98.5; 100.0]) compared to the qPCR at 98.5 (95% PPI [94.6; 99.9]). The median estimated negative predictive values of qPCR was consistently higher than those of the BC at all estimated prevalences, and the superiority of the qPCR increased with increasing within-herd prevalence. The median positive predictive values of BC was in general higher than the estimates for the qPCR, however, at the highest prevalence the predictive ability of both tests were similar.
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Microclimatic temperatures at Danish cattle farms, 2000–2016: quantifying the temporal and spatial variation in the transmission potential of Schmallenberg virus

Microclimatic temperatures provide better estimates of vector-borne disease transmission parameters than standard meteorological temperatures, as the microclimate represent the actual temperatures to which the vectors are exposed. The objectives of this study were to quantify farm-level geographic variations and temporal patterns in the extrinsic incubation period (EIP) of Schmallenberg virus transmitted by Culicoides in Denmark through generation of microclimatic temperatures surrounding all Danish cattle farms.

Methods

We calculated the hourly microclimatic temperatures at potential vector-resting sites within a 500 m radius of 22,004 Danish cattle farms for the months April to November from 2000 to 2016. We then modeled the daily EIP of Schmallenberg virus at each farm, assuming vectors choose resting sites either randomly or based on temperatures (warmest or coolest available) every hour. The results of the model output are presented as 17-year averages.

Results: The difference between the warmest and coolest microhabitats at the same farm was on average 3.7 °C (5th and 95th percentiles: 1.0 °C to 7.8 °C). The mean EIP of Schmallenberg virus (5th and 95th percentiles) for all cattle farms during spring, summer, and autumn was: 23 (18–33), 14 (12–18) and 51 (48–55) days, respectively, assuming Culicoides select resting sites randomly. These estimated EIP values were considerably shorter than those estimated using standard meteorological temperatures obtained from a numerical weather prediction model for the same periods: 43 (39–52), 21 (17–24) and 57 (55–58) days, respectively. When assuming that vectors actively select the coolest resting sites at a farm, the EIP was 2.3 (range: 1.1 to 4.1) times longer compared to that of the warmest sites at the same farm. Conclusions: We estimated a wide range of EIP in different microclimatic habitats surrounding Danish cattle farms, stressing the importance of identifying the specific resting sites of vectors when modeling vector-borne disease transmission. We found a large variation in the EIP among different farms, suggesting disease transmission may vary substantially between regions, even within a small country. Our findings could be useful for designing risk-based surveillance, and in the control and prevention of emerging and re-emerging vector-borne diseases.
Migrating birds and carnivores introduce ticks and tick borne pathogens to Denmark – but are they also a public health risk?

Since the end of the ice age, spring migrating birds from Africa and Europe and autumn migrating birds from Northern Scandinavia have entered Denmark, and recently a small wave of long migrating carnivores have started arriving in Denmark from Central Europe. Theoretically, migrating birds could introduce new tick species as well as tick-associated pathogens to Denmark. These migrating animals may also carry ticks and pathogens which already exist in native tick populations in Denmark. The potential supplement of native ticks and existing pathogens to the established high density tick populations in Danish forest and nature areas can be expected to be of little practical importance. However, some of the infected ticks, introduced by migrating birds, may be deposited in private gardens and public parks that are otherwise not able to sustain a viable tick population. Migrating birds may therefore introduce a low level risk of tick borne infections to urban areas. Also the recent unexpected wave of long migrating golden jackals (Canis aureus) and grey wolves (Canis lupus), arriving at the Danish peninsula of Jutland, constitutes an emerging risk of introduction of especially Dermacentor spp ticks and their associated pathogens from Germany and Central Europe. Here, we present the results of screening migrating birds and a golden jackal for ticks as well as ticks collected by flagging in selected urban areas in Denmark. The collected ticks were screened for exotic tick species and 38 different tick borne pathogens. We show that the risk is not just theoretical and we suggest that these introductions may have a practical public health impact.

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Mining the Effects of Duration and Size of the Control Zones on the Consequences of a Hypothetical African Swine Fever Epidemic in Denmark

African swine fever (ASF) is a notifiable infectious disease. The disease is endemic in certain regions in Eastern Europe constituting a risk of ASF spread toward Western Europe. Therefore, as part of contingency planning, it is important to continuously explore strategies that can effectively control an epidemic of ASF. A previously published and well documented simulation model for ASF virus spread between herds was used to examine the epidemiologic and economic impacts of the duration and size of the control zones around affected herds. In the current study, scenarios were run, where the duration of the protection and surveillance zones were reduced from 50 and 45 days to 35 and 25 days or to 35 and 25 days, respectively. These scenarios were run with or without enlargement of the surveillance zone around detected herds from 10 to 15 km. The scenarios were also run with only clinical or clinical and serological surveillance of herds within the zones. Sensitivity analysis was conducted on influential input parameters in the model. The model predicts that reducing the duration of the protection and surveillance zones has no impact on the epidemiological consequences of the epidemics, while it may result in a substantial reduction in the total economic losses. In addition, the model predicts that increasing the size of the surveillance zone from 10 to 15 km may reduce both the epidemic duration and the total economic losses, in case of large epidemics. The ranking of the control strategies by the total costs of the epidemics was not influenced by changes of input parameters in the sensitivity analyses.

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Multiband modulation spectroscopy for determination of sex and species of mosquitoes in flight

We present a dual-wavelength polarimetric measurement method to distinguish species and sexes of disease transmitting mosquitoes in flight. By measuring co- and de-polarized backscattered light at 808 and 1550 nm, the degree of linear polarization, wingbeat frequency, reflectance, spectral ratio and glossiness of mosquitoes can be retrieved. Body and wing contributions to these signals can be separated. Whereas the optical cross-section is sensitive to the aspect of observation, thus the heading direction of the insect in flight, we demonstrate that polarimetric- and spectral-band ratios are largely invariant to the aspect of observation. We show that wing glossiness, as well as wing- and body-spectral ratios are particularly efficient in distinguishing Anopheles coluzzii and Anopheles arabiensis, two closely related species of malaria vectors. Spectral- and polarimetric ratios relate to microstructural and melanization features of the wing and body of these species. We conclude that multiband modulation spectroscopy is a useful expansion of the parameter space that can be used to improve specificity of entomological lidars.

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Persistence of antimicrobial resistance genes from sows to finisher pigs

Antimicrobial resistance in pigs has been under scrutiny for many years. However, many questions remain unanswered, including whether the initial antimicrobial resistance level of a pig will influence the antimicrobial resistance found at slaughter. Faecal samples from finishers pigs from 681 farms and from sows from 82 farms were collected, and levels of seven antimicrobial resistance genes, ermB, ermF, sulI, sulII, tet(M), tet(O), and tet(W), were quantified by high-capacity qPCR. There were 40 pairs of observations where the finishers were born in the farms of the sows. The objective of this study was to evaluate whether the levels of AMR genes found in finisher pigs at slaughter were associated with the levels in the farm where the finishers were born, and whether the levels of the AMR genes were equal in the sow and finisher pig populations. We found a significant positive correlation between the levels of AMR genes in finishers and the sows in the farms where the pigs were born for some of the genes (ermB (ρ = 0.47, p-value = 0.002), ermF (ρ = 0.41, p-value = 0.03), and tet(O) (ρ = 0.33, p-value = 0.04)). Furthermore, there were significant differences between AMR gene levels for the sow and finisher populations for ermB, ermF, sulI, sulII, tet(O), and tet(W), though not for tet(M).
Prevalence of Onchocerca in Danish wild deer

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Short time window for transmissibility of African swine fever virus from a contaminated environment

Since the introduction of African swine fever virus (ASFV) into the Baltic states and Poland in 2014, the disease has continued to spread within these regions. In 2017, the virus spread further west and the first cases of disease were reported in the Czech Republic and Romania, in wild boar and domestic pigs, respectively. To control further spread, knowledge of different modes of transmission, including indirect transmission via a contaminated environment, is crucial. Up until now, such an indirect mode of transmission has not been demonstrated. In this study, transmission via an environment contaminated with excretions from ASFV-infected pigs was investigated. Following euthanasia of pigs that were infected with an isolate of ASFV from Poland (POL/2015/Podlaskie/Lindholm), healthy pigs were introduced into the pens, in which the ASFV-infected pigs had been housed. Introduction was performed at 1, 3, 5 or 7 days, following euthanasia of the infected pig groups. Pigs, that were introduced into the contaminated environment after 1 day, developed clinical disease within 1 week, and both ASFV DNA and infectious virus were isolated from their blood. However, pigs introduced into the contaminated pens after 3, 5 or 7 days did not develop any signs of ASFV infection and no viral DNA was detected in blood samples obtained from these pigs within the following 3 weeks. Thus, it was shown that exposure of pigs to an environment contaminated with ASFV can result in infection. However, the time window for transmissibility of ASFV seems very limited, and, within our experimental system, there appears to be a rapid decrease in the infectivity of ASFV in the environment.

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Spatial and temporal variation in the abundance of Culicoides biting midges (Diptera: Ceratopogonidae) in nine European countries

Biting midges of the genus Culicoides (Diptera: Ceratopogonidae) are vectors of bluetongue virus (BTV), African horse sickness virus and Schmallenberg virus (SBV). Outbreaks of both BTV and SBV have affected large parts of Europe. The spread of these diseases depends largely on vector distribution and abundance. The aim of this analysis was to identify and quantify major spatial patterns and temporal trends in the distribution and seasonal variation of observed Culicoides abundance in nine countries in Europe. We gathered existing Culicoides data from Spain, France, Germany, Switzerland, Austria, Denmark, Sweden, Norway and Poland. In total, 31,429 Culicoides trap collections were available from 904 ruminant farms across these countries between 2007 and 2013. The Obsoletus ensemble was distributed widely in Europe and accounted for 83% of all 8,842,998 Culicoides specimens in the dataset, with the highest mean monthly abundance recorded in France, Germany and southern Norway. The Pulicaris ensemble accounted for only 12% of the specimens and had a relatively southerly and easterly spatial distribution compared to the Obsoletus ensemble. Culicoides imicola Kieffer was only found in Spain and the southernmost part of France. There was a clear spatial trend in the accumulated annual abundance from southern to northern Europe, with the Obsoletus ensemble steadily increasing from 4000 per year in southern Europe to 500,000 in Scandinavia. The Pulicaris ensemble showed a very different pattern, with an increase in the accumulated annual abundance from 1600 in Spain, peaking at 41,000 in northern Germany and then decreasing again toward northern latitudes. For the two species ensembles and C. imicola, the season began between January and April, with later start dates and increasingly shorter vector seasons at more northerly latitudes. We present the first maps of seasonal Culicoides abundance in large parts of Europe covering a gradient from southern Spain to northern Scandinavia. The identified temporal trends and spatial patterns are useful for planning the allocation of resources for international prevention and surveillance programmes in the European Union.

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A Cow- and Herd-specific Bio-Economic Model of Intramammary Infections in Dairy Cows

Introduction. Mastitis, or intramammary infection (IMI), is one of the most significant diseases in dairy herds worldwide. It is caused by environmental and contagious bacteria. Simulation models have proven useful for evaluating the effect of different control strategies. However, previous published models are not cow-specific and therefore not so detailed in the simulation of host-pathogen interactions. If a simulation model is to be used by dairy farmers as a decision-making tool, it needs to be cow-specific because daily management decisions are made on cow level. Furthermore, as IMI is often caused by more than one pathogen in the same herd, such a simulation model should also be pathogen-specific to account for different transmission characteristics and treatment effects. Moreover, as different strains of pathogens can have different transmission routes (i.e. environmental, contagious or mixed), the model should be able to reflect this diversity. Our objective was thus to create a pathogen-, cow- and herd-specific bio-economic simulation model that could simulate multiple pathogens and strains at the same time within a dairy herd. This model should be able to simulate realistic scenarios for specific herds, thus being a tool for decision-making for individual farmers. Methods: We used an existing mechanistic, stochastic simulation model framework to create an IMI simulation model. This mechanistic model simulates a dairy herd in great detail; i.e. with individual lactation curves for all cows, continuous movement of cows between farm sections and continuous culling decisions made by the farmer. We expanded the model to simulate the individual quarters of cows. This procedure made it possible for cows to have up to four different infections at a time, one per quarter. We implemented two different transmission modes, namely environmental transmission based on a continuous reservoir of pathogens in the farm, and contagious IMI originating from other infected animals in the herd. Currently, the environmental pathogen included is Escherichia coli, and the contagious pathogens are Staphylococcus aureus, Streptococcus agalactiae and Streptococcus uberis. The contagious transmission is simulating transmission, e.g. via milk liners, and depends on the number of quarters with contagious pathogens in the herd. We chose to focus on these four pathogens because they are common in Danish dairy farms. We modelled the increase in somatic cell count (SCC) due to subclinical infection. The reduction in milk yield for individual cows is then based on their SSC. Thus we are able to estimate the economic consequences of each IMI pathogen in the herd, simulate different control scenarios and estimate their epidemiological and economic effects.
A cross-sectional field study on potential associations between feed quality measures and usage of antimicrobials in commercial mink (Neovison vison)

Feed quality is generally assumed to affect health status in animal production. In previous studies, the feed producer has been found to affect the occurrence of gastrointestinal disease and antimicrobial use in Mink (Neovison vison). Mink are fed with moist, freshly produced feed, based on perishable ingredients. The objective of this study was to investigate the potential effect of specific feed parameters on antimicrobial use on herd level. The study was cross-sectional, including 1472 mink herds, responsible for 97% of oral antimicrobials prescribed for Danish mink during the study period, 2012-2014. Data were obtained from the national veterinary prescription database (VetStat), Copenhagen Fur database, and the Voluntary Feed Control (Mink producers Organization). All feed batches subject to feed control were included. A multivariable variance analysis was carried out analysing the effect of the feed parameters total volatile nitrogen, dry matter, crude protein and fat; total bacterial count (21 °C), and counts of sulphite producing bacteria (21 °C), Clostridium spp., faecal cocci (FC) (44 °C), yeast, and mould; presence of Salmonella spp. and Clostridium perfringens (dichotome). Three outcome variables were applied: prescription of oral antimicrobial on herd level within time slots of 3, 5 or 7 days after feeding. Two binomial models were developed, adjusting for significant effects (p < 0.0001) of Ps. aeruginosa infection, herd size, month (season) and year. Antimicrobial prescription was significantly (p < 0.0001) associated with FC (all time slots, both models). A negative association (p < 0.0001) with crude protein on antimicrobial prescription within a 7 day slot suggested an association between low content of crude protein and antimicrobial use. The associations need to be confirmed in controlled studies, and ideally, potential causalities should be investigated. The perspective of such findings could be the development of tests for control of feed ingredients prior to use in the feed production.
A cross-sectional study of oral antibacterial treatment patterns in relation to specific diarrhoeal pathogens in weaner pigs

According to international guidelines, the use of antibacterials should be evidence based and prudent. This register-based, cross-sectional study investigates the potential effect of laboratory findings on the patterns of antibacterial oral (batch) medication of weaner pigs, and the level of compliance with national guidelines for antibacterial use. The study population includes 1,736 weaner herds (~65% of all Danish weaner pigs) that were subject to laboratory analysis from the National Veterinary Institute on Brachyspira pilosicoli, Lawsonia intracellularis, and E.coli (F4 and F18) in 2014. Antibacterial prescription data were obtained from the national database, VetStat. These showed that antibacterial prescriptions for use in weaner pigs was 8.6% lower in spring 2015 compared to spring 2014. The antibacterial use per pig tended (p = 0.08) to decrease more in herds with negative laboratory results compared to herds with a moderate or massive occurrence of either of the pathogens. Irrespective of the laboratory findings on diarrhoeal pathogens, tetracyclines were the most frequently used antibacterials by a substantial margin, both 3 months prior to and 2-5 months after laboratory analysis. According to the national guidelines, tetracyclines are the second or third-choice antibacterial for treatment of diarrhoeal pathogens, due to resistance and co-resistance patterns. Compliance with the guidelines increased in 14% of the herds, mostly following identification of B. pilosicoli within the herd. Between 10% and 20% of the herds did not use batch treatment, despite the presence of moderate–massive amounts of the pathogens.
A mechanistic model for spread of livestock-associated methicillin-resistant Staphylococcus aureus (LA-MRSA) within a pig herd

Before an efficient control strategy for livestock-associated methicillin resistant *Staphylococcus aureus* (LA-MRSA) in pigs can be decided upon, it is necessary to obtain a better understanding of how LA-MRSA spreads and persists within a pig herd, once it is introduced. We here present a mechanistic stochastic discrete-event simulation model for spread of LA-MRSA within a farrow-to-finish sow herd to aid in this. The model was individual-based and included three different disease compartments: susceptible, intermittent or persistent shedder of MRSA. The model was used for studying transmission dynamics and within-farm prevalence after different introductions of LA-MRSA into a farm. The spread of LA-MRSA throughout the farm mainly followed the movement of pigs. After spread of LA-MRSA had reached equilibrium, the prevalence of LA-MRSA shedders was predicted to be highest in the farrowing unit, independent of how LA-MRSA was introduced. LA-MRSA took longer to spread to the whole herd if introduced in the finisher stable, rather than by gilts in the mating stable. The more LA-MRSA positive animals introduced, the shorter time before the prevalence in the herd stabilised. Introduction of a low number of intermittently shedding pigs was predicted to frequently result in LA-MRSA fading out. The model is a potential decision support tool for assessments of short and long term consequences of proposed intervention strategies or surveillance options for LA-MRSA within pig herds.
A multivariate dynamic linear model for early warnings of diarrhea and pen fouling in slaughter pigs

We present a method for providing early, but indiscriminant, predictions of diarrhea and pen fouling in grower/finisher pigs. We collected data on dispensed feed amount, water flow, drinking bouts frequency, temperature at two positions per pen, and section level humidity from 12 pens (6 double pens) over three full growth periods. The separate data series were co-modeled at pen level with time steps of one hour, using a multivariate dynamic linear model. The step-wise forecast errors of the model were unified using Cholesky decomposition. An alarm was raised if the unified error exceeded a set threshold a sufficient number of times, consecutively. Using this method with a 7 day prediction window, we achieved an area under the receiver operating characteristics curve of 0.84. Shorter prediction windows yielded lower performances, but longer prediction windows did not affect the performance.
Antimicrobial resistance among pathogenic bacteria from mink (Neovison vison) in Denmark

Background: For proper treatment of bacterial infections in mink, knowledge of the causative agents and their antimicrobial susceptibility patterns is crucial. The used antimicrobials are in general not registered for mink, i.e. most usage is "off-label". In this study, we report the patterns of antimicrobial resistance among pathogenic bacteria isolated from Danish mink during the period 2014-2016. The aim of this investigation was to provide data on antimicrobial resistance and consumption, to serve as background knowledge for new veterinary guidelines for prudent and optimal antimicrobial usage in mink. Results: A total number of 308 Escherichia coli isolates, 41 Pseudomonas aeruginosa, 36 Streptococcus canis, 30 Streptococcus dysgalactiae, 55 Staphylococcus delphini, 9 Staphylococcus aureus, and 20 Staphylococcus schleiferi were included in this study. Among E. coli, resistance was observed more frequently among the hemolytic isolates than among the non-hemolytic ones. The highest frequency of resistance was found to ampicillin, 82.3% and 48.0% of the hemolytic and the non-hemolytic isolates, respectively. The majority of the P. aeruginosa isolates were only sensitive to...
ciprofloxacin and gentamicin. Among the *Staphylococcus spp.*, the highest occurrence of resistance was found for tetracycline. Regarding the nine *S. aureus*, one isolate was resistant to cefoxitin indicating it was a methicillin-resistant *Staphylococcus aureus*. Both β-hemolytic *Streptococcus* species showed high levels of resistance to tetracycline and erythromycin. The antimicrobial consumption increased significantly during 2007-2012, and fluctuated at a high level during 2012-2016, except for a temporary drop in 2013-2014. The majority of the prescribed antimicrobials were aminopenicillins followed by tetracyclines and macrolides. Conclusions: The study showed that antimicrobial resistance was common in most pathogenic bacteria from mink, in particular hemolytic *E. coli*. There is a need of guidelines for prudent use of antimicrobials for mink.

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Antimicrobial resistance in Danish pigs: A cross sectional study of the association between antimicrobial resistance and geography, exposure to antimicrobials, and trade

Antimicrobial resistance is a worldwide problem of paramount importance for both humans and animals. To combat the emergence of antimicrobial resistance, the problem must be targeted in all major reservoirs as it is assumed that a high level of AMR genes in environmental reservoirs can increase the risk of human pathogens becoming resistant. Pigs might constitute an important reservoir. Therefore, it is important to manage antimicrobial resistance in pigs. Before effective actions can be initiated, it is crucial to know which factors are associated with the levels of antimicrobial resistance in pigs. The Danish pig farm is an ideal place to study AMR, as the pigs are all kept together in a confined space and managed in a similar manner. Furthermore, movements of pigs between farms and the purchase of antimicrobials for use at the farm are registered in national databases, thus facilitating the collection of information on relevant factors. The aim of this PhD project was to study the relationship between the levels of antimicrobial resistance genes and three factors in Danish pig farms: the geographical location of the farm, the exposure to antimicrobials, and the trade patterns. Data collection was necessary in order to fulfill the aim of the project, and early in the project it became evident that a thorough consideration of how the data should be collected was needed. This resulted in three different projects, each contributing to the planning process. Throughout the entire PhD project, the focus was on seven antimicrobial resistance genes - ermB, ermF, sulI, sulII, tet(M), tet(O), and tet(W). The levels of these genes were determined using a quantitative real-time polymerase chain reaction (qPCR). The erm genes confer resistance against macrolides, the sul genes confer resistance against sulfonamides, and the tet genes confer resistance against tetracyclines. It was necessary to determine the minimum number of individual faecal samples that should be pooled together to represent the average level of antimicrobial resistance genes in the farm. It was estimated that a sample pooled from individual samples from five pigs was optimal. The pooling method was optimised, and was found to have strong agreement with previously used pooling methods. Samples were collected from 687 Danish pig farms in February and March 2015. However, 6 farms did not fulfil the criteria for the target population and were excluded. The samples were collected at five abattoirs located on Zealand and in Jutland. The sample material was faeces, and it was collected by squeezing a small amount out of the rectum at the slaughter line. After collection the samples were sent to the laboratory. The samples were pooled into one aliquot per farm and DNA was extracted from the faecal material. The antimicrobial resistance gene levels were then measured using quantitative real-time PCR. As the samples were collected at the abattoir it was not possible to know in advance which farms were available for sampling. Consequently, it was not possible to estimate whether the sampled farms were representative of the target and study populations prior to sampling. However, an evaluation of the representativeness of sampled farms (in terms of farm size and geographical location) was carried out post-sampling. It was found that the
sampled farms were larger than nonsampled farms. Furthermore, there was an undersampled area in the western part of Jutland and an oversampled area in the northern part of Jutland. A simulation study showed that the sampling procedure would inevitably result in a bias towards larger farms and with some non-randomness in the spatial distribution. One of the aims of this PhD project was to estimate the quantitative relationship between the antimicrobial resistance gene levels and antimicrobial exposure. Previous studies have indicated that antimicrobial exposure in early periods of a pig’s life can influence the antimicrobial resistance genes levels found later in life. In order to quantify the relationship, an estimate of the antimicrobial exposure throughout the entire lifetime of a slaughter pig was required. An algorithm to estimate the LEA was therefore developed. Previous studies have shown that livestock farms in close proximity share common pathogens. Furthermore, there have been indications that phenotypic antimicrobial resistance can be spatially clustered. Therefore, the spatial pattern of the antimicrobial resistance gene levels was assessed, and both areas with high levels and areas with low levels of some of the genes were found. However, it was concluded that the geographical location of the farm had only a minor effect on the antimicrobial resistance gene levels. Antimicrobial exposure is the most important risk factor for the development of antimicrobial resistance. However, previous studies of the relationship between antimicrobial resistance and antimicrobial exposure have focused on phenotypic antimicrobial resistance in a small number of farms. In this PhD project, the focus was on genotypic antimicrobial resistance. The quantitative relationship between the levels of seven antimicrobial resistance genes and the lifetime exposure of 11 different antimicrobial classes was estimated. It was found that some antimicrobial classes had a positive correlation with the levels of some antimicrobial resistance genes, but a negative correlation with other antimicrobial resistance genes. In conclusion, it was found that even though exposure to antimicrobials was associated with the antimicrobial resistance gene levels, it could only explain 10% - 42% of the variation in the gene levels. The microflora of a pig is established soon after birth. The source of the microflora is bacteria in the environment and from the sow. It has been shown that antimicrobial exposure of the sow will influence the antimicrobial resistance levels in the piglet. Therefore, the correlation between the levels of antimicrobial resistance genes in finisher farms and that of the sow farms with which they had trade connections was assessed. A significant correlation was found for most of the antimicrobial resistance genes with correlation coefficients ranging from 0.06 to 0.47. Of the three factors that were studied in this PhD project, only the antimicrobial exposure and the level of antimicrobial resistance in the sow farm with a trade connection were found to have a considerable effect on the antimicrobial resistance genes. However, it became apparent during the project that many other factors could affect the levels of antimicrobial resistance genes. This could lay the foundation for future studies.

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A prospective observational longitudinal study of new-onset seizures and newly diagnosed epilepsy in dogs

Seizures are common in dogs and can be caused by non-epileptic conditions or epilepsy. The clinical course of newly diagnosed epilepsy is sparsely documented. The objective of this study was to prospectively investigate causes for seizures (epileptic and non-epileptic) in a cohort of dogs with new-onset untreated seizures, and for those dogs with newly diagnosed epilepsy to investigate epilepsy type, seizure type and the course of disease over time, including the risk of seizure recurrence. Untreated client-owned dogs experiencing new-onset seizures were prospectively enrolled in a longitudinal observational study including clinical investigations and long-term monitoring at the Copenhagen University Hospital for Companion Animals. A baseline clinical assessment was followed by investigator/owner contact every eight weeks from inclusion to death or end of study. Inclusion of dogs was conducted from November 2010 to September 2012, and the study terminated in June 2014. One hundred and six dogs were included in the study. Seventy-nine dogs (74.5%) were diagnosed with epilepsy: 61 dogs (77.2%) with idiopathic epilepsy, 13 dogs (16.5%) with structural epilepsy and five dogs (6.3%) with suspected structural epilepsy. A non-epileptic cause for seizures was identified in 13 dogs and suspected in 10 dogs. Four dogs in which no cause for seizures was identified experienced only one seizure during the study. In dogs with idiopathic epilepsy 60% had their second epileptic seizure within three months of seizure onset. Twenty-six dogs with idiopathic epilepsy (43%) completed the study without receiving antiepileptic treatment. The natural course of idiopathic epilepsy (uninfluenced by drugs) was illustrated by highly individual and fluctuating seizure patterns, including long periods of remission. Cluster seizures motivated early treatment. In a few dogs with a high seizure frequency owners declined treatment against the investigators advice. Epilepsy is the most likely diagnosis in dogs presenting with new-onset seizures. The course of idiopathic epilepsy is highly individual and might not necessarily require long-term treatment. This must be considered when advising owners about what to expect with regard to treatment and prognosis.
A Robust Statistical Model to Predict the Future Value of the Milk Production of Dairy Cows Using Herd Recording Data

The future value of an individual dairy cow depends greatly on its projected milk yield. In developed countries with developed dairy industry infrastructures, facilities exist to record individual cow production and reproduction outcomes consistently and accurately. Accurate prediction of the future value of a dairy cow requires further detailed knowledge of the costs associated with feed, management practices, production systems, and disease. Here, we present a method to predict the future value of the milk production of a dairy cow based on herd recording data only. The method consists of several steps to evaluate lifetime milk production and individual cow somatic cell counts and to finally predict the average production for each day that the cow is alive. Herd recording data from 610 Danish Holstein herds were used to train and test a model predicting milk production (including factors associated with milk yield, somatic cell count, and the survival of individual cows). All estimated parameters were either herd- or cow-specific. The model prediction deviated, on average, less than 0.5 kg from the future average milk production of dairy cows in multiple herds after adjusting for the effect of somatic cell count. We conclude that estimates of future average production can be used on a day-to-day basis to rank cows for culling, or can be implemented in simulation models of within-herd disease spread to make operational decisions, such as culling versus treatment. An advantage of the approach presented in this paper is that it requires no specific knowledge of disease status or any other information beyond herd recorded milk yields, somatic cell counts, and reproductive status.

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A simulation study to evaluate the performance of five statistical monitoring methods when applied to different time-series components in the context of control programs for endemic diseases

Disease monitoring and surveillance play a crucial role in control and eradication programs, as it is important to track implemented strategies in order to reduce and/or eliminate a specific disease. The objectives of this study were to assess the performance of different statistical monitoring methods for endemic disease control program scenarios, and to explore what impact of variation (noise) in the data had on the performance of these monitoring methods. We simulated 16 different scenarios of changes in weekly sero-prevalence. The changes included different combinations of increases, decreases and constant sero-prevalence levels (referred as events). Two space-state models were used to model the time series, and different statistical monitoring methods (such as univariate process control algorithms–Shewart Control Chart, Tabular Cumulative Sums, and the V-mask- and monitoring of the trend component–based on 99% confidence intervals and the trend sign) were tested. Performance was evaluated based on the number of iterations in which an alarm was raised for a given week after the changes were introduced. Results revealed that the Shewhart Control Chart was better at detecting increases over decreases in sero-prevalence, whereas the opposite was observed for the Tabular Cumulative Sums. The trend-based methods detected the first event well, but performance was poorer when adapting to several consecutive events. The V-Mask method seemed to perform most consistently, and the impact of noise in the baseline was greater for the Shewhart Control Chart and Tabular Cumulative Sums than for the V-Mask and trend-based methods. The performance of the different statistical monitoring methods varied when monitoring increases and decreases in disease sero-prevalence. Combining two of more methods might improve the potential scope of surveillance systems, allowing them to fulfill different objectives due to their complementary advantages.
Bacterial antimicrobial resistance (AMR) in pigs is an important public health concern due to its possible transfer to humans. We aimed at quantifying the relationship between the lifetime exposure of antimicrobials and seven antimicrobial resistance genes in Danish slaughter pig farms. AMR gene levels were quantified by qPCR of total-community DNA in faecal samples obtained from 681 batches of slaughter pigs. The lifetime exposure to antimicrobials was estimated at batch level for the piglet, weaner, and finisher periods individually for the sampled batches. We showed that the effect of antimicrobial exposure on the levels of AMR genes was complex and unique for each individual gene. Several antimicrobial classes had both negative and positive correlations with the AMR genes. From 10-42% of the variation in AMR gene levels could be explained in the final regression models, indicating that antimicrobial exposure is not the only important determinant of the AMR gene levels.
Associations between Antibacterial Treatment and the Prevalence of Tail- Biting-Related Sequelae in Danish Finishers at Slaughter

Secondary infections as a result of tail biting cause substantial economic losses in pig production and are a subject of concern for animal welfare. The use of first-choice antibacterial agents in the treatment of tail biting in finishing pigs is hypothesized to be negatively correlated with the development of systemic infection. This would be expected to reduce the prevalence of post-mortem pyemic sequelae (such as osteomyelitis and abscesses) in finishers with tail-bite lesions. We performed a register-based study that included three Danish databases, holding information on the purchase of antibacterials at herd level (VetStat), herd demographics (Central Husbandry Register), and relevant observations at slaughter (meat inspection data). We included all finishers from indoor production finisher herds that met the inclusion criterion of at least one slaughtered finisher with a recorded tail-bite observation during 2015 at the single largest Danish abattoir. The final dataset held 1,070 herds with one or more tail-bite observations, from which 14,411 of 2,906,626 finishers (0.50%) had an individual record of a tail bite. Within this group of finishers with tail-bite observations, the recorded tail-biting-related sequelae included osteomyelitis (8.1%), abscesses in the hindquarters (10.5%), abscesses in the forequarters (2.3%), abscesses in the mid-section of the carcass (2.9%), abscesses in the limbs (2.4%), and chronic arthritis (0.5%). Due to a high-herd prevalence (>25%), osteomyelitis and abscesses in the hindquarters were selected for further analysis. The occurrence of osteomyelitis and hindquarter abscesses in individual finishers with tail-bite observations was described using a generalized linear mixed effects model with binomial response and logit link. Herd was included as a random effect, while herd size and various antibacterial treatments were tested for inclusion in the model as fixed effects. The final models indicated a significant association between herd size and both osteomyelitis (p = 0.014) and hindquarter abscesses (p < 0.001), with larger herds (2,001–12,000 registered finisher pigs) showing a reduced risk. Further, a negative association was found between the occurrence of hindquarter abscesses and the use of oral pleuromutilin (p = 0.022). The significant association with herd size highlights the potential importance of management
Big data - modelling of midges in Europe using machine learning techniques and satellite imagery

Biting midges (Diptera, Ceratopogonidae) of the genus Culicoides are important vectors of pathogens causing diseases in free living and production animals and can lead to large economic losses in many European countries. In Europe, Culicoides imicola and the Obsoletus group are considered to be the main vectors of bluetongue virus that mostly affects ruminants such as cattle and sheep. Spatio-temporal modelling of vector distribution and abundance allows us to identify high risk areas for virus transmission and can aid in applying effective surveillance and control measures.

We used presence-absence and monthly abundance data of Culicoides from 1005 sites across 9 countries (Spain, France, Denmark, Poland, Switzerland, Austria, Poland, Sweden, Norway) collected between the years 2007 and 2013. The dataset included information on the vector species abundance (number of specimens caught per night), GPS coordinates of each trap, start and end dates of trapping. We used 120 environmental predictor variables together with Random Forest machine learning algorithms to predict the overall species distribution (probability of occurrence) and monthly abundance in Europe. We generated maps for every month of the year, to visualize the abundance of C. imicola and Obsoletus group in Europe as well as distribution maps showing the probability of occurrence.

We were able to create predictive maps of both Culicoides sp. occurrence and abundance using Random Forest models, and although the variance was large, the predicted abundance values for each site had a positive correlation with the observed abundance. We found relatively large spatial variations in probability of occurrence and abundance for both C. imicola and the Obsoletus group. For C. imicola probability of occurrence and abundance was higher in southern Spain, where as the Obsoletus group had higher probability of occurrence and abundance in central and northern Europe such as France and Germany. Temporal variation was also observed with higher abundance occurring during summer months and low or no abundance during winter months for both C. imicola and the Obsoletus group, although abundance was generally higher for a longer period of time for C. imicola than for the Obsoletus group.

Using machine learning techniques, we were able to model the spatial distribution in Europe for C. imicola and the Obsoletus group in terms of abundance and suitability (probability of occurrence). Our maps corresponded well with the previously reported distribution for C. imicola and the Obsoletus group. The observed seasonal variation was also consistent with reported population dynamics for Culicoides, as it depends on environmental factors such as temperature and rainfall. Longer seasonal abundance for C. imicola compared to the Obsoletus group can be explained by the species distribution, as C. imicola is limited to the southern parts of Europe where the warm season lasts longer, whereas the Obsoletus group is found further north. The outputs obtained here will be used as input for epidemiological models and can be helpful for determining high risk areas for disease transmission.

General information
Biosecurity Conditions in Small Commercial Chicken Farms, Bangladesh 2011-2012

In Bangladesh, highly pathogenic avian influenza H5N1 is endemic in poultry. This study aimed to understand the biosecurity conditions and farmers' perception of avian influenza biosecurity in Bangladeshi small commercial chicken farms. During 2011-2012, we conducted observations, in-depth interviews and group discussions with poultry farmers in 16 farms and in-depth interviews with seven local feed vendors from two districts. None of the farms were completely segregated from people, backyard poultry, other animals, households, other poultry farms or large trees. Wild birds and rodents accessed the farms for poultry feed. Farmers usually did not allow the buyers to bring egg trays inside their sheds. Spraying disinfectant in the shed and removing feces were the only regular cleaning and disinfection activities observed. All farmers sold or used untreated feces as fish feed or fertilizer. Farmers were more concerned about Newcastle disease and infectious bursal disease than about avian influenza. Farmers' understanding about biosecurity and avian influenza was influenced by local vendors. While we seldom observed flock segregation, some farmers used measures that involved additional cost or effort to protect their flocks. These farmers could be motivated by interventions to protect their investment from diseases they consider harmful. Future interventions could explore the feasibility and effectiveness of low-cost alternative biosecurity measures.
Computational algorithm for lifetime exposure to antimicrobials in pigs using register data – the LEA algorithm

Accurate and detailed data on antimicrobial exposure in pig production are essential when studying the association between antimicrobial exposure and antimicrobial resistance. Due to difficulties in obtaining primary data on antimicrobial exposure in a large number of farms, there is a need for a robust and valid method to estimate the exposure using register data. An approach that estimates the antimicrobial exposure in every rearing period during the lifetime of a pig using register data was developed into a computational algorithm. In this approach data from national registers on antimicrobial purchases, movements of pigs and farm demographics registered at farm level are used. The algorithm traces batches of pigs retrospectively from slaughter to the farm(s) that housed the pigs during their finisher, weaner, and piglet period. Subsequently, the algorithm estimates the antimicrobial exposure as the number of Animal Defined Daily Doses for treatment of one kg pig in each of the rearing periods. Thus, the antimicrobial purchase data at farm level are translated into antimicrobial exposure estimates at batch level. A batch of pigs is defined here as pigs sent to slaughter at the same day from the same farm. In this study we present, validate, and optimise a computational algorithm that calculate the lifetime exposure of antimicrobials for slaughter pigs. The algorithm was evaluated by comparing the computed estimates to data on antimicrobial usage from farm records in 15 farm units. We found a good positive correlation between the two estimates. The algorithm was run for Danish slaughter pigs sent to slaughter in January to March 2015 from farms with more than 200 finishers to estimate the proportion of farms that it was applicable for. In the final process, the algorithm was successfully run for batches of pigs originating from 3,026 farms with finisher units (77% of the initial population). This number can be increased if more accurate register data can be obtained. The algorithm provides a systematic and repeatable approach to estimating the antimicrobial exposure throughout the rearing period, independent of rearing site for finisher batches, as a lifetime exposure measurement.

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Determinants for Treatments in Relation to Udder Health in Danish Dairy Cattle Farms

Regular cow level registrations in the Danish Cattle Database include registrations about e.g. milk yield, SCC and calvings, but also about diseases and antibiotic treatments of cows. These data could potentially be a useful source of information for the development of herd-specific udder health management programs tailored to the farmer's preference. With tailored programs farmers may be more motivated to adopt effective management programs that can also enhance a prudent use of antibiotics.

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Determinants of antimicrobial treatment for udder health in Danish dairy cattle herds

Societal pressure to limit the use of antibiotics in livestock production systems, including dairy cattle systems, is consistently increasing. To motivate farmers to reduce antibiotic usage, it is important to understand the factors that determine whether a cow will be treated with antibiotics or not. If farmers' usual practices regarding antibiotic treatments are taken into account, they may be motivated to adopt control measures that can facilitate prudent use of antibiotics and are at the same time cost-effective. In this study, we analyzed database recordings of milk yield and somatic cell count from the routine milk recording scheme, clinical registrations of mastitis and PCR results, and cow factors such as days in milk and parity in relation to antibiotic treatments for 518 dairy herds in Denmark. Farm-wise logistic regressions were used to predict antimicrobial treatment based on these factors. The resulting regression coefficients of 422 herds were further analyzed by principal component analysis and clustering to determine the driving predictors for treatment in
different groups of farms. The results showed that determinants that were most important for predicting antibiotic treatments vary from one farm to another. Health indicators such as PCR or somatic cell count were most indicative for treatment on some farms, whereas other groups seemed to depend more on production factors (milk yield) or later culling of the cows. This shows that farmers behave differently and differences can be identified in register data. This information can be considered when developing cost-effective herd-specific control measures of mastitis to promote prudent use of antibiotics in Danish dairy cattle farms.

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- Organisations: National Veterinary Institute, Epidemiology, University of Copenhagen, SEGES Cattle
- Authors: Gussmann, M. K. (Intern), Græsbøll, K. (Intern), Toft, N. (Intern), Nielsen, S. S. (Ekstern), Farre, M. (Ekstern), Kirkeby, C. T. (Intern), Halasa, T. (Intern)
- Pages: 505-517
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  - Web of Science (2016): Indexed yes
  - Scopus rating (2016): CiteScore 2.66 SJR 1.304 SNIP 1.464
  - Web of Science (2016): Indexed yes
  - BFI (2015): BFI-level 2
  - Scopus rating (2015): SJR 1.464 SNIP 1.498 CiteScore 2.63
  - Web of Science (2015): Indexed yes
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  - Scopus rating (2014): SJR 1.43 SNIP 1.505 CiteScore 2.78
  - Web of Science (2014): Indexed yes
  - BFI (2013): BFI-level 2
  - Scopus rating (2013): SJR 1.407 SNIP 1.597 CiteScore 2.82
  - ISI indexed (2013): ISI indexed yes
  - Web of Science (2013): Indexed yes
  - BFI (2012): BFI-level 2
  - Scopus rating (2012): SJR 1.451 SNIP 1.718 CiteScore 2.79
  - ISI indexed (2012): ISI indexed yes
  - Web of Science (2012): Indexed yes
  - BFI (2011): BFI-level 2
  - Scopus rating (2011): SJR 1.411 SNIP 1.59 CiteScore 2.59
  - ISI indexed (2011): ISI indexed yes
  - Web of Science (2011): Indexed yes
  - BFI (2010): BFI-level 2
  - Scopus rating (2010): SJR 1.351 SNIP 1.517
  - Web of Science (2010): Indexed yes
  - BFI (2009): BFI-level 2
  - Scopus rating (2009): SJR 1.321 SNIP 1.717
  - Web of Science (2009): Indexed yes
  - BFI (2008): BFI-level 2
  - Scopus rating (2008): SJR 1.226 SNIP 1.556
  - Web of Science (2008): Indexed yes
  - Scopus rating (2007): SJR 0.978 SNIP 1.894
Efficiency of the Clinical Veterinary Diagnostic Practices and Drug Choices for Infectious Diseases in Livestock in Bangladesh

As in most low-income countries, adequate laboratory facilities are not available in Bangladesh to assist veterinarians in diagnosing animal diseases. We aimed to determine the efficiency of veterinary diagnoses for two common ruminant diseases in Bangladesh: Peste des petits ruminants (PPR) and foot-and-mouth disease (FMD). We conducted the study from May 2009 to August 2010 in three government veterinary hospitals where veterinarians collected samples from sick livestock and recorded the presumptive diagnosis on the basis of clinical presentations. Samples were tested for PPR and FMD using real-time RT-PCR. We estimated the sensitivity, specificity, positive predictive value (PPV) and negative predictive value (NPV) of the presumptive diagnoses when compared to laboratory tests. We tested 539 goats for PPR and 340 cattle and goats for FMD. Our results indicate that the veterinarians' presumptive diagnoses were different from laboratory findings for both PPR (P < 0.05) and FMD (P < 0.05). The overall sensitivity of the presumptive clinical diagnoses was 54% (95% CI: 47–61%) while specificity was 81% (95% CI: 78–84%) compared to real-time RT-PCR tests. The kappa value obtained in our validation process for PPR (kappa: 0.25) and FMD (kappa 0.36) indicated a poor performance of the presumptive diagnoses. Most of the animals (93%) were treated with antibiotics. Our findings indicate that veterinarians can detect animals not infected with FMD or PPR but miss the true cases. The clinical competency of these veterinarians needs to be improved and access to laboratory diagnostic facilities could help veterinarians to improve the diagnostics and outcomes. The rational use of antibiotics by veterinarians in animals must be ensured.

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Organisations: National Veterinary Institute, Epidemiology, University of Florida, EcoHealth Alliance, Ministry of Fisheries and Livestock, International Centre for Diarrhoeal Disease Research
Pages: 1329-1333
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Journal: Transboundary and Emerging Diseases
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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.16 SJR 0.994 SNIP 1.096
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.258 SNIP 1.262 CiteScore 2.29
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.038 SNIP 1.19 CiteScore 2.23
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.953 SNIP 1.123 CiteScore 2.33
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.917 SNIP 1.149 CiteScore 2.04
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.941 SNIP 1.146 CiteScore 2.05
ISI indexed (2011): ISI indexed yes
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Scopus rating (2010): SJR 0.747 SNIP 0.986
Clinical diagnostic practices, Presumptive diagnoses, Sensitivity, Specificity, Bangladesh, PPR, FMD

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Organisations: National Veterinary Institute, Epidemiology, Diagnostic & Development, Bacteriology & Parasitology, Pathology
Authors: Bødker, R. (Intern), Chriél, M. (Intern), Isbrand, A. (Intern), Jensen, T. K. (Intern), Schou, K. K. (Intern)
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Journal: Dansk Veterinaertidsskrift
Volume: 2017
Issue number: 16
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BFI (2008): BFI-level 1
Original language: Danish
Publication: Communication › Journal article – Annual report year: 2017
Epidemiological and economic consequences of purchasing livestock infected with Mycobacterium avium subsp. paratuberculosis

Paratuberculosis (PTB) is a chronic disease which may lead to reduced milk yield, lower animal welfare and death in cattle. The causative agent is Mycobacterium avium subsp. paratuberculosis (MAP). The economic consequences are particularly important incentives in the control and eradication of the infection. One strategy to control PTB in a herd is to purchase animals from farms with a low risk of MAP infection. We wanted to investigate the epidemiological and economic consequences of buying livestock from different supplier farms of low, medium or high risk, as well as farms with unknown status. We also wanted to estimate the probability of spontaneous fadeout if the farmer of an initially MAP-free herd bought a specified number of infected animals in a single year, or continually bought infected animals. This was achieved through simulation modeling, and the effects of consistently introducing one, five or ten infected animals annually into an initially infection-free herd was also modeled. Our findings show that once infected, a farm can relatively safely purchase animals from other low and medium-risk farms without experiencing an increase in the prevalence, highlighting the importance of certification programmes. Furthermore, farms free of MAP are highly susceptible and cannot purchase more than a small number of animals per year without having a high risk of being infected. The probability of spontaneous fadeout after 10 years was 82% when introducing a single infected animal into an initially MAP-free herd. When purchasing ten infected animals, this probability was 46%. The continual purchase of infected animals resulted in very low probabilities of spontaneous fadeout. We demonstrated that MAP-free farms can purchase a small number of animals, preferably from certified farms, each year and still remain free of MAP. Already infected farms have little risk of increasing the prevalence on a farm when purchasing animals from other farms.

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Organisations: National Veterinary Institute, Epidemiology, Technical University of Denmark, University of Copenhagen
Authors: Kirkeby, C. T. (Intern), Græsbøll, K. (Intern), Nielsen, S. S. (Ekstern), Toft, N. (Intern), Halasa, T. (Ekstern)
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Web of Science (2016): Indexed yes
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Scopus rating (2015): SJR 0.925 SNIP 0.97 CiteScore 1.86
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.885 SNIP 0.987 CiteScore 1.81
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.829 SNIP 0.833 CiteScore 1.85
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.743 SNIP 1.043 CiteScore 1.94
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.157 SNIP 1.455 CiteScore 2.66
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.072 SNIP 1.4
BFI (2009): BFI-level 1
Estimation of the transmission dynamics of African swine fever virus within a swine house

The spread of African swine fever virus (ASFV) threatens to reach further parts of Europe. In countries with a large swine production, an outbreak of ASF may result in devastating economic consequences for the swine industry. Simulation models can assist decision makers setting up contingency plans. This creates a need for estimation of parameters. This study presents a new analysis of a previously published study. A full likelihood framework is presented including the impact of model assumptions on the estimated transmission parameters. As animals were only tested every other day, an interpretation was introduced to cover the weighted infectiousness on unobserved days for the individual animals (WIU).

Based on our model and the set of assumptions, the within- and between-pen transmission parameters were estimated to $\beta_w = 1.05$ (95% CI 0.62-1.72), $\beta_b = 0.46$ (95% CI 0.17-1.00), respectively, and the WIU = 1.00 (95% CI 0-1). Furthermore, we simulated the spread of ASFV within a pig house using a modified SEIR-model to establish the time from infection of one animal until ASFV is detected in the herd. Based on a chosen detection limit of 2.55% equivalent to 10 dead pigs out of 360, the disease would be detected 13-19 days after introduction.
Evaluation of Strategies to Control a Potential Outbreak of Foot-and-Mouth Disease in Sweden

To minimize the potential consequences of an introduction of foot-and-mouth disease (FMD) in Europe, European Union (EU) member states are required to present a contingency plan. This study used a simulation model to study potential outbreak scenarios in Sweden and evaluate the best control strategies. The model was informed by the Swedish livestock structure using herd information from cattle, pig, and small ruminant holdings in the country. The contact structure was based on animal movement data and studies investigating the movements between farms of veterinarians, service trucks, and other farm visitors. All scenarios of outbreak control included depopulation of detected herds, 3km protection and 10 km surveillance zones, movement tracing, and 3 days national standstill. The effect of availability of surveillance resources, i.e., number of field veterinarians per day, and timeliness of enforcement of interventions, was assessed. With the estimated currently available resources, an FMD outbreak in Sweden is expected to be controlled (i.e., last infected herd detected) within 3 weeks of detection in any evaluated scenario. The density of farms in the area where the epidemic started would have little impact on the time to control the outbreak, but spread in high density areas would require more surveillance resources, compared to areas of lower farm density. The use of vaccination did not result in a reduction in the
expected number of infected herds. Preemptive depopulation was able to reduce the number of infected herds in extreme scenarios designed to test a combination of worst-case conditions of virus introduction and spread, but at the cost of doubling the number of herds culled. This likely resulted from a combination of the small outbreaks predicted by the spread model, and the high efficacy of the basic control measures evaluated, under the conditions of the Swedish livestock industry, and considering the assumed control resources available. The results indicate that the duration and extent of FMD outbreaks could be kept limited in Sweden using the EU standard control strategy and a 3 days national standstill.

**General information**

State: Published
Organisations: National Veterinary Institute, Epidemiology, National Veterinary Institute Sweden
Authors: Dórea, F. C. (Ekstern), Nöremark, M. (Ekstern), Widgren, S. (Ekstern), Frössling, J. (Ekstern), Boklund, A. (Intern), Hisham Beshara Halasa, T. (Intern), Ståhl, K. (Ekstern)
Publication date: 2017
Main Research Area: Technical/natural sciences

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Farm-level risk factors for Fasciola hepatica infection in Danish dairy cattle as evaluated by two diagnostic methods

The prevalence of bovine fasciolosis in Denmark is increasing but appropriate guidelines for control are currently lacking. In order to help develop a control strategy for liver fluke, a risk factor study of farm management factors was conducted and the utility of bulk tank milk (BTM ELISA) as a tool for diagnosis in Danish dairy cattle farms was assessed. This case-control study aimed to identify farm-level risk factors for fasciolosis in Danish dairy farms (>50 animals slaughtered in 2013) using two diagnostic methods: recordings of liver condemnation at slaughter, and farm-level Fasciola hepatica antibody levels in BTM. A case farm was defined as having a minimum of 3 incidents of liver condemnation due to liver fluke at slaughter (in any age group) during 2013, and control farms were located within 10 km of at least one case farm and had no history of liver condemnation due to liver fluke during 2011-2013. The selected farmers were interviewed over telephone about grazing and control practices, and BTM from these farms was collected and analysed by ELISA in 2014. The final complete dataset consisting of 131 case and 63 control farms was analysed using logistic regression. Heifers grazing on wet pastures, dry cows grazing on wet pastures, herd size, breed and concurrent beef cattle production were identified as risk factors associated with being classified as a case farm. With the categorised BTM ELISA result as the response variable, heifers grazing on wet pastures, dry cows grazing on wet pastures, and purchase of cows were identified as risk factors. Within the case and control groups, 74.8 and 12.7% of farms were positive for fasciolosis on BTM ELISA, respectively. The differences are likely to be related to the detection limit of the farm-level prevalence by the BTM ELISA test, time span between slaughter data and BTM, and the relatively low sensitivity of liver inspection at slaughter. Control of bovine fasciolosis in Denmark should target heifers and dry cows through grazing management and appropriate anthelmintic treatment, and BTM ELISA can be a useful diagnostic tool for fasciolosis in Danish dairy farms.

**General information**

State: Published
Organisations: National Veterinary Institute, Epidemiology, University of Copenhagen, SEGES, Danish Agriculture & Food Council, Norwegian Veterinary Institute
Authors: Takeuchi-Storm, N. (Ekstern), Denwood, M. (Ekstern), Hansen, T. V. A. (Ekstern), Halasa, T. (Intern), Rattenborg, E. (Ekstern), Boes, J. (Ekstern), Enemark, H. L. (Ekstern), Thamsborg, S. M. (Ekstern)
Number of pages: 11
Publication date: 2017
Foderkvalitet og andre faktorer af betydning for forbruget af antibiotika på minkgårde

Antibiotikaforbruget hos mink er steget gradvist gennem det seneste århundrede, og forbruget på den enkelte gård påvirkes af en række faktorer. Tidligere studier har vist at forekomsten af diare og ordination af antibiotika er influeret af foderleverandøren. Formålet med dette studie (Jensen et al. 2017) var at undersøge for eventuelle effekter af de foderparametre, som indgår i den frivillige foderkontrol, på ordination af antibiotika til mink. Studiet inkluderede alle undersøgte foderbatch fra 12 fodercentraler og tilknyttede 1472 minkgårde i perioden 2012–2014. De undersøgte foderparametre omfattede både kemiske parametre og mikrobiologiske parametre. Data blev analyseret ved multivariat variansanalyse i to modeller. I den første model var responsvariablen ordination af antibiotika på en given gård, dvs. andelen af gård som fik antibiotika i tilknytning til udfodring af en give batch. Analysenerne korrigerede for kendte faktorer med indflydelse på antibiotikaforbruget (p < 0.0001), herunder
årstids variation, tidstrends, besætningsstørrelse og udbrud af Pseudomonas aeruginosa. I alle modeller var kimtallet for fæcale coccer signifikant (p < 0.0001) relateret til ordination af antibiotika.

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, Diagnostic & Development, Department of Applied Mathematics and Computer Science, Statistics and Data Analysis, Kopenhagen Fur
Authors: Jensen, V. F. (Intern), Chriél, M. (Intern), Sommer, H. M. (Intern), Struve, T. (Ekstern), Clausen, J. (Ekstern)
Pages: 95-98
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Mink (neovison vison), Foderkvalitet, Antibiotika, Faktorer
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Forekomst af antibiotikaresistens i bakterieisolater fra danske mink

General information
State: Published
Organisations: National Veterinary Institute, Diagnostic & Development, Bacteriology & Parasitology, Epidemiology, Technical University of Denmark
Authors: Chriél, M. (Intern), Corvera Kløve Lassen, D. (Ekstern), Larsen, G. (Intern), Jensen, V. F. (Intern), Pedersen, K. (Intern)
Pages: 153-158
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Place of publication: Aarhus N
Publisher: Kopenhagen Fur
Main Research Area: Technical/natural sciences
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DTU3.pdf
Publication: Research - peer-review › Book chapter – Annual report year: 2017

Forskere designer fleksibel strategi mod kvægseydom

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology
Authors: Kirkeby, C. T. (Intern)
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Pages (from-to): 4-4
Newspaper: D T U Avisen
Volume: 2017
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Ratings:
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ISI indexed (2012): ISI indexed no
Harmonizing methods for wildlife abundance estimation and pathogen detection in Europe—a questionnaire survey on three selected host-pathogen combinations

Background: The need for wildlife health surveillance as part of disease control in wildlife, domestic animals and humans on the global level is widely recognized. However, the objectives, methods and intensity of existing wildlife health surveillance programs vary greatly among European countries, resulting in a patchwork of data that are difficult to merge and compare. This survey aimed at evaluating the need and potential for data harmonization in wildlife health in Europe. The specific objective was to collect information on methods currently used to estimate host abundance and pathogen prevalence. Questionnaires were designed to gather detailed information for three host-pathogen combinations: (1) wild boar and Aujeszky’s disease virus, (2) red fox and Echinococcus multilocularis, and (3) common vole and Francisella tularensis.

Results: We received a total of 70 responses from 19 European countries. Regarding host abundance, hunting bags are currently the most widely accessible data source for widely distributed mid-sized and larger mammals such as red fox and wild boar, but we observed large differences in hunting strategies among countries as well as among different regions within countries. For small rodents, trapping is the method of choice, but practical applications vary among study sites. Laboratory procedures are already largely harmonized but information on the sampled animals is not systematically collected.

Conclusions: The answers revealed that a large amount of information is available for the selected host-pathogen pairs and that in theory methods are already largely harmonized. However, the comparability of the data remains strongly compromised by local differences in the way, the methods are applied in practice. While these issues may easily be overcome for prevalence estimation, there is an urgent need to develop tools for the routine collection of host abundance data in a harmonized way. Wildlife health experts are encouraged to apply the harmonized APHAEA protocols in epidemiological studies in wildlife and to increase cooperation.

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State: Published
Organisations: National Veterinary Institute, Epidemiology, University of Bern, Erasmus Medical Center, Università degli Studi di Torino, Friedrich-Loeffler-Institute
Authors: Schulz, J. (Intern), Ryser-Degiorgis, M. (Ekstern), Kuiken, T. (Ekstern), Ferroglio, E. (Ekstern), Ulrich, R. G. (Ekstern), Conraths, F. J. (Ekstern), Gortazar, C. (Ekstern), Staubach, C. (Ekstern), Partners, A. P. (Ekstern)
Number of pages: 10
Publication date: 2017
Main Research Area: Technical/natural sciences
Identification of Dermacentor reticulatus Ticks Carrying Rickettsia raoultii on Migrating Jackal, Denmark

From a migrating golden jackal (Canis aureus), we retrieved 21 live male Dermacentor reticulatus ticks, a species not previously reported from wildlife in Denmark. We identified *Rickettsia raoultii* from 18 (86%) of the ticks. This bacterium is associated with scalp eschar and neck lymphadenopathy after tick bite syndrome among humans.

**General information**

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**Organisations:** National Veterinary Institute, Bacteriology & Parasitology, Diagnostic & Development, Pathology, Epidemiology  
**Authors:** Schou, K. K. (Intern), Chriél, M. (Intern), Isbrand, A. (Intern), Jensen, T. K. (Intern), Bedker, R. (Intern)  
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Scopus rating (2016): CiteScore 4.92 SJR 3.305 SNIP 2.206  
Web of Science (2016): Indexed yes  
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Scopus rating (2015): SJR 3.026 SNIP 2.033 CiteScore 4.23  
Web of Science (2015): Indexed yes  
BFI (2014): BFI-level 2  
Scopus rating (2014): SJR 3.437 SNIP 2.437 CiteScore 4.59
Improving institutional memory on challenges and methods for estimation of pig herd antimicrobial exposure based on data from the Danish Veterinary Medicines Statistics Program (VetStat)

With the increasing occurrence of antimicrobial resistance, more attention has been directed towards surveillance of both human and veterinary antimicrobial use. Since the early 2000s, several research papers on Danish pig antimicrobial
usage have been published, based on data from the Danish Veterinary Medicines Statistics Program (VetStat). VetStat was established in 2000, as a national database containing detailed information on purchases of veterinary medicine. This paper presents a critical set of challenges originating from static system features, which researchers must address when estimating antimicrobial exposure in Danish pig herds. Most challenges presented are followed by at least one robust solution. A set of challenges requiring awareness from the researcher, but for which no immediate solution was available, were also presented. The selection of challenges and solutions was based on a consensus by a cross-institutional group of researchers working in projects using VetStat data. No quantitative data quality evaluations were performed, as the frequency of errors and inconsistencies in a dataset will vary, depending on the period covered in the data. Instead, this paper focuses on clarifying how VetStat data may be translated to an estimation of the antimicrobial exposure at herd level, by suggesting uniform methods of extracting and editing data, in order to obtain reliable and comparable estimates on pig antimicrobial consumption for research purposes.

**General information**
State: Published
Organisations: National Veterinary Institute, Epidemiology, National Food Institute, Research Group for Genomic Epidemiology, University of Copenhagen
Authors: Dupont, N. H. (Ekstern), Fertner, M. (Intern), Birkegård, A. C. (Intern), Dalhoff Andersen, V. (Intern), Nielsen, G. B. (Ekstern), Kruse, A. B. (Ekstern), de Knegt, L. V. (Intern)
Number of pages: 25
Publication date: 2017
Main Research Area: Technical/natural sciences

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P_Vetstat_paper_Versao_Leo_Repository_Preparation_for_ArXiv_01_ArXiv_240517.pdf
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**Infektion med TBE-virus i Danmark 2013-2016**

**General information**
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Organisations: National Veterinary Institute, Epidemiology, Statens Serum Institut, State Serum Institute
Authors: Ocias, L. F. (Ekstern), Petersen, A. (Ekstern), Krogfelt, K. (Ekstern), Rosenstierne, M. W. (Forskerdatabase), Fomsgaard, A. (Ekstern), Bedker, R. (Intern)
Number of pages: 2
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Main Research Area: Technical/natural sciences

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**Bibliographical note**
https://www.ssi.dk/Aktuelt/Nyhedsbreve/EPI-NYT/2017/Uge%2040%20-%202017.aspx<br/>OBS forfatterne står allersidst i artiklen
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Publication: Communication › Journal article – Annual report year: 2017
Methods for estimating disease transmission rates: Evaluating the precision of Poisson regression and two novel methods

Precise estimates of disease transmission rates are critical for epidemiological simulation models. Most often these rates must be estimated from longitudinal field data, which are costly and time-consuming to conduct. Consequently, measures to reduce cost like increased sampling intervals or subsampling of the population are implemented. To assess the impact of such measures we implement two different SIS models to simulate disease transmission: A simple closed population model and a realistic dairy herd including population dynamics. We analyze the accuracy of different methods for estimating the transmission rate. We use data from the two simulation models and vary the sampling intervals and the size of the population sampled. We devise two new methods to determine transmission rate, and compare these to the frequently used Poisson regression method in both epidemic and endemic situations. For most tested scenarios these new methods perform similar or better than Poisson regression, especially in the case of long sampling intervals. We conclude that transmission rate estimates are easily biased, which is important to take into account when using these rates in simulation models.
Microclimatic temperatures increase the potential for vector-borne disease transmission in the Scandinavian climate

We quantified the difference between the meteorological temperature recorded by the Danish Meteorological Institute (DMI) weather stations and the actual microclimatic temperatures at two or three different heights at six potential insect habitats. We then compared the impact of the hourly temperature on the extrinsic incubation period (EIP) of six pathogens. Finally, we developed a regression model, enabling us to predict the microclimatic temperatures of different habitats based on five standard meteorological parameters readily available from any meteorological institution. Microclimatic habitats were on average 3.5–5°C warmer than the DMI recorded temperatures during midday and 1–3°C cooler at midnight. The estimated EIP for five of the six microclimatic habitats was shorter than the estimates based on DMI temperatures for all pathogens studied. The microclimatic temperatures also predicted a longer season for virus development compared to DMI temperatures. Based on DMI data of hourly temperature, solar radiation, wind speed, rain and humidity, we were able to predict the microclimatic temperature of different habitats with an R2 of 0.87–0.96. Using only meteorological temperatures for vector-borne disease transmission models may substantially underestimate both the daily potential for virus development and the duration of the potential transmission season.

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, Danish Meteorological Institute
Authors: Haider, N. (Intern), Kirkeby, C. T. (Intern), Kristensen, B. (Intern), Kjær, L. J. (Intern), Havskov Sørensen, J. (Ekstern), Bødker, R. (Intern)
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Scientific Reports
Microclimatic temperatures of Danish cattle farms: a better understanding of the variation in transmission potential of Schmallenberg virus

Background: Insects inhabiting the surroundings of a cattle farm are exposed to microclimatic temperatures of the habitats surrounding the farm. Microclimatic temperatures are key drivers of the extrinsic incubation period (EIP), the speed by which an infected insect becomes infectious. The objective of this study was to quantify the variation of EIP of Schmallenberg virus among Danish cattle farms and identify possible spatial patterns of the EIPs. Methods: We quantified 21 different land cover classes within a 500 meter radius of all cattle farms in Denmark (N=22092) using CORINE land cover and regrouped them into four major land cover types: dry meadow, wet meadow, hedges, and forest. We then obtained the meteorological temperatures and other parameters (solar radiation, wind speed, humidity) near the farm from the Danish Meteorological Institute (DMI) for the period of 2000-2016. Using recently developed microclimatic temperature prediction models for those four major land cover types, we calculated the hourly microclimatic temperatures of each farm based on their surrounding habitat types and meteorological parameters. We then modelled the daily EIP of Schmallenberg virus for each farm for each year of the period of 2000-2016 using both hourly DMI and hourly microclimatic temperatures and calculated mean EIP of 17 years for each farm. Finally, we plotted the average spatial pattern of farm level EIP for spring (May-June), summer (July-August) and autumn (September-October) in Denmark for the 17 years. Results: Of the 22092 cattle farms, we were able to predict the hourly microclimatic temperatures of 22006 farms (99.6%) - the rest of the farms had habitats either not suitable for insects resting or the microclimatic model was not able to calculate the temperature of the surrounding land covers. We found a surprisingly large between-farm variation in EIP between farms on a specific day. For example, in the year 2016, the EIP of all farms varied (5th and 95th percentiles) from 9-19 days on May 1st, 12-23 days on July 1st and 11-21 days on September 1st. The mean EIP of Schmallenberg virus [inter quantile range (IQR)] of all the cattle farms during spring, summer, and autumn for 17 years period were 16 [13-17], 15 [13-16] and 40 [38-42] days respectively, when using microclimatic temperatures. These estimated EIP values were much shorter compared to EIP estimated using DMI temperatures for the same periods of spring (29 [27-30]), summer (21 [19-24]), and autumn (56 [55-58]) days respectively. For the summer period, we observed a large area where
farms with shorter EIP for Schmallenberg virus were grouped together, comprising southern Funen and associated islands, Lolland, Falster, and southern Zealand. Conclusion: Microclimatic temperature is highly important for understanding and predicting insect-borne virus transmission on Danish cattle farms. We were able to predict the daily farm level EIP of Schmallenberg virus for 17 years. We found large variation in EIP between farms and also a spatial pattern with a strong geographical trend suggesting that disease transmission may vary substantially between regions even in a small country like Denmark – and this could be useful for designing risk based surveillance for emerging and reemerging vector-borne diseases.

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, Danish Meteorological Institute
Authors: Haider, N. (Intern), Cuellar, A. C. (Intern), Kjær, L. J. (Intern), Havskov Sørensen, J. (Ekstern), Bedker, R. (Intern)
Publication date: 2017
Event: Abstract from 11th Annual meeting Epizone, Paris, France.
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Modelling risk of tick exposure in southern Scandinavia using machine learning techniques, satellite imagery, and human population density maps
Vector-borne diseases such as Lyme disease and tick-borne encephalitis have become more common in recent decades and present a real health problem in many parts of Europe. Risk assessment, control, and prevention of these diseases require a better understanding of vector abundance as well as risk factors determining human exposure to ticks. There is a great need for analyses and models that can predict how vectors and their associated diseases are distributed and how this relates to high risk areas for human exposure. As a part of the ScandTick Innovation project, we surveyed ticks at approximately 30 sites (forests and meadows) in each of Denmark, southern Norway and south-eastern Sweden. At each site we measured presence/absence of ticks, and used the data obtained along with environmental satellite images to run Boosted Regression Tree machine learning algorithms to predict overall spatial distribution (probability of presence) in southern Scandinavia. Together with the predicted distribution maps, we used human density maps to determine areas with high risk of exposure to ticks. For nymphs, the predicted distribution found corresponded well with known distributions of ticks in Scandinavia, with more widespread distribution in Denmark compared to Norway and Sweden. In the Norwegian region, probability of presence was markedly higher nearer the coastline and the data shows a latitudinal boundary in the Swedish region above which probability of presence was low or close to zero. Presence of larvae was much more clustered in the observed data, which was also reflected in the predicted distribution maps for the region. Whereas the predicted distribution of larvae was mostly even throughout Denmark, larvae were primarily around the coastlines in Norway and Sweden. When combining these distribution maps with human population density maps and accounting for area accessibility, we could assess the proportion of the population living in areas where ticks were present. Our data showed that although ticks are found in a limited proportion of the total region area (particularly for Norway and Sweden), areas with high population densities tend to overlap with these zones. Machine learning techniques allow us to predict for larger areas without having to perform extensive sampling all over the region in question, and we were able to produce models and maps with high predictive value. The results from these models help us pinpoint areas with high risk of exposure to ticks and thus potentially tick-borne diseases.

General information
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Organisations: National Veterinary Institute, Epidemiology, Bacteriology & Parasitology, University of Agder, Norwegian Institute of Public Health, Swedish University of Agricultural Sciences
Authors: Kjær, L. J. (Intern), Korslund, L. (Ekstern), Kjelland, V. (Ekstern), Slettan, A. (Ekstern), Andreassen, Å. K. (Ekstern), Paulsen, K. M. (Ekstern), Christensson, M. (Ekstern), Kjellander, P. (Ekstern), Teräväinen, M. (Ekstern), Soleng, A. (Ekstern), Edgar, K. S. (Ekstern), Lindstedt, H. H. (Ekstern), Schou, K. K. (Intern), Bedker, R. (Internal)
Publication date: 2017
Event: Abstract from 4th Conference on Neglected Vectors and Vector-Borne Diseases, Chania, Greece.
Main Research Area: Technical/natural sciences
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Modelling spread of MRSA within a pig herd

General information
State: Published
Modelling tick abundance using machine learning techniques and satellite imagery

Recently, focus on tick-borne diseases has increased as diseases such as Lyme disease and tickborne encephalitis have become more widespread and represent a real health problem in many parts of Europe. Effective control and prevention of these diseases requires a better understanding of the factors affecting the vectors. There is a great need for analyses and models that can predict how vectors and their associated diseases are distributed now and possibly in the future. As a part of the ScandTick Innovation project, we surveyed and collected ticks at approximately 30 sites in each of Denmark, southern Norway and south-eastern Sweden. At each site we measured presence/absence and relative tick abundance using north- and east-facing line transect, where number of larvae, nymphs and adult females and males were counted at eight 50 m transects. We used the data obtained along with environmental satellite images to run Boosted Regression Tree machine learning algorithms to predict overall distribution (presence/absence of ticks) and relative tick abundance of nymphs and larvae in southern Scandinavia. For nymphs, the predicted abundance had a positive correlation with observed abundance and the spatial variation found corresponded well with known abundance and distributions of ticks in Scandinavia, with higher abundance and more widespread distribution in Denmark compared to Norway and Sweden. Because abundance was strongly correlated with forested habitats the risk areas were much larger in Sweden and Norway compared to Denmark. In both the Norwegian and Swedish regions, abundance was markedly higher nearer the coastline. Presence of larvae was much more clustered in the observed data, which was also reflected in the predicted abundance and distribution maps for the region. Whereas the predicted distribution of larvae was mostly even throughout Denmark, it was primarily around the coastlines in Norway and Sweden. Abundance was fairly low overall except in some fragmented patches corresponding to forested habitats in the region. Machine learning techniques allow us to predict for larger areas without having to perform extensive sampling all over the region in question. The results from these models can be used in epidemiological models and can help us determine areas under risk of disease transmission and help us interpret human incidence data. Next step will be to analyze the collected ticks for pathogens and using the same machine learning techniques to develop prevalence maps of the ScandTick region.

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Authors: Kjaer, L. J. (Intern), Korslund, L. (Ekstern), Kjelland, V. (Ekstern), Slettan, A. (Ekstern), Andreassen, Å. K. (Ekstern), Paulsen, K. M. (Ekstern), Christensson, M. (Ekstern), Kjellander, P. (Ekstern), Teräväinen, M. (Ekstern), Soleng, A. (Ekstern), Edgar, K. S. (Ekstern), Lindstedt, H. H. (Ekstern), Schou, K. K. (Intern), Bødker, R. (Intern)
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Mortality in Danish Swine herds: Spatio-temporal clusters and risk factors

The aim of this study was to explore spatio-temporal mortality patterns in Danish swine herds from December 2013 to October 2015, and to discuss the use of mortality data for syndromic surveillance in Denmark. Although it has previously been assessed within the context of syndromic surveillance, the value of mortality data generated on a regular and mandatory basis from all swine herds remains unexplored in terms of swine surveillance in Denmark.

A total of 5010 farms were included in the analysis, corresponding to 1896 weaner herds, 1490 sow herds and 3839 finisher herds. The spatio-temporal analysis included data description for spatial, temporal, and spatio-temporal cluster analysis for three age groups: weaners (up to 30 kg), sows and finishers. Logistic regression models were used to assess the potential factors associated with finisher and weaner herds being included within multiple-herd clusters. The spatio-temporal distribution of mortality changed over time, and suggested a general increase in mortality for the
months of January and July for the three age groups. A large number of single-herd clusters (i.e. clusters with only one herd), and fewer multiple-herd clusters (i.e. clusters with at least two herds) were found. The herd size affected whether weaner herds were within multiple-herd clusters, and factors such farm type, SPF status and presence of atrophic rhinitis had an impact on finisher herds being inside vs. outside multiple-herd clusters in the univariable analysis. However, due to a strong correlation between variables, only farm type remained in the multivariable analysis for the finisher herds. The higher mortality observed for the months of January and July could be linked to infrequent updates of the data used to calculate mortality. The presence of single-herd clusters might indicate welfare and disease issues, while multiple-herd clusters could suggest the presence of infectious diseases within the cluster area. The impact of farm type is linked to the fact that larger farms specialize in only one age group, with high biosecurity and more specialized personnel, and subsequently a lower mortality. Mortality data have a potential use in disease surveillance. However, detected clusters might not be due to disease, but the result of changes such as herd management practices. Further analysis to explore other spatio-temporal monitoring methods is needed before mortality data can be incorporated into a Danish disease monitoring system.

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, University of Southern Denmark
Authors: Lopes Antunes, A. C. (Intern), Ersbøll, A. K. (Ekstern), Bihrmann, K. (Forskerdatabase), Toft, N. (Intern)
Pages: 41-48
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Main Research Area: Technical/natural sciences

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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.185 SNIP 1.329
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.26 SNIP 1.23 CiteScore 2.1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.267 SNIP 1.421 CiteScore 2.37
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.247 SNIP 1.552 CiteScore 2.49
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.274 SNIP 1.452 CiteScore 2.45
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.211 SNIP 1.303 CiteScore 2.24
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.155 SNIP 1.28
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.022 SNIP 1.34
Web of Science (2009): Indexed yes
Network analysis of pig movements: Loyalty patterns and contact chains of different holding types in Denmark

Understanding animal movements is an important factor for the development of meaningful surveillance and control programs, but also for the development of disease spread models. We analysed the Danish pig movement network using static and temporal network analysis tools to provide deeper insight in the connection between holdings dealing with pigs, such as breeding and multiplier herds, production herds, slaughterhouses or traders. Pig movements, which occurred between 1\textsuperscript{st} January 2006 and 31\textsuperscript{st} December 2015 in Denmark, were summarized to investigate temporal trends such as the number of active holdings, the number of registered movements and the number of pigs moved. To identify...
holdings and holding types with potentially higher risk for introduction or spread of diseases via pig movements, we determined loyalty patterns, annual network components and contact chains for the 24 registered holding types. The total number of active holdings as well as the number of pig movements decreased during the study period while the holding sizes increased. Around 60-90% of connections between two pig holdings were present in two consecutive years and around one third of the connections persisted within the considered time period. Weaner herds showed the highest level of in-loyalty, whereas we observed an intermediate level of in-loyalty for all breeding sites and for production herds. Boar stations, production herds and trade herds showed a high level of out-loyalty. Production herds constituted the highest proportion of holdings in the largest strongly connected component. All production sites showed low levels of in-going contact chains and we observed a high level of out-going contact chain for breeding and multiplier herds. Except for livestock auctions, all transit sites also showed low levels of out-going contact chains. Our results reflect the pyramidal structure of the underlying network. Based on the considered disease, the time frame for the calculation of network measurements needs to be adapted. Using these adapted values for loyalty and contact chains might help to identify holdings with high potential of spreading diseases and thus limit the outbreak size or support control or eradication of the considered pathogen.
Scopus rating (2009): SJR 2.473 SNIP 0.985
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.323 SNIP 0.96
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.289 SNIP 0.525
Web of Science (2006): Indexed yes
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Pas på med indkøb af dyr med paratuberkulose

General information
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Organisations: National Veterinary Institute, Epidemiology
Authors: Kirkeby, C. T. (Intern)
Pages: 14-15
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Main Research Area: Technical/natural sciences

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Original language: Danish
Source: PublicationPreSubmission
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Predicting tick abundance in Southern Scandinavia using machine learning techniques and satellite imagery – a part of the ScandTick Innovation project

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Organisations: National Veterinary Institute, Epidemiology, Bacteriology & Parasitology, University of Agder, Norwegian Institute of Public Health, Swedish University of Agricultural Sciences
Authors: Kjær, L. J. (Intern), Korslund, L. (Ekstern), Kjelland, V. (Ekstern), Slettan, A. (Ekstern), Andreassen, Å. K. (Ekstern), Paulsen, K. M. (Ekstern), Christensson, M. (Ekstern), Kjellander, P. (Ekstern), Teräväinen, M. (Ekstern), Soleng, A. (Ekstern), Edgar, K. S. (Ekstern), Lindstedt, H. H. (Ekstern), Schou, K. K. (Intern), Bødker, R. (Intern)
Number of pages: 1
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Event: Abstract from NorTick Conference 2017, Oslo, Norway.
Main Research Area: Technical/natural sciences
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NorTick_abstract.pdf
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Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2017
Reporting guidelines for diagnostic accuracy studies that use Bayesian latent class models (STARD-BLCM)

Evaluation of medical tests is usually based on comparing their results to those from a perfect reference (gold standard) procedure. The Standards for Reporting of Diagnostic Accuracy (STARD) initiative (http://www.equator-network.org/reporting-guidelines/stard/) developed reporting guidelines for studies designed to estimate the accuracy of tests when disease status is known. The original STARD statement was initially published in seven journals, while an updated version — STARD2015 — has been recently released. More than 200 biomedical journals encourage its use in their instructions to authors. An affordable, reliable, and noninvasive reference standard does not always exist as is the case for infectious diseases with a long latent period (e.g., in chronic infections such as tuberculosis). In such situations test accuracy can be estimated using latent class models that do not require knowledge of disease status (i.e., disease status is a latent variable). Statistical methods were introduced in this context by Hui and Walter and have been successfully applied since then, with the majority of the work being carried out in a Bayesian framework. While STARD provides useful reporting guidelines for diagnostic accuracy studies when a reference standard is available, it required modification and extension to address crucial aspects that are unique to latent class analysis: In the absence of a perfect reference test, the target condition must be explicitly described when performing a latent class analysis to estimate test accuracy. Latent class models, in conjunction with what the tests under evaluation actually detect (e.g., organisms or immune responses to organisms), define the latent status. Thus, a definition/interpretation of the latent disease or infection under consideration from a biological perspective is critical to communicate effectively the contextual meaning of the sensitivity and specificity estimates. A detailed description of the latent class model and its assumptions is required. A meta-analysis found that 28% of the studies that used latent class models to estimate diagnostic test accuracy failed to report any evidence that assumptions were verified or that the underlying models were of adequate fit to the data at hand. Bayesian latent class analysis requires reporting the details and justification of the prior distributions used in the primary and sensitivity analysis. This task takes on increased importance when using non-identifiable latent class models. We adapted the STARD checklist in order to fulfill the reporting requirements for diagnostic test accuracy studies that use Bayesian latent class models. The new guidelines, termed Standards for the Reporting of Diagnostic accuracy studies that use Bayesian Latent Class Models, have been recently published and are available online (https://www.equator-network.org/reporting-guidelines/stard-blcm/). Further, a mailing list has been created and those interested can freely subscribe (http://lists.uth.gr/mailman/listinfo/lcmate). Standards for the Reporting of Diagnostic accuracy studies that use Bayesian Latent Class Models is relevant to both Bayesian and frequentist estimation methods but the focus is on the former. It should prove to be a useful tool for the sound application of latent class models in the evaluation of diagnostic tests and promote optimal reporting practices for studies that use such models.
Risk based surveillance of vector born infections - the daily transmission potential of Schmallenberg in Denmark 2013 to 2016

General information
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Organisations: National Veterinary Institute, Epidemiology
Authors: Bødker, R. (Intern), Haider, N. (Intern)
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Risk factors associated with diarrhea in Danish commercial mink (Neovison vison) during the pre-weaning period

Pre-weaning diarrhea in mink, also known as "sticky kits", is a syndrome and outbreaks occur every year on commercial mink farms in all mink producing countries. Morbidity and mortality can be considerable on a farm with huge economic consequences for the farmer as well as compromised welfare for the mink kits. Although efforts have been taken to identify etiologic agents involved in outbreaks, the syndrome is still regarded as multifactorial and recurring problems on the same farms draw attention to management and environmental risk factors. In the pre-weaning period from May to June 2015, a case control study was carried out on 30 Danish mink farms. Data concerning management, biosecurity, hygiene, feed consumption, antibacterial prescription and production efficiency were analyzed. The proportion of 1-year old females, farm size (total number of females), energy supply per female in the late gestation period, and dogs
accessing the farm area were significantly associated with being a case farm. Case farms were prescribed almost twice the amount of antibacterials per gestational unit (female and litter) as in control farms. Farmers on case farms spent significantly more time nursing and treating the animals and experienced more females with mastitis compared to farmers on control farms. No significant differences in cleaning practices or hygienic measures between case and control farms were found and there were no differences in drinking water quality, bedding material, composition neither of color types nor in management regarding litter equalization. Results from this study showed an association between the occurrence of pre-weaning diarrhea on mink farms and parity profile, farm size and feeding intensity in the gestational period. The access of dogs to the farm area was a significant risk factor, but needs further clarification.

**General information**

State: Published
Organisations: National Veterinary Institute, Epidemiology, University of Copenhagen, Copenhagen Fur
Authors: Birch, J. M. (Ekstern), Agger, J. F. (Ekstern), Dahlin, C. (Ekstern), Jensen, V. F. (Intern), Hammer, A. S. (Ekstern), Struve, T. (Ekstern), Jensen, H. E. (Ekstern)
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BFI (2016): BFI-level 1
Web of Science (2016): Indexed yes
Scopus rating (2016): CiteScore 1.01 SJR 0.484 SNIP 0.775
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.409 SNIP 1.445 CiteScore 0.98
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.644 SNIP 1.113 CiteScore 1.54
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.494 SNIP 1.001 CiteScore 1.41
ISI indexed (2013): ISI indexed no
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BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.57 SNIP 0.798 CiteScore 1.26
ISI indexed (2012): ISI indexed no
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.649 SNIP 0.99 CiteScore 1.42
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.541 SNIP 1.007
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.401 SNIP 0.698
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.33 SNIP 0.608
Scopus rating (2007): SJR 0.12 SNIP 0.539
Scopus rating (2006): SJR 0.155 SNIP 0.888
Web of Science (2006): Indexed yes
Risk factors associated with spatio-temporal clusters of high mortality in Danish swine herds

What were our motivation and objective? Mortality data are recorded to fulfill the European Commission requirements which ensures a continuous data flow for a surveillance system. Before using these data as part of a syndromic surveillance system, it is necessary to understand why increasing changes in mortality happen. The aim of this study was to identify spatio-temporal clusters of high mortality in Danish swine herds and associated risk factors.

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Organisations: National Veterinary Institute, Epidemiology, University of Southern Denmark
Authors: Lopes Antunes, A. C. (Intern), Ersbøll, A. K. (Ekstern), Bihrmann, K. (Ekstern), Toft, N. (Intern)
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Risk factors associated with spatio-temporal clusters of high mortality in Danish swine herds

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Electronic versions:
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Relations
Activities:
Sampling pig farms at the abattoir in a cross-sectional study – Evaluation of a sampling method

A cross-sectional study design is relatively inexpensive, fast and easy to conduct when compared to other study designs. Careful planning is essential to obtaining a representative sample of the population, and the recommended approach is to use simple random sampling from an exhaustive list of units in the target population. This approach is rarely feasible in practice, and other sampling procedures must often be adopted. For example, when slaughter pigs are the target population, sampling the pigs on the slaughter line may be an alternative to on-site sampling at a list of farms. However, it is difficult to sample a large number of farms from an exact predefined list, due to the logistics and workflow of an abattoir. Therefore, it is necessary to have a systematic sampling procedure and to evaluate the obtained sample with respect to the study objective. We propose a method for 1) planning, 2) conducting, and 3) evaluating the representativeness and reproducibility of a cross-sectional study when simple random sampling is not possible. We used an example of a cross-sectional study with the aim of quantifying the association of antimicrobial resistance and antimicrobial consumption in Danish slaughter pigs. It was not possible to visit farms within the designated timeframe. Therefore, it was decided to use convenience sampling at the abattoir. Our approach was carried out in three steps: 1) planning: using data from meat inspection to plan at which abattoirs and how many farms to sample; 2) conducting: sampling was carried out at five abattoirs; 3) evaluation: representativeness was evaluated by comparing sampled and non-sampled farms, and the reproducibility of the study was assessed through simulated sampling based on meat inspection data from the period where the actual data collection was carried out. In the cross-sectional study samples were taken from 681 Danish pig farms, during five weeks from February to March 2015. The evaluation showed that the sampling procedure was reproducible with results comparable to the collected sample. However, the sampling procedure favoured sampling of large farms. Furthermore, both under-sampled and over-sampled areas were found using scan statistics. In conclusion, sampling conducted at abattoirs can provide a spatially representative sample. Hence it is a possible cost-effective alternative to simple random sampling. However, it is important to assess the properties of the resulting sample so that any potential selection bias can be addressed when reporting the findings.
Semiquantitative Decision Tools for FMD Emergency Vaccination Informed by Field Observations and Simulated Outbreak Data

We present two simple, semiquantitative model-based decision tools, based on the principle of first 14 days incidence (FFI). The aim is to estimate the likelihood and the consequences, respectively, of the ultimate size of an ongoing FMD epidemic. The tools allow risk assessors to communicate timely, objectively, and efficiently to risk managers and less technically inclined stakeholders about the potential of introducing FMD suppressive emergency vaccination. To explore the FFI principle with complementary field data, we analyzed the FMD outbreaks in Argentina in 2001, with the 17 affected provinces as the units of observation. Two different vaccination strategies were applied during this extended epidemic. In a series of 5,000 Danish simulated FMD epidemics, the numbers of outbreak herds at day 14 and at the end of the epidemics were estimated under different control strategies. To simplify and optimize the presentation of the resulting data for urgent decisions to be made by the risk managers, we estimated the sensitivity, specificity, as well as the negative and positive predictive values, using a chosen day-14 outbreak number as predictor of the magnitude of the number of remaining post-day-14 outbreaks under a continued basic control strategy. Furthermore, during an ongoing outbreak, the actual cumulative number of detected infected herds at day 14 will be known exactly. Among the number of epidemics lasting >14 days out of the 5,000 simulations under the basic control scenario, we selected those with an assumed accumulated number of detected outbreaks at day 14. The distribution of the estimated number of detected outbreaks at the end of the simulated epidemics minus the number at day 14 was estimated for the epidemics lasting more than 14 days. For comparison, the same was done for identical epidemics (i.e., seeded with the same primary outbreak herds) under a suppressive vaccination scenario. The results indicate that, during the course of an FMD epidemic, simulated likelihood predictions of the remaining epidemic size and of potential benefits of alternative control strategies can be
Serological evidence of hepatitis E virus infection in pigs and jaundice among pig handlers in Bangladesh

Hepatitis E virus (HEV) is the most common cause of viral hepatitis in humans. Pigs may act as a reservoir of HEV, and pig handlers were frequently identified with a higher prevalence of antibodies to HEV. The objectives of this study were to identify evidence of HEV infection in pigs and compare the history of jaundice between pig handlers and people not exposed to pigs and pork. Blood and faecal samples were collected from 100 pigs derived from three slaughterhouses in the Gazipur district of Bangladesh from January to June, 2011. We also interviewed 200 pig handlers and 250 non-exposed people who did not eat pork or handled pigs in the past 2 years. We tested the pig sera for HEV-specific antibodies using a competitive ELISA and pig faecal samples for HEV RNA using real-time RT-PCR. Of 100 pig sera, 82% (n = 82) had detectable antibody against HEV. Of the 200 pig handlers, 28% (56/200) demonstrated jaundice within the past 2 years, whereas only 17% (43/250) of controls had a history of jaundice (p < .05). Compared to non-exposed people, those who slaughtered pigs (31% versus 15%, p < .001), reared pigs (37% versus 20%, p < .001), butch-ered pigs (35% versus 19%, p < .001) or involved in pork transportation (28% versus 13%, p < .001) were more likely to be affected with jaundice in the preceding 2 years. In multivariate logistic regression analysis, exposure to pigs (odds ratio [OR]: 2.2, 95% CI: 1.2–3.9) and age (OR: 0.97, 95% CI: 0.95–0.99) was significantly associated with jaundice in the past 2 years. Pigs in Bangladesh demonstrated evidence of HEV infection, and a history of jaundice was significantly more frequent in pig handlers. Identifying and genotyping HEV in pigs and pig handlers may provide further evidence of the pig's role in zoonotic HEV transmission in Bangladesh.
Simulating control of paratuberculosis in Danish dairy herds

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, University of Copenhagen
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Bangladesh, Hepatitis E virus, Jaundice, Pig handlers, Pigs, Pork, Zoonotic HEV
Spatial patterns of antimicrobial resistance genes in a cross-sectional sample of pig farms with indoor non-organic production of finishers

Antimicrobial resistance (AMR) in pig populations is a public health concern. There is a lack of information of spatial distributions of AMR genes in pig populations at large scales. The objective of the study was to describe the spatial pattern of AMR genes in faecal samples from pig farms and to test if the AMR genes were spatially randomly distributed with respect to the geographic distribution of the pig farm population at risk. Faecal samples from 687 Danish pig farms were collected in February and March 2015. DNA was extracted and the levels of seven AMR genes (ermB, ermF, sulI, sulII, tet(M), tet(O) and tet(W)) were quantified on a high-throughput real-time PCR array. Spatial differences for the levels of the AMR genes measured as relative quantities were evaluated by spatial cluster analysis and creating of risk maps using kriging analysis and kernel density estimation. Significant spatial clusters were identified for ermB, ermF, sulII and tet(W). The broad spatial trends in AMR resistance evident in the risk maps were in agreement with the results of the cluster analysis. However, they also showed that there were only small scale spatial differences in the gene levels. We conclude that the geographical location of a pig farm is not a major determinant of the presence or high levels of AMR genes assessed in this study.

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Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
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Scopus rating (2013): SJR 1.313 SNIP 1.126 CiteScore 2.57
ISI indexed (2013): ISI indexed yes
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The Standards for the Reporting of Diagnostic Accuracy (STARD) statement, which was recently updated to the STARD2015 statement, was developed to encourage complete and transparent reporting of test accuracy studies. Although STARD principles apply broadly, the checklist is limited to studies designed to evaluate the accuracy of tests when the disease status is determined from a perfect reference procedure or an imperfect one with known measures of test accuracy. However, a reference standard does not always exist, especially in the case of infectious diseases with a long latent period. In such cases, a valid alternative to classical test evaluation involves the use of latent class models that do not require a priori knowledge of disease status. Latent class models have been successfully implemented in a Bayesian framework for over 20 years. The objective of this work was to identify the STARD items that require modification and develop a modified version of STARD for studies that use Bayesian latent class analysis to estimate diagnostic test accuracy in the absence of a reference standard. Examples and elaborations for each of the modified items are provided. The new guidelines, termed STARD-BLCM (Standards for Reporting of Diagnostic accuracy studies that use Bayesian Latent Class Models), will facilitate improved quality of reporting on the design, conduct and results of diagnostic accuracy studies that use Bayesian latent class models.
Transmission differentials for multible pathogens as inferred from their prevalence in larva, nymph and suit of *Ixodes ricinus* (Acari: *Ixodidae*)

*Ixodes ricinus* serves as vector for a range of microorganisms capable of causing clinical illness in humans. The microorganisms occur in the same vector populations and are generally affected by the same tick-host interactions. Still, the instars have different host preferences which should manifest in different transmission patterns for various microorganisms in the tick populations, i.e., most microorganisms increase in prevalence rate from larvae to nymphs because their reservoirs are among small mammals and birds that serve as blood hosts for larvae. Other microorganisms, like *Anaplasma phagocytophilum*, mainly increase in prevalence rates from nymphs to adults, because their reservoirs are larger ungulates that serve as primary blood hosts for nymphs and adults. We sampled a representative sample of ticks from 12 locations on Zealand and Funen, Denmark, and investigated the differences in prevalence rate of infection in larvae, nymphs and adults for multiple pathogens. Prevalence of infection for larvae, nymphs and adults, respectively, was: 0, 1.5 and 4.5% for *Borrelia burgdorferi*; 0, 4.2 and 3.9% for *Borrelia garinii*; 0, 6.6 and 6.1% for *Borrelia afzelii*; 0, 0 and 0.6% for *Borrelia valaisiana*; 0, 3.7 and 0.6% for *Borrelia spielmani*; 0, 0.7 and 1.2% for *Babesia divergens*; 0, 0, 0.6% for *Babesia venatorum*; 0, 1.5 and 6.1% for *A. phagocytophilum*. The results were in general compatible with the hypothesis i.e., that differences in blood host for larvae and nymphs define differences in transmission of infectious agents, but other factors than differences in blood hosts between larvae and nymphs may also be important to consider.

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Organisations: National Veterinary Institute, Bacteriology & Parasitology, Epidemiology, University of Copenhagen, Agence nationale de la sécurité sanitaire, alimentation, environnement et travail
Authors: Jensen, P. M. (Ekstern), Christoffersen, C. S. (Ekstern), Moutailler, S. (Ekstern), Michelet, L. (Ekstern), Schou, K. K. (Intern), Bødker, R. (Intern)
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Transmission of African swine fever virus from infected pigs by direct contact and aerosol routes

In 2014, African swine fever virus (ASFV) was introduced into the Baltic states and Poland. Since then, the disease has continued to spread within these regions, and recently, cases were reported in the Czech Republic and Romania. Currently, there is an increasing risk of ASFV introduction into Western Europe. Hence, there is an urgent need to assess current contingency plans. For this purpose, knowledge of modes-of-transmission and clinical outcome in pigs infected with new European ASFV strains is needed. In the present study, two experiments were conducted in pigs using an isolate of ASFV from Poland (designated here POL/2015/Podlaskie/Lindholm). In both studies, pigs were inoculated intranasally with the virus and contact pigs were exposed to the experimentally infected pigs, either directly (contact within and between pens) or by air. Pigs exposed to the virus by intranasal inoculation, by direct contact to infected animals and by aerosol developed acute disease characterized by viremia, fever and depression. Infectious virus was first detected in blood obtained from the inoculated pigs and then sequentially among the within-pen, between-pen and air-contact pigs. ASFV DNA and occasionally infectious virus was found in nasal-, oral-, and rectal swabs obtained from the pigs, and ASFV DNA was detected in air samples. No anti-ASFV antibodies were detected in sera.

In conclusion, the study shows that the currently circulating strain of ASFV can be efficiently transmitted via direct contact and by aerosols. Also, the results provide quantitative transmission parameters and knowledge of infection stages in pigs infected with this ASFV.

General information
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Organisations: National Veterinary Institute, Virology, Epidemiology, National Veterinary Research Institute, Centro de Investigación en Sanidad Animal
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BFI (2009): BFI-level 2
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Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.043 SNIP 1.322
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.022 SNIP 1.401
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.078 SNIP 1.262
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.869 SNIP 1.259
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.913 SNIP 1.186
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.84 SNIP 1.112
Web of Science (2002): Indexed yes
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Treatment Patterns for Mastitis in Danish Dairy Cattle Farms

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Vectorborne zoonoses

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What tools are useful for monitoring endemic diseases? A simulation study based on different time-series components.
Control and eradication programs play an important role in disease monitoring and surveillance. It is important to follow up on implemented strategies to reduce and/or eliminate a specific disease. The objectives of this study were to investigate the performance of different detection methods, including methods commonly used in biosurveillance as well as state space models, for monitoring the effect of endemic disease control and eradication programs. We simulated 16 different scenarios of changes in disease sero-prevalence, inspired by real-world data from the Danish PRRS (Porcine Reproductive and Respiratory Syndrome) monitoring program. The changes included increases, decreases and/or constant sero-prevalence levels in different combinations. Two state space models were used to model the simulated data and different monitoring methods, such as univariate process control algorithms (UPCA) and monitoring of the trend component were tested. The performance was evaluated as the proportion of iterations with an alarm for a given week. Results revealed that the different UPCA performed differently with respect to detecting increasing and decreasing changes in sero-prevalence. The trend-based methods performed well for detecting the first event but its performance was poorer in adapting to several consecutive events. The different monitoring methods had different performances in monitoring increasing and decreasing changes in disease sero-prevalence, showing that the objectives of the monitoring program should be taken into account when choosing which methods to use. The principles used in this study can also be applied in disease surveillance of (re-)emerging diseases.
Monitoring diseases based on register data: Methods and application in the Danish swine production

The spread of diseases is one of the most important threats to animal production and public health. Disease spread causes considerable economic losses for the agricultural sector and constitutes trade-limiting factors, as transmission to countries free from disease should be avoided. Monitoring and surveillance systems are critical for the timely and effective control of infectious diseases. The ability of a system to detect changes in the disease burden depends on the choice of data source. Many factors can lead to inconsistent data collection among populations and it is therefore important to assess the quality of data before use in disease monitoring and surveillance. Over the past decade, several studies have focused on using statistical control methods to detect outbreaks of (re-)emerging diseases in the context of syndromic surveillance – both in human and veterinary medicine – in an attempt to supplement traditional sentinel surveillance. However, it may not be possible to generalize the performance of these methods to the context of other countries (where data have different characteristics), or to the context of endemic diseases. Lower incidence rates are normally expected for endemic diseases compared to highlyinfectious (re-emerging) diseases, due to control measures such as vaccination or health management programs. Furthermore, the data collected differ from those obtained from traditional surveillance (generally related to incidence monitoring), due to its focus on the endemic scenario, with less frequently sampled data. This reflects the added complexity of monitoring endemic diseases, as disease burden is affected not only by the incidence, but also by the duration and recovery rate. The aim of this thesis was to evaluate existing register data related to veterinary health, as a tool for monitoring swine diseases in Denmark. This included: i) describing and evaluating the quality of data (regarding the potential for disease monitoring and surveillance) in Danish databases related to swine health; ii) assessing the feasibility of studying changes in data records over time to detect changes that might indicate disease spread between swine herds; iii) evaluating the performance of different time-series methods for the monitoring and surveillance of endemic diseases, as well as assessing the impact of noise in the data on the results when using these methods. Some of the work presented was focused on endemic diseases, using Porcine Reproductive and Respiratory Syndrome (PRRS) as example. Interviews were conducted with relevant stakeholders in order to assess the data quality of seven databases: the Central Husbandry Register (CHR), the swine movement database (SMD), the national Danish database of drugs for veterinary use (VetStat), laboratorydiagnostic data from the National Veterinary Institute – Technical University of Denmark (DTU-Vet lab) and the Pig Research Centre - SEGES (VSP-SEGES lab), the
Specific Pathogen Free System (SPF System) and the Meat Inspection database. The guidelines from the European Centre for Disease Prevention and Control (ECDC) for monitoring data quality and surveillance systems were used. The findings showed that limitations included delayed transfer of data to databases and incomplete representation of Danish swine herds. Laboratory submission data for testing PRRS were used to study temporal changes in data records, due to the large amount of diagnostic data available. The laboratory data proved to be useful for monitoring temporal patterns of disease occurrence. The fact that some Danish swine herds are tested monthly allows for changes in disease prevalence and incidence to be monitored, which is an example of sentinel surveillance. However, for other herds, the frequency of testing (i.e. the representativeness of the data) depends on factors such as the herd status, farmer compliance, the value of the animal, commercial purposes and ongoing control and eradication programs. This limitation did not apply to the mortality data, which is available for all Danish swine herds on a monthly basis. However, observed changes might be due to disease occurrence, or as a result of changes in herd management or a lack of accuracy in the calculation of mortality. Several scenarios representative of changes in endemic disease sero-prevalence programs were simulated to test the performance of different monitoring methods. These included univariate process control algorithms applied directly to the simulated data, as well as using the forecast errors and trend-based methods. The performance of these methods was evaluated based on the sensitivity and time taken to detect changes, which showed that some methods were more efficient than others for specific patterns. Therefore, choosing a single temporal monitoring method is challenging, and the objectives of the monitoring program and the differing performance of the methods in detecting a specific pattern should be taken into account. Changes in the noise of the data had an impact on the univariate process control algorithms, while the trend-based methods provided a consistent approach to monitoring changes in disease or sero-prevalence. The findings of this thesis may serve as a basis for the improvement of monitoring swine diseases in Denmark. Although the available databases have the potential for use in disease monitoring and surveillance of swine herds in Denmark, improvements are needed for accurate and real-time implementation. Further research relating to the improvement of data quality, as well as combining different data sources for monitoring endemic diseases in Denmark is needed.

General information
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Organisations: National Veterinary Institute, Epidemiology
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Spatial Distribution and Abundance of Culicodes Imicola and Obsoletus Group in Europe

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Spatio-temporal flooding fluctuation analysis: wetland management Bañado La Estrella, Chaco región, Argentina
The wetlands are widely distributed over the Chaco region. Despite their wide territorial extension and major functional role, Bañado la Estrella wetlands have not been appropriately mapped, and this is not a protected area nowadays. Wetlands are ecosystems that depend on periodical flooding, which determine the presence of soils with hydromorphic features and species adapted to permanent or temporary flooding conditions. The bed of the Pilcomayo River began regressing to the west about 30 years ago, creating a wetlands known as the “Bañado la Estrella”. We propose an integrated approach, based on satellite imagery analysis (Landsat TM), the NDWI index (Normalized Difference Water) and decision trees, to analyze and characterize seasonal variations (1992-2012) and to map seasonal flooding. We use information about land use and herd distribution (anthropogenic use) and validate it with field data. Four classes of flooding frequency were defined: permanent flooded areas (80-100 % of the time pixels showed water presence), usually flooded areas (60-100% of the time) and regularly flooded areas (40-60% of the time) during the 1992-2012 period. We are able to delimitate and quantify the total area of Bañado la Estrella wetlands which occupies 1682 km² including the permanently, usually and regularly flooded areas. This spatio temporal analysis shows that during the dry period the permanently flooded areas were reduced 462 km² of the total wetland area while the usually flooded area occupied 2 % of the total area and the regularly flooded area occupied 5%. Our results suggest that this method can be used to delimitate different zones, gathering together hydrodynamic and anthropogenic activities, in order to be used as tool for the creation of a future protect area in Argentina.

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Organisations: National Veterinary Institute, Epidemiology, Universidad Nacional de Tucuman, ProYungas Foundation
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Flooding fluctuations, Wetlands management, Protect area

Big Data fra jord til bord

Danske landmænd og virksomhederne i fødevaresektoren har gode forudsætninger for at drage nytte af den rivende udvikling inden for indsamling og bearbejdning af data:

• Danmark har en stærk fødevaresektor. Det skyldes bl.a., at alle dele af værdikæden arbejder tæt sammen. Fra primærproducenterne, over forarbejdningsindustrien, agroindustrien til videns- og forskningsmiljøerne. Effektiv ressourceudnyttelse og fokus på optimering i hele værdikæden gør sektoren i stand til at konkurriere på verdensmarkedet.

• Danske fødevarevirksomheder har altid været gode til at opdyrke nye forretningsmodeller og finde nye innovative veje til øget værdiskabelse. For eksempel gennem smartere måder at producere på, levere produkterne på eller at indarbejde større værdi i produkterne, så de kan sælges med større fortrin.

• Dansk landbrug og hele værdikæden i fødevaresektoren producerer store mængder af data. Det skyldes bl.a. et højt automationsniveau og myndighedernes krav til dokumentation af fødevarekvaliteten, når de danske producenter leverer fødevarer til forbrugerne verden over. Der er imidlertid et stort spring fra at råde over store mængder af data til at bruge dem aktivt i forretningsudviklingen. Denne rapport viser, hvordan Big Data kan være ét af omdrejningspunkter

General information

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Organisations: Office for Innovation & Sector Services, Department of Applied Mathematics and Computer Science, Statistics and Data Analysis, National Food Institute, Division of Risk Assessment and Nutrition, Research Group for Analytical Food Chemistry, National Veterinary Institute, Epidemiology, Department of Management Engineering, Management Science, Transport DTU, Operations Management, Department of Bio and Health Informatics, IT Service, High Performance Computing, DI Itek, Landbrug og Fødevarer, City Pressekontor
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EFSA (European Food Safety Authority) and ECDC (European Centre for Disease Prevention and Control), 2014. The European Union Summary Report on Trends and Sources of Zoonoses, Zoonotic Agents and Food-borne Outbreaks In 2012

Zoonoses are infections and diseases that are naturally transmissible, directly or indirectly, for example via contaminated foodstuffs, between animals and humans. The severity of these diseases in humans varies from subclinical infection or mild symptoms to life-threatening conditions. In order to prevent zoonoses from occurring, it is important to identify which animals and foodstuffs are the main sources of infection. For this purpose information aimed at protecting human health is collected and analysed from all European Union Member States.

In 2012, 27 Member States submitted information on the occurrence of zoonoses, zoonotic agents and food-borne outbreaks to the European Commission and the European Food Safety Authority. Furthermore, information on cases of zoonoses reported in humans was provided by the European Centre for Disease Prevention and Control. In addition, three European countries that were not European Union Member States provided information. The European Food Safety Authority and the European Centre for Disease Prevention and Control jointly analysed the data, the results of which are published in this annual European Union Summary Report, which covers 15 zoonoses and food-borne outbreaks.

In 2012, the notification rate and confirmed number of cases of human campylobacteriosis in the European Union
The number of salmonellosis cases in humans decreased by 4.7 % compared with 2011. A statistically significant decreasing trend in the European Union was observed over the period 2008-2012. In total, 91,034 confirmed human cases were reported in 2012. A statistically significant increasing trend in the number of reported cases compared with 2011 (132 cases), but a 33.5 % decrease compared with 2010 (349 cases). 2012 was the first year in which Member States were specifically invited to report data on West Nile virus in the European Union. There was an overall 75.8 % increase in the number of reported cases compared with 2011 (132 cases), but a 33.5 % decrease compared with 2010 (349 cases). 2012 was the first year in which Member States were specifically invited to report data on West Nile virus in animals. Most data were from solipeds, notably horses, and less information was received from birds and other animal species. Test-positive solipeds were reported by Southern European countries but few test-positive horses were also found. The reported prevalence of bovine tuberculosis in cattle increased slightly at European Union level, but remained at a very low level. This slight increase was, however, due to one Member State that reported an increase in prevalence of bovine tuberculosis for the fourth consecutive year.

The number of confirmed human tuberculosis cases due to Mycobacterium bovis in the European Union in 2012 was 125. This was a decrease compared with 2011, with a few Member States accounting for the majority of the reported cases. The reported prevalence of bovine tuberculosis in cattle increased slightly at European Union level, but remained at a very low level. This slight increase was, however, due to one Member State that reported an increase in prevalence of bovine tuberculosis for the fourth consecutive year.

Trichinella caused 301 confirmed human cases in the European Union. Although the number of cases was slightly higher in 2012 than in 2011, human trichinellosis cases remained at a low level in the European Union compared with 2009 and previous years. In 2012, the prevalence of Trichinella in pigs was similar to that observed in 2011. The parasite was more prevalent in wildlife than in farmed animals. However, seven out of the nine strong-evidence outbreaks reported were due to consumption of pig meat.

Toxoplasma was reported by the Member States from pigs, sheep, goats, hunted wild boar and hunted deer, in 2011 and 2012. In addition, positive findings were detected in cats (the natural hosts), cattle and dogs as well as several other animal species, indicating the wide distribution of the parasite among different animal and wildlife species.

One domestically acquired human case and one imported human case of rabies were reported in the European Union in 2012. In addition, positive findings were detected in cats (the natural hosts), cattle and dogs as well as several other animal species, indicating the wide distribution of the parasite among different animal and wildlife species.

The number of confirmed brucellosis cases in humans was 328 at European Union level, which was almost the same as in 2011. The number of brucellosis-positive cattle, and sheep and goat herds continued to decrease, although marginally compared with 2011.

A total of 5,671 confirmed verocytotoxigenic Escherichia coli infections were reported in 2012, which was a decrease of 40 % compared with 2011. Of those cases in which the serogroup was known, most were caused by serogroup O157, followed by O26 and O91. There was an increasing European Union trend of confirmed human verocytotoxigenic Escherichia coli infections in 2008-2012. Even without the 2011 data the European Union trend for verocytotoxigenic Escherichia coli infections during 2008–2010 was significantly increasing. Human pathogenic verocytotoxigenic Escherichia coli strains were detected by the reporting Member States from fresh bovine meat occasionally and at low levels. The human pathogenic verocytotoxigenic Escherichia coli serogroups isolated from the bovine meat and cattle samples included VTEC O157, O26, O91, O103 and O145.

The number of listeriosis cases in humans increased slightly compared with 2011, and 1,642 confirmed human cases were reported in 2012. A statistically significant increasing trend in the number of reported cases compared with 2011 (132 cases), but a 33.5 % decrease compared with 2010 (349 cases). 2012 was the first year in which Member States were specifically invited to report data on West Nile virus in animals. Most data were from solipeds, notably horses, and less information was received from birds and other animal species. Test-positive solipeds were reported by Southern European countries but few test-positive horses were also found.
A total of 5,363 food-borne outbreaks were reported in the European Union, resulting in 55,453 human cases, 5,118 hospitalisations and 41 deaths. Most of the reported outbreaks were caused by Salmonella, bacterial toxins, viruses and Campylobacter. The most important food sources of the outbreaks were eggs and egg products, followed by mixed food and fish and fish products. Overall, 16 waterborne outbreaks were reported in 2012, caused by calicivirus, verocytotoxigenic E. coli, Cryptosporidium parvum and rotavirus.

General information
State: Published
Organisations: National Food Institute, Division of Risk Assessment and Nutrition, National Veterinary Institute, Epidemiology, Research Group for Genomic Epidemiology
Authors: EFSA Journal
Number of pages: 312
Publication date: 2014

Publication information
Place of publication: Parma, Italy
Publisher: European Food Safety Authority
Original language: English

Series: The EFSA Journal
Volume: 12(2)
Number: 3547
ISSN: 1830-5458
Main Research Area: Technical/natural sciences
Zoonoses, Monitoring, Salmonella, Campylobacter, Listeria, Parasites, Food-borne outbreaks
Electronic versions:
EUSR_2012.pdf
Source: PublicationPreSubmission
Source-ID: 119656492
Publication: Commissioned - peer-review › Report – Annual report year: 2015

European Food Safety Authority, European Centre for Disease Prevention and Control; The European Union Summary Report on Trends and Sources of Zoonoses, Zoonotic Agents and Food-borne Outbreaks in 2009
The European Food Safety Authority and the European Centre for Disease Prevention and Control have analysed the information on the occurrence of zoonoses and food-borne outbreaks in 2009 submitted by 27 European Union Member States. In 2009, 108,614 salmonellosis cases in humans were reported and the statistically significant decreasing trend in the case numbers continued. Eighteen Member States reached the European Union Salmonella reduction target for breeding flocks of fowl, 17 Member States met their reduction target for laying hens and 18 Member States met the reduction target for broilers. In foodstuffs, Salmonella was most often detected in fresh poultry and pig meat. Campylobacteriosis was the most commonly reported zoonosis with 198,252 human cases. Campylobacter was most often detected in fresh broiler meat. The number of listeriosis cases in humans increased by 19.1 % compared to 2008, with 1,645 cases in 2009. Listeria was seldom detected above the legal safety limit from ready-to-eat foods. Member States reported 3,573 verotoxigenic Escherichia coli (VTEC), 7,595 yersiniosis and 401 brucellosis cases in humans, while VTEC bacteria were mostly found from cattle and bovine meat and Yersinia from pigs and pig meat. Brucellosis and tuberculosis decreased in cattle, sheep and goat populations. In humans 1,987 Q fever cases were detected in 2009, and 1,259 human cases of toxoplasmosis were mainly detected in wild life. There were 1,259 human cases of toxoplasmosis reported and in animals Toxoplasma was most often found in sheep and goats. Rabies was recorded in one person in the European Union and the disease was also found in animals. Most of the 5,550 reported food-borne outbreaks were caused by Salmonella, viruses and bacterial toxins and the most important food sources were eggs, mixed or buffet meals and pig meat.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Risk Assessment and Nutrition, National Veterinary Institute, Epidemiology, Research Group for Microbial Food Safety
Authors: EFSA Journal
Number of pages: 378
Publication date: 2011

Publication information
Place of publication: Parma, Italy
Publisher: European Food Safety Authority
Original language: English
Projects:

**Disease databases**
The general purpose of the project is to explore the potential use and value of different data sources as a monitoring tool for detection of diseases in Danish swine herds. The project is a continuation of the PhD project "Veterinary Epidemiology with the focus on monitoring livestock disease using diagnostic databases", in which different databases and monitoring methods were explored in the context of endemic diseases.
As a starting point, the project will be focused on methods to detect changes in mortality and to find possible links among diseases occurrence, antibiotic usage, and other data streams (such as meat inspection and laboratory diagnostic data).

National Veterinary Institute

**Epidemiology**
Period: 01/01/2017 → 31/12/2019
Number of participants: 3
Project participant:
Lopes Antunes, Ana Carolina (Intern)
Jensen, Vibeke Frøkjær (Intern)
Toft, Nils (Intern)

**Activities:**

**Interactive, web-based health data visualisation with RStudio Shiny**
Period: 26 Mar 2018 → 28 Mar 2018
Ana Carolina Lopes Antunes (Participant)

National Veterinary Institute

**Epidemiology**
Degree of recognition: International

**Related event**

**Interactive, web-based health data visualisation with RStudio Shiny**
26/03/2018 → 28/03/2018
Uppsala, Sweden
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**What to look for when monitoring endemic disease? Translating large volumes of data into valuable data for disease surveillance**
Period: 5 Mar 2018
Ana Carolina Lopes Antunes (Invited speaker)

National Veterinary Institute

**Epidemiology**

**Related event**
High quality pork 2018
05/03/2018 → 06/03/2018
Da Nang, Viet Nam
Activity: Talks and presentations › Conference presentations

Simulating control of paratuberculosis in Danish dairy herds
Period: 15 Nov 2017
Carsten Thure Kirkeby (Guest lecturer)
National Veterinary Institute
Epidemiology
Description
Presentation for CPH Cattle
Documents:
Abstract CKIR CPH Cattle

Related event

Copenhagen Cattle 2017
15/11/2017 → 15/11/2017
Copenhagen, Denmark
Activity: Talks and presentations › Conference presentations

Risk factors associated with spatio-temporal clusters of high mortality in Danish swine herds
Period: 4 Oct 2017
Ana Carolina Lopes Antunes (Guest lecturer)
National Veterinary Institute
Epidemiology
Description
Presented at the ECVPH AGM & Annual Scientific Conference 2017
Degree of recognition: International
Documents:
Proceedings -ECVPH-2017-v06

Related event

ECVPH AGM & Annual Scientific Conference 2017
02/10/2017 → 04/10/2017
Liege, Belgium
Activity: Talks and presentations › Conference presentations

How can we improve public health, food hygiene, and animal welfare in developing country slaughterhouses?
Period: 3 Oct 2017
Ana Carolina Lopes Antunes (Organizer)
National Veterinary Institute
Epidemiology
Degree of recognition: International

Related event

How can we improve public health, food hygiene, and animal welfare in developing country slaughterhouses?
03/10/2017 → …
Liege, Belgium
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

ECVPH AGM & Annual Scientific Conference 2017
Period: 2 Oct 2017 → 4 Oct 2017
Dynamics of intra-mammary infections causing pathogens: A herd-, cow- and strain-specific model.
Period: 21 Sep 2017
Carsten Thure Kirkeby (Guest lecturer)
National Veterinary Institute
Epidemiology

Description
Presentation at the EMRW meeting 2017
Degree of recognition: International
Links:
http://cphcattle.ku.dk/seminarer/emrw/

Related external organisation
University of Copenhagen
Thorvaldsensvej 40, DK-1871 Frederiksberg C, Copenhagen, Denmark
Activity: Talks and presentations › Conference presentations

Maul- und Klauenseuche – verschiedene Bekämpfungsmethoden und ihre Auswirkungen
Period: 6 Sep 2017 → 8 Sep 2017
Carola Sauter-Louis (Other)
Christoph Staubach (Other)
Thomas Selhorst (Other)
Tariq Hisham Beshara Halasa (Guest lecturer)
Christine Pottgiese (Other)
Jorn Gethmann (Other)
Carolina Probst (Other)
Brend Haas (Other)
Franz J. Conraths (Other)
National Veterinary Institute
Epidemiology

Description
Poster presentation in the DVG-Epidemiologie Conference, DACH-Epi 2017, 6th -8th September 2017, Hall in Tirol, Austria
Degree of recognition: International

Related event
the DVG-Epidemiologie Conference,
06/09/2017 → 08/09/2017
Activity: Talks and presentations › Conference presentations

Modelling of disease spread
Period: 5 Jun 2017 → 23 Jun 2017
Ana Carolina Lopes Antunes (Participant)
National Veterinary Institute
Epidemiology

Related event

Modelling of disease spread
05/06/2017 → 23/06/2017
Lyngby, Denmark
Activity: Other

ETALEE 2017
Period: 23 May 2017 → 24 May 2017
Carsten Thure Kirkeby (Participant)
National Veterinary Institute
Epidemiology

Description

The aim of the conference is to shine the spot light on forms of teaching and learning that motivate, activate and engage students. The conference aims to provide a meeting place where you can interact and exchange experiences with colleagues from other engineering education institutions. Thus, you are encouraged to bring good examples from your teaching practice on the use of active learning (article in danish - english) in engineering education.

The conference will be a mixture of active keynotes, practical Hands-on sessions, Explore sessions, an active Poster session and social arrangements.
Degree of recognition: International
Links:
http://www.etalee.dk

Related event

ETALEE 2017: Exploring Teaching for Active Learning in Engineering Education 2017
23/05/2017 → 24/05/2017
Odense, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

International Conference in Animal Health Surveillance 3
Period: 1 May 2017 → 4 May 2017
Ana Carolina Lopes Antunes (Speaker)
National Veterinary Institute
Epidemiology
Degree of recognition: International

Related event

International Conference in Animal Health Surveillance 3
01/05/2017 → 04/05/2017
Rotorua, New Zealand
Activity: Talks and presentations › Conference presentations

What tools are useful for monitoring endemic diseases? A simulation study based on different time-series components.
Period: 1 May 2017 → 4 May 2017
Ana Carolina Lopes Antunes (Speaker)
National Veterinary Institute
Epidemiology
Degree of recognition: International

Related event
International Conference in Animal Health Surveillance 3
01/05/2017 → 04/05/2017
Rotorua, New Zealand
Activity: Talks and presentations ▶ Conference presentations

EVALUATION OF ADAPTIVE TEST STRATEGIES FOR CONTROL AND ERADICATION OF PARATUBERCULOSIS WITHIN DAIRY CATTLE HERDS
Period: 29 Mar 2017 → 31 Mar 2017
Carsten Thure Kirkeby (Invited speaker)
National Veterinary Institute

Epidemiology

Links:

Related event
2017 Annual Meeting of SVEPM 2017, 29-31 March, Inverness, Scotland
29/03/2017 → 31/03/2017
Scotland, United Kingdom
Activity: Talks and presentations ▶ Conference presentations

Danish OIKOS Annual Meeting
Period: 10 Mar 2017 → 11 Mar 2017
Najmul Haider (Speaker)
National Veterinary Institute

Epidemiology

Description
Oral Presentation in The Danish OIKOS Annual Meeting 2017
Title: Vector-borne diseases transmission and microclimate

Authors: Najmul Haider, Carsten Kirkeby, Birgit Kristensen, Lene Jung Kjaer, Jens Havskov Sørensen, Rene Bedker
Degree of recognition: Regional
Documents:
OIKOS2017_ScientificProgramme_ver2

Related event
Danish OIKOS Annual Meeting
10/03/2017 → 11/03/2017
Frederiksberg, Denmark
Activity: Talks and presentations ▶ Conference presentations

Sørensen, AIV, Boklund, A, Toft, N, Espinosa-Gongora, C, Larsen, J & Halasa, T: Modelling within-herd spread of MRSA
Period: 1 Feb 2017
Anna Irene Vedel Sørensen (Speaker)
National Veterinary Institute

Epidemiology

Description
Oral presentation
Spatiotemporal flooding fluctuation analysis: wetland management Bañado La Estrella, Chaco region, Argentina

We propose an integrated approach, based on satellite imagery analysis (Landsat TM), the NDWI index (Normalized Difference Water) and decision trees, to analyze and characterize seasonal variations (1992-2012) and to map seasonal flooding in Bañado La Estrella wetlands.

Documents:
Abstract Book-china conference

Related event
10th INTERCOL International Wetlands Conference
Period: 19 Sep 2016 → 24 Sep 2016
Ana Carolina Cuellar (Participant)
National Veterinary Institute

Epidemiology

Description
Spatiotemporal flooding fluctuation analysis: wetland management Bañado La Estrella, Chaco region, Argentina

We propose an integrated approach, based on satellite imagery analysis (Landsat TM), the NDWI index (Normalized Difference Water) and decision trees, to analyze and characterize seasonal variations (1992-2012) and to map seasonal flooding in Bañado La Estrella wetlands.

Degree of recognition: International
Documents:
Abstract Book-china conference

Related event
10th INTERCOL International Wetlands Conference
19/09/2016 → 24/09/2016
Changshu, China
Activity: Attending an event › Participating in or organising a conference

University of Southern Denmark
Ana Carolina Lopes Antunes (Visiting researcher)
National Veterinary Institute

Epidemiology
Activity: Visiting an external institution › Visiting another research institution

Food and Agriculture Organization of the United Nations (FAO) Participatory Epidemiology Forum
Period: Oct 2015 → …
Ana Carolina Lopes Antunes (Participant)
National Veterinary Institute

Epidemiology
Degree of recognition: International
Links:
Activity: Other

National Veterinary Institute Sweden
Period: Feb 2015 → Mar 2015
Ana Carolina Lopes Antunes (Visiting researcher)
National Veterinary Institute
Prizes:

**MSD Animal Health names 2018 High Quality Pork Ph.D. award**  
Ana Carolina Lopes Antunes (Recipient)  
National Veterinary Institute, Epidemiology

**Details**  
Awarded date: 2018  
Degree of recognition: International  
Prize: Prizes, scholarships, distinctions

**Poster Prize**  
Anna Irene Vedel Sørensen (Recipient)  
National Veterinary Institute, Epidemiology

**Description**  
Poster prize awarded for the poster: "Modelling spread of MRSA within a pig herd"

**Details**  
Awarded date: 30 Mar 2017  
Granting Organisations: Society for Veterinary Epidemiology and Preventive Medicine  
event: 2017 Annual Meeting of SVEPM 2017, 29-31 March, Inverness, Scotland  
Prize: Prizes, scholarships, distinctions

**Roberto Chizzoline Memorial Poster Award 2017**  
Ana Carolina Lopes Antunes (Recipient)  
National Veterinary Institute, Epidemiology

**Description**  
Poster presented at the ECVPH AGM & Annual Scientific Conference 2017

**Details**  
Awarded date: 4 Oct 2017  
Degree of recognition: International  
Granting Organisations: European College of Veterinary Public Health  
Prize: Prizes, scholarships, distinctions

Press clippings:

**Uudforskede data giver ny viden om svins dødelighed**  
Ana Carolina Lopes Antunes  
19/12/2017  
National Veterinary Institute, Epidemiology

**Media coverage (1)**

**Uudforskede data giver ny viden om svins dødelighed**  
19/12/2017  
Denmark, Web  
Ana Carolina Lopes Antunes  
Press / Media