Research outputs:

Screening for multiple tick-borne pathogens in Ixodes ricinus ticks from birds in Denmark during spring and autumn migration seasons

Presently, it is uncertain to what extent seasonal migrating birds contribute to the introduction of ticks and tick-associated pathogens in Denmark. To quantify this phenomenon, we captured birds during the spring and autumn migration at three field sites in Denmark and screened them for ticks. Bird-derived ticks were identified to tick species and screened for 37 tick-borne pathogens using real-time PCR. Overall, 807 birds, representing 44 bird species, were captured and examined for ticks during the spring (292 birds) and autumn migrations (515 birds). 10.7% of the birds harboured a total of 179 Ixodes ricinus ticks (38 ticks in spring and 141 in the autumn) with a mean infestation intensity of 2.1 ticks per bird. The European robin (Erithacus rubecula), the common blackbird (Turdus merula), and the common redstart (Phoenicurus phoenicurus) had the highest infestation intensities. 60.9% of the ticks were PCR-positive for at least one tick-borne pathogen. Borrelia DNA was found in 36.9% of the ticks. The Borrelia species detected were B. spielmanii (15.1%), B. valaisiana (13.4%), B. garinii (12.3%), B. burgdorferi s.s. (2.2%), B. miyamotoi (1.1%), and B. afzelii (0.6%). In addition, 10.6% and 1.7% of the samples were PCR-positive for spotted fever group rickettsiae and Candidatus Neoehrlichia mikurensis. All of the tick-borne pathogens that we found in the present study are known to occur in Danish forest populations of I. ricinus. Our study indicates that migrating birds can transport ticks and their pathogens from neighboring countries to Denmark including sites in Denmark without a sustainable tick population. Thus, a tick-borne pathogen affecting human or animal health emerging at one location in Europe can rapidly be introduced to other countries by migrating birds. These movements are beyond national veterinary control. The current globalization, climatic and environmental changes affect the potential for introduction and establishment of ticks and tick-borne pathogens in Northern Europe. It is therefore important to quantify the risk for rapid spread and long distance exchange of tick-borne pathogens in Europe.
Emerging vector borne infections in Europe - prevention, early detection, control and the impact of wildlife

Vector borne infections continue to emerge and spread in Europe. Climate, environmental change and globalisation may be important drivers but there is no simple explanation for this development.

**General information**

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Organisations: National Veterinary Institute, Epidemiology
Contributors: Bødker, R.
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Infection of pigs with African swine fever virus via ingestion of stable flies (Stomoxys calcitrans)

Within Eastern Europe, African swine fever virus (ASFV) has unexpectedly spread to farms with high biosecurity. In an attempt to explain this process, pigs were allowed to ingest flies that had fed on ASFV-spiked blood, which had a realistic titre for an infected pig. Some of the pigs became infected with the virus. Thus, ingestion of blood-sucking flies, having fed on ASFV-infected wild boar before entering stables, represents a potential route for disease transmission.

**General information**

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Organisations: National Veterinary Institute, Virology, Epidemiology
Contributors: Olesen, A. S., Lohse, L., Hansen, M. F., Boklund, A., Halasa, T., Belsham, G. J., Rasmussen, T. B., Bøtner, A., Bødker, R.
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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 jack 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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**Monthly variation in the probability of presence of adult Culicoides populations in nine European countries and the implications for targeted surveillance**

**BACKGROUND:** Biting midges of the genus Culicoides (Diptera: Ceratopogonidae) are small hematophagous insects responsible for the transmission of bluetongue virus, Schmallenberg virus and African horse sickness virus to wild and domestic ruminants and equids. Outbreaks of these viruses have caused economic damage within the European Union. The spatio-temporal distribution of biting midges is a key factor in identifying areas with the potential for disease spread. The aim of this study was to identify and map areas of neglectable adult activity for each month in an average year.

Average monthly risk maps can be used as a tool when allocating resources for surveillance and control programs within Europe.

**METHODS:** We modelled the occurrence of C. imicola and the Obsoletus and Pulicaris ensembles using existing entomological surveillance data from Spain, France, Germany, Switzerland, Austria, Denmark, Sweden, Norway and Poland. The monthly probability of each vector species and ensembles being present in Europe based on climatic and environmental input variables was estimated with the machine learning technique Random Forest. Subsequently, the monthly probability was classified into three classes: Absence, Presence and Uncertain status. These three classes are useful for mapping areas of no risk, areas of high-risk targeted for animal movement restrictions, and areas with an uncertain status that need active entomological surveillance to determine whether or not vectors are present.

**RESULTS:** The distribution of Culicoides species ensembles were in agreement with their previously reported distribution in Europe. The Random Forest models were very accurate in predicting the probability of presence for C. imicola (mean AUC = 0.95), less accurate for the Obsoletus ensemble (mean AUC = 0.84), while the lowest accuracy was found for the Pulicaris ensemble (mean AUC = 0.71). The most important environmental variables in the models were related to temperature and precipitation for all three groups.

**CONCLUSIONS:** The duration periods with low or null adult activity can be derived from the associated monthly distribution maps, and it was also possible to identify and map areas with uncertain predictions. In the absence of ongoing vector surveillance, these maps can be used by veterinary authorities to classify areas as likely vector-free or as likely risk areas from southern Spain to northern Sweden with acceptable precision. The maps can also focus costly entomological surveillance to seasons and areas where the predictions and vector-free status remain uncertain.
Nye blodsugere krydser grænsen


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Predicting and mapping human risk of exposure to Ixodes ricinus nymphs in northern Europe using climatic and environmental data

In recent years, focus on tick-borne diseases has increased as diseases such as Lyme disease and tick-borne encephalitis have become more common and represent a health problem in many parts of Scandinavia. More effective prevention of infections requires a better understanding of the factors affecting the vector abundance as well as human exposure to the vectors. Hence, 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 tick nymphs at 159 sites (forests and meadows) in Denmark, southern Norway and south-eastern Sweden. At each site we measured presence/absence, and used the data obtained along with environmental data from satellite images to run Boosted Regression Tree machine learning algorithms to predict overall distribution in southern Scandinavia. Together with the predicted distribution maps, we used human population density maps to identify and plot areas with high risk of exposure to ticks.

The predicted distribution and the spatial variation found corresponded well with known distributions of ticks in Scandinavia (sensitivity: 91%, specificity: 60%), and we found that the model was predominantly temperature-driven. Because presence was strongly correlated with forested habitats the risk areas were much larger in Sweden and Norway compared to Denmark. When combining these distribution maps with human population density maps, we were able to quantify the proportion of people living in areas with tick presence in Scandinavia. We found that although tick nymphs were restricted to a small proportion of the modelled area, high proportions of the human populations (67-79%) lived within these same areas. The model suggests that a potential future range expansion of I. ricinus in Scandinavia is likely but may only affect a relatively small additional proportion of the human population.

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Organisations: Epidemiology, National Veterinary Institute, Statistics and Data Analysis, Department of Applied Mathematics and Computer Science, Bacteriology & Parasitology, Norwegian Institute of Public Health, University of Agder, Norwegian University of Life Sciences, University of Agricultural Sciences
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Prevalence of tick-borne viruses in Ixodes ricinus assessed by high-throughput real-time PCR

Ticks are one of the principal arthropod vectors of human and animal infectious diseases. Whereas the prevalence of tick-borne encephalitis virus in ticks in Europe is well studied, there is less information available on the prevalence of the other tick-borne viruses (TBVs) existing worldwide. The aim of this study was to improve the epidemiological survey tools of TBVs by the development of an efficient high-throughput test to screen a wide range of viruses in ticks. In this study, we developed a new high-throughput virus-detection assay based on parallel real-time PCRs on a microfluidic system, and used it to perform a large scale epidemiological survey screening for the presence of 21 TBVs in 18,135 nymphs of I. ricinus collected from five European countries. This extensive investigation has (i) evaluated the prevalence of four viruses present in the collected ticks, (ii) allowed the identification of viruses in regions where they were previously undetected. In conclusion, we have demonstrated the capabilities of this new screening method that allows the detection of numerous TBVs in a large number of ticks. This tool represents a powerful and rapid system for TBVs surveillance in Europe and could be easily customized to assess viral emergence.
Relative abundance and geographical variation of Culex pipiens and Culex torrentium (Diptera: Culicidae) in CO₂-baited traps in Denmark

European Culex pipiens and Culex torrentium are morphological fairly similar mosquito species with potentially different vector competences for pathogenic viruses. The relative abundance of the two species is therefore important for quantifying the potential for disease transmission in Denmark. Mosquitoes were sampled from 74 different sites in Denmark with CO₂ and octenol-baited suction traps. A total of 285 Culex specimens were identified to species using a restriction enzyme assay. Culex pipiens was the dominating species with 220 (77%) specimens caught at 22 different sites, while 65 (23%) specimens were identified as C. torrentium and only caught at 4 sites. The ratio of the two species differed significantly between sites with C. torrentium dominating in just a single location. Both mosquito species were predominantly caught late in the Danish mosquito season, from mid-August and onwards.

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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.
Survival and localization of African swine fever virus in stable flies (Stomoxys calcitrans) after feeding on viremic blood using a membrane feeder

Since 2014, African swine fever virus (ASFV) has been spreading within Eastern Europe. Within affected regions, the virus has infected some farms with high biosecurity and a marked seasonality of outbreaks in domestic pigs has been observed. ASFV transmission from stable flies, Stomoxys calcitrans, has previously been shown both mechanically and via ingestion of whole flies. Hence, blood-feeding flies may offer one explanation for the introductions into high biosecurity farms and for the observed seasonality. The aim of this study was to further elucidate the potential role of stable flies in ASFV transmission. Different parts of flies were analyzed for the presence of viral DNA and infectious virus at different time points following in vitro feeding of the flies on blood from an ASFV-infected pig. Using qPCR, ASFV DNA was detectable in mouth parts of flies for at least 12 h and remained in head and body samples from the flies for up to three days following feeding. Infectious virus was detected in fly body samples prepared at 3 h and 12 h after feeding. The presence of infectious ASFV in stable flies following feeding on viremic blood means that such flies are capable of transporting infectious virus. The detection of ASFV DNA in the flies for up to three days following feeding suggests that qPCR analysis of blood-feeding flies during ASFV outbreaks could be a useful method to elucidate the role of these flies in ASFV transmission under field conditions.
Tag ikke engflåter med hjem fra ferien

Engflåten Dermacentor reticulatus spreder sig hastigt i Vesteuropa, og sammen med flåten udbredes også blodparasitten Babesia canis. B. canis kan forårsage en alvorlig infektion i hunde, men parasitten kan ikke spredes af vores almindelige skovflåt. Heldigvis er engflåten endnu ikke etableret i Danmark, og man kan derfor stadigvæk trygt færdes med sin hund i den danske natur.
The annual, temporal and spatial pattern of Setaria tundra outbreaks in Finnish reindeer: a mechanistic transmission model approach

In northern Finland (Lapland), reindeer are reared as semi-domesticated animals. The region has a short summer season of 2-3 months, yet reindeer are infected with the mosquito-borne filarioid parasite Setaria tundra. The infection causes peritonitis and perihepatitis, which cause significant economic losses due to reduced body weight of infected animals. The objective of this study was to: (i) describe the spatial and temporal pattern of outbreaks in three different areas across Finnish Lapland; and (ii) construct a temperature-driven mechanistic transmission model to quantify the potential role of temperature on intensity of S. tundra transmission in reindeer. We developed a temperature-driven transmission model able to predict the number of S. tundra potentially transmitted from an infectious reindeer. We applied the model to the years 2004-2015, and compared the predictions to the proportion of reindeer whose livers were condemned due to S. tundra infection at the time of slaughter. The mean proportion of liver condemnation increased in reindeer slaughtered in late autumn/winter compared to earlier dates. The outbreaks were geographically clustered each year but there were no fixed foci where outbreaks occurred. Larger outbreaks were recorded in the southern regions of reindeer-herding areas compared to the central or northern parts of Lapland. Our model showed that temperatures never allowed for transmission of more than a single generation of S. tundra each season. In southern (Kuusamo) and central (Sodankylä) Lapland, our model predicted an increasing trend from 1979 to 2015 for both the duration of the effective transmission period of S. tundra (P <0.001) and for the potential number of L3 S. tundra larvae being transmitted from an infectious reindeer (P <0.001). The effective transmission period for S. tundra in reindeer is very short in Lapland, but it increased over the period studied. Only one generation of S. tundra can be transmitted in one season among reindeer in Lapland. Increasing temperatures may facilitate a range expansion and increasing duration of effective transmission period for S. tundra.
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. imicula and the Obsoletus group, although abundance was generally higher for a longer period of time for C. imicula 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. imicula compared to the Obsoletus group can be explained by the species distribution, as C. imicula 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.
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.

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Infektion med TBE-virus i Danmark 2013-2016

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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.
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 re-emerging vector-borne diseases.
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**

State: Published

Organisations: National Veterinary Institute, Epidemiology, Bacteriology & Parasitology, University of Agder, Norwegian Institute of Public Health, Swedish University of Agricultural Sciences


Publication date: 2017

Peer-reviewed: Yes

Event: Abstract from 4th Conference on Neglected Vectors and Vector-Borne Diseases, Chania, Greece.

Electronic versions:

Kjaer_1_oral_2.pdf
Source: PublicationPreSubmission
Source-ID: 137132505

Research output: Research - peer-review » Conference abstract for conference – Annual report year: 2017

**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.

**General information**

State: Published

Organisations: National Veterinary Institute, Epidemiology, Bacteriology & Parasitology, University of Agder, Norwegian Institute of Public Health, Swedish University of Agricultural Sciences

Predicting tick abundance in Southern Scandinavia using machine learning techniques and satellite imagery – a part of the ScandTick Innovation project

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, Bacteriology & Parasitology, University of Agder, Norwegian Institute of Public Health, Swedish University of Agricultural Sciences

Risk based surveillance of vector born infections - the daily transmission potential of Schmallenberg in Denmark 2013 to 2016

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology
Contributors: Bødker, R., Haider, N.

Transmission differentials for multiple 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 spielmani; 0, 3.7 and 0.6% for Borrelia valaisiana; 0, 0 and 0.6% 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.
Vectorborne zoonoses

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, Bacteriology & Parasitology, Technical University of Denmark
Contributors: Bødker, R., Vrbová, E., Schou, K. K.
Pages: 20-21
Publication date: 2017

Host publication information
Title of host publication: Annual Report on Zoonoses in Denmark 2016
Place of publication: Søborg
Publisher: National Food Institute, Technical University of Denmark
Editors: Helwigh, B., Christensen, J., Müller, L.
(Annual Report on Zoonoses in Denmark).
Electronic versions:
Annual_Report_2016_FINAL.pdf
Source: PublicationPreSubmission
Source-ID: 133498715
Research output: Commissioned › Report chapter – Annual report year: 2017

Communicating spatial risk of tick-borne infections - Creating a ScandTick Innovation website based on surveillance data

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Section for Bacteriology, Pathology and Parasitology
Contributors: Clausen, C. G., Schou, K. K., Kirkeby, C., Bødker, R.
Number of pages: 1
Publication date: 2016
Peer-reviewed: Yes
Event: Poster session presented at 3rd Conference on Neglected Vectors and Vector-Borne Diseases (EurNegVec): with MC and WG Meeting of the COST Action TD1303, Zaragoza, Spain.
Electronic versions:
EurNegVec_Poster_FINAL.pdf
Source: PublicationPreSubmission
Source-ID: 124140618
Research output: Research - peer-review › Poster – Annual report year: 2016

Communicating spatial risk of tick-borne infections: Creating a ScandTick Innovation website based on surveillance data

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Section for Bacteriology, Pathology and Parasitology
Contributors: Clausen, C. G., Schou, K. K., Kirkeby, C., Bødker, R.
Number of pages: 1
Publication date: 2016
Peer-reviewed: Yes
Event: Poster session presented at SVEPM, Elsinore, Denmark.
Electronic versions:
Cecilie_G._Clausen.pdf
Source: PublicationPreSubmission
Source-ID: 123370078
Research output: Research - peer-review › Poster – Annual report year: 2016
Comparative Risk Analysis of Two Culicoides-Borne Diseases in Horses: Equine Encephalosis More Likely to Enter France than African Horse Sickness

African horse sickness (AHS) and equine encephalosis (EE) are Culicoides-borne viral diseases that could have the potential to spread across Europe if introduced, thus being potential threats for the European equine industry. Both share similar epidemiology, transmission patterns and geographical distribution. Using stochastic spatiotemporal models of virus entry, we assessed and compared the probabilities of both viruses entering France via two pathways: importation of live-infected animals or importation of infected vectors. Analyses were performed for three consecutive years (2010–2012). Seasonal and regional differences in virus entry probabilities were the same for both diseases. However, the probability of EE entry was much higher than the probability of AHS entry. Interestingly, the most likely entry route differed between AHS and EE: AHS has a higher probability to enter through an infected vector and EE has a higher probability to enter through an infectious host. Consequently, different effective protective measures were identified by ‘what-if’ scenarios for the two diseases. The implementation of vector protection on all animals (equine and bovine) coming from low-risk regions before their importation was the most effective in reducing the probability of AHS entry. On the other hand, the most significant reduction in the probability of EE entry was obtained by the implementation of quarantine before import for horses coming from both EU and non-EU countries. The developed models can be useful to implement risk-based surveillance.
Microclimate temperature play a vital role for vector borne disease transmission in the cool scandinavian climate

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Technical University of Denmark
Microclimatic temperature play a vital role for vector borne disease transmission in the cool Scandinavian climates

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology
Contributors: Haider, N., Kristensen, B., Kirkeby, C., Toft, N., Bødker, R.
Pages: 69-70
Publication date: 2016

Host publication information
Title of host publication: 3rd Conference on Neglected Vectors and Vector-Borne Diseases (EurNegVec): with MC and WG Meeting of the COST Action TD1303: Abstract book
Place of publication: ZARAGOZA
Publisher: European Science Foundation
Electronic versions:
abstractszaragoza.pdf
Research output: Research - peer-review › Conference abstract in proceedings – Annual report year: 2016

Predicting spatial distribution of pathogens transmitted by ticks in northern Europe

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Section for Bacteriology, Pathology and Parasitology, Wageningen University & Research, National Veterinary Institute, ANSES - French Agency for Food, Environmental and Occupational Health & Safety, Central Veterinary Institute, Animal and Plant Health Agency
Contributors: Cuellar, A. C., Schou, K. K., Moutailler, S., Fach, P., Delannoy, S., van der Wal, F., de Koeier, A., Chirico, J., Aspán, A., Juremalm, M., Mansfield, K., Phipps, P., Fooks, T., Bødker, R.
Pages: 78-79
Publication date: 2016

Host publication information
Title of host publication: 3rd Conference on Neglected Vectors and Vector-Borne Diseases (EurNegVec): with MC and WG Meeting of the COST Action TD1303: Abstract book
Place of publication: ZARAGOZA
Publisher: European Science Foundation
Electronic versions:
abstractszaragoza.pdf
Research output: Research - peer-review › Conference abstract in proceedings – Annual report year: 2016

Predicting spatial distribution of pathogens transmitted by ticks in Northern Europe

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Section for Bacteriology, Pathology and Parasitology, ANSES - French Agency for Food, Environmental and Occupational Health & Safety, Central Veterinary Institute, National Veterinary Institute, Animal and Plant Health Agency
Predicting spatial prevalence of tick pathogens in Northern Europe using satellite imagery

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Section for Bacteriology, Pathology and Parasitology, ANSES - French Agency for Food, Environmental and Occupational Health & Safety, Wageningen University & Research, Animal and Plant Health Agency, National Veterinary Institute
Number of pages: 1
Publication date: 2016
Peer-reviewed: Yes
Event: Poster session presented at SVEPM, Elsinore, Denmark.
Electronic versions:
Cuellar_Ana_Carolina.pdf
Source: PublicationPreSubmission
Source-ID: 123456579
Research output: Research - peer-review › Poster – Annual report year: 2016

Spatial Distribution and Abundance of Culicoides Imicola and Obsolutes Group in Europe

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, Department of Applied Mathematics and Computer Science, Statistics and Data Analysis, Aarhus University, Roskilde University, National Veterinary Institute, Bernhard Nocht Institute for Tropical Medicine, Norwegian Veterinary Institute, Institute for Veterinary Public Health, Centre de cooperation Internationale en Recherche Agronomique pour le Développement, Universite de Strasbourg, EID Méditerranée, University of the Balearic Islands, University of Zaragoza, Avia-GIS, University of Zurich
Number of pages: 1
Publication date: 2016
Peer-reviewed: Yes
Event: Abstract from 3rd Conference on Neglected Vectors and Vector-Borne Diseases, Zaragoza, Spain.
Electronic versions:
Cuellar_Abstract_Zaragoza2.pdf
Source: PublicationPreSubmission
Source-ID: 123456579
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2017

Spatial distribution and abundance of culicoides imicola and obsolutes group in Europe

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Department of Applied Mathematics and Computer Science, Statistics and Data Analysis, Roskilde University, National Veterinary Institute, Bernhard Nocht Institute for Tropical Medicine, Norwegian Veterinary Institute, Institute for Veterinary Public Health, Centre de cooperation Internationale en Recherche Agronomique pour le Développement, Universite de Strasbourg, EID Méditerranée, Aarhus University, National Veterinary Research Institute
Spatial risk of tick borne infections – creating a ScandTick Innovation website for both the public and the health sector based on surveillance data

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Section for Bacteriology, Pathology and Parasitology
Contributors: Clausen, C. G., Schou, K. K., Kirkeby, C., Bødker, R.
Number of pages: 1
Publication date: 2016
Peer-reviewed: Yes
Electronic versions:
Abstract_NordTick_Creating_a_ScandTick_Innovation_website_20april2016.pdf
Source: PublicationPreSubmission
Source-ID: 123456779
Research output: Research - peer-review » Conference abstract for conference – Annual report year: 2016

The impact of microclimatic temperature on vector-borne disease transmission in Denmark

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology
Contributors: Haider, N., Kristensen, B., Kirkeby, C., Toft, N., Bødker, R.
Number of pages: 1
Publication date: 2016
Peer-reviewed: Yes
Event: Poster session presented at SVEPM, Elsinore, Denmark.
Electronic versions:
Haider_Najmul.pdf
Source: PublicationPreSubmission
Source-ID: 123369531
Research output: Research - peer-review » Poster – Annual report year: 2016

The potential for vector borne infections in the Nordic area now and in the future

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Technical University of Denmark
Contributors: Bødker, R., Cuellar, A. C., Haider, N.
Publication date: 2016
Media of output: PowerPoint

Event Information
Event: Workshop on mosquitoes and biting midges (Culicidae, Ceratopogonidae: Culicoides)
Location: NINA, Høgskoleringen 9, Trondheim, Norway
Electronic versions:
Rene_Boedker_Trondheim_June_2016_final_PDF.pdf
West Nile fever: En virussygdom, der spredes sig i Europa
Status over West Nile virus i Europa og det danske overvågningsprogram.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Section for Virology, Danish Veterinary and Food Administration, University of Copenhagen
Contributors: Lohse, L., Madsen, J. J., Huda, A., Bødker, R., Thorup, K., Polacek, C., Bøtner, A.
Pages: 10-13
Publication date: 2016
Peer-reviewed: No

Publication information
Journal: Dansk Veterinaertidsskrift
Volume: 2016
Issue number: 8
ISSN (Print): 0106-6854
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: English
Electronic versions:
West_Nile_fever_DVT_08_2016.pdf
URLs:
Source: PublicationPreSubmission
Source-ID: 124120862
Research output: Research Journal article – Annual report year: 2016

Battling Bluetongue and Schmallenberg virus: Local scale behavior of transmitting vectors

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Statistics and Data Analysis, National Veterinary Institute, Section for Epidemiology
Contributors: Stockmarr, A., Kirkeby, C., Bødker, R.
Publication date: 2015
Media of output: PowerPoint

Event information
Event: World Congress on Infectious Diseases 2015
Location: London, United Kingdom
Electronic versions:
Infectious_Diseases_1008_2015_Anders_Stockmarr.pdf
Prevalence, risk factors and spatial analysis of infections with liver flukes in Danish cattle herds

Liver fluke infection, also known as fasciolosis, is a world-wide prevalent zoonotic parasitic disease infecting a wide range of host species and is caused by Fasciola hepatica. Despite the substantial economic and animal welfare effects of the disease, knowledge on its prevalence and the factors related to its occurrence and distribution are scarce in Denmark. A retrospective study was performed using liver inspection data of approximately 1.5 million cattle for the period 2011 to 2013. Spatial analysis was carried out to explore whether the data on F. hepatica infection was clustered in space as this could help understand whether or not the infection was driven by local environmental factors. Both global and local spatial autocorrelation techniques were used. Herd level and environmental risk factors were evaluated for their association with prevalence of F. hepatica infection using Generalized Estimating Equations.

Prevalence, risk factors and spatial analysis of liver fluke infections in Danish cattle herds

Background: Fasciola hepatica, a trematode parasite (liver fluke), infects a wide range of host species causing fasciolosis. The disease is prevalent world-wide and causes considerable economic losses to the livestock industry. Fasciolosis is regarded as an emerging food-borne zoonosis. To promote awareness among farmers and to implement strategies to control the infection, this study examined the prevalence, spatial distribution and risk factors for Fasciola hepatica infection in Danish cattle herds. Methods: A retrospective population based study was performed using meat inspection data of approximately 1.5 million cattle slaughtered in the period 2011 to 2013. Annual cumulative prevalence of recorded liver fluke findings was calculated for each year. Global and local spatial cluster analysis was used to identify and map spatial patterns of Fasciola hepatica positive and negative herds to explore environmental indicators of infection. Herd level, trade and environmental risk factors were evaluated for association with infection using logistic regression. Herd infection status as predicted from the final risk factor model was compared with the observed status using heat maps to assess how well the model fitted the observed spatial pattern. Results: During the investigated period (2011-2013), an increase in annual herd prevalence was noted (2011-25.6%; 2012-28.4%; 2013-29.3%). The spatial analysis suggested significant clustering of positive and negative herds. Presence of streams, wetlands and pastures on farms showed a significant association with the presence of infection in cattle herds. Buying animals from positive herds was a risk factor on conventional farms. Additionally, risk of being infected with Fasciola hepatica was higher in non-dairy herds of medium size (≥ 30 and <100) when compared to dairy and large (≥ 100) cattle herds. The observed spatial pattern could be reproduced by predictions of the risk factor model. Conclusions: This study showed an increase in annual herd level prevalence (2011 to 2013) indicating that an increasing proportion of herds are infected with Fasciola hepatica infection every year in Denmark. Fasciolosis was found to be associated with both herd and environmental factors where the infection was influenced by local factors that clustered geographically.
Risk of entry and transmission for two Culicoides - borne diseases in horse: comparison of Africa n horse sickness and Equine encephalosis for France

General information
State: Published
The impact of a decade of research on vector borne diseases

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology
Number of pages: 131
Publication date: 2015

Publication information
Publisher: CIRAD
Original language: English
Electronic versions:
EDENEXT_BOOK_Final_Pages_Basse_def.pdf
DOIs:
10.13140/RG.2.1.4382.6400

Bibliographical note
Not complete author list
Source: PublicationPreSubmission
Source-ID: 115475584
Research output: Research - peer-review › Book – Annual report year: 2015

The joint risk score for vector-borne diseases used for early detection

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Utrecht University, INRA Institut National de La Recherche Agronomique, Friedrich-Loeffler-Institute, National Veterinary Institute
Number of pages: 1
Publication date: 2015

Host publication information
Title of host publication: Proceedings of the 14th international symposium on veterinary epidemiology and economics
Place of publication: Yucatan, Mexico
Article number: P104
Research output: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015

Establishment of the West Nile virus vector, Culex modestus, in a residential area in Denmark

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Technical University of Denmark
Contributors: Bødker, R., Kiltgard, K., Byriel, D. B., Kristensen, B.
Number of pages: 3
Publication date: 2014
Peer-reviewed: Yes
High-throughput screening of tick-borne pathogens in Europe

Due to increased travel, climatic, and environmental changes, the incidence of tick-borne disease in both humans and animals is increasing throughout Europe. Therefore, extended surveillance tools are desirable. To accurately screen tick-borne pathogens, a large-scale epidemiological study was conducted on 7050 Ixodes ricinus nymphs collected from France, Denmark, and the Netherlands using a powerful new high-throughput approach. This advanced methodology permitted the simultaneous detection of 25 bacterial, and 12 parasitic species (including; Borrelia, Anaplasma, Ehrlichia, Rickettsia, Bartonella, Candidatus Neoehrlichia, Coxiella, Francisella, Babesia, and Theileria genus) across 94 samples. We successfully determined the prevalence of expected (Borrelia burgdorferi sensu lato, Anaplasma phagocytophilum, Rickettsia helvetica, Candidatus Neoehrlichia mikurensis, Babesia divergens, Babesia venatorum), unexpected (Borrelia miyamotoi) and rare (Bartonella henselae) pathogens in the three European countries. Moreover, we detected Borrelia spielmanii, Borrelia miyamotoi, Babesia divergens, and Babesia venatorum for the first time in Danish ticks. This surveillance method represents a major improvement in epidemiological studies, able to facilitate comprehensive testing of tick-borne pathogens, and which can also be customized to monitor emerging diseases.
Multiple detection of pathogens in ticks: development of a high throughput real time PCR chip used as a new epidemiologic investigative tool

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Section for Bacteriology, Pathology and Parasitology, ANSES - French Agency for Food, Environmental and Occupational Health & Safety, National Veterinary Institute, Central Veterinary Institute, National Institute of Public Health and the Environment
Publication date: 2014
Peer-reviewed: Yes

Publication information
Journal: Parasites & Vectors
Volume: 7
Issue number: Suppl 1
Article number: 012
ISSN (Print): 1756-3305
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.29 SJR 1.702 SNIP 1.295
Web of Science (2017): Impact factor 3.163
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.23 SJR 1.534 SNIP 1.313
Web of Science (2016): Impact factor 3.035
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.61 SJR 1.72 SNIP 1.396
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.31 SJR 1.568 SNIP 1.595
Web of Science (2014): Impact factor 3.43
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.52 SJR 1.56 SNIP 1.474
Web of Science (2013): Impact factor 3.251
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 3.43 SJR 1.224 SNIP 1.354
Web of Science (2012): Impact factor 3.246
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 3.06 SJR 1.071 SNIP 1.302
Web of Science (2011): Impact factor 2.937
ISI indexed (2011): ISI indexed yes
Nye aktive redskaber til passiv overvågning

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology
Contributors: Bødker, R.
Pages: 30-32
Publication date: 2014
Peer-reviewed: Yes

Publication information
Journal: Dansk Veterinaertidsskrift
Volume: 2014
Issue number: 04
ISSN (Print): 0106-6854
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: Danish
Electronic versions:
DVT.pdf
URLs:
Optimal vaccination strategies against vector-borne diseases
Using a process oriented semi-agent based model, we simulated the spread of Bluetongue virus by Culicoides, biting midges, between cattle in Denmark. We evaluated the minimum vaccination cover and minimum cost for eight different preventive vaccination strategies in Denmark.

The simulation model replicates both a passive and active flight of midges between cattle distributed on pastures and cattle farms in Denmark. A seasonal abundance of midges and temperature dependence of biological processes were included in the model. The eight vaccination strategies were investigated under four different grazing conditions. Furthermore, scenarios were tested with three different index locations stratified for cattle density. The cheapest way to vaccinate cattle with a medium risk profile (less than 1000 total affected cattle) was to vaccinate cattle on pasture. Regional vaccination displayed better results when index cases were in the vaccinated areas. However, given that the long-range spread of midge borne disease is still poorly quantified, more robust national vaccination schemes seem preferable.

Rapid Spread of Schmallenberg Virus-infected Biting Midges (Culicoides spp.) across Denmark in 2012
Detection of Schmallenberg virus RNA, using real-time RT-PCR, in biting midges (Culicoides spp.) caught at 48 locations in 2011 and four well-separated farms during 2012 in Denmark, revealed a remarkably rapid spread of virus-infected midges across the country. During 2012, some 213 pools of obsoletus group midges (10 specimens per pool) were
examined, and of these, 35 of the 174 parous pools were Schmallenberg virus RNA positive and 11 of them were positive in the heads. Culicoides species-specific PCRs identified both C. obsoletus and C. dewulfi as vectors of Schmallenberg virus.

**General information**
- **State:** Published
- **Organisations:** National Veterinary Institute, Section for Virology, Section for Epidemiology
- **Contributors:** Rasmussen, L. D., Kirkeby, C., Bødker, R., Kristensen, B., Rasmussen, T. B., Belsham, G., Bøtner, A.
- **Pages:** 12-16
- **Publication date:** 2014
- **Peer-reviewed:** Yes

**Publication information**
- **Journal:** Transboundary and Emerging Diseases
- **Volume:** 61
- **Issue number:** 1
- **ISSN (Print):** 1865-1674
- **Ratings:**
  - BFI (2019): BFI-level 1
  - Web of Science (2019): Indexed yes
  - BFI (2018): BFI-level 1
  - Web of Science (2018): Indexed yes
  - BFI (2017): BFI-level 1
  - Scopus rating (2017): CiteScore 2.87 SJR 1.147 SNIP 1.488
  - Web of Science (2017): Impact factor 3.504
  - Web of Science (2017): Indexed yes
  - BFI (2016): BFI-level 1
  - Scopus rating (2016): CiteScore 2.16 SJR 1.046 SNIP 0.998
  - Web of Science (2016): Impact factor 3.585
  - Web of Science (2016): Indexed yes
  - BFI (2015): BFI-level 1
  - Scopus rating (2015): CiteScore 2.29 SJR 1.305 SNIP 1.249
  - Web of Science (2015): Impact factor 2.714
  - Web of Science (2015): Indexed yes
  - BFI (2014): BFI-level 1
  - Scopus rating (2014): CiteScore 2.23 SJR 1.048 SNIP 1.207
  - Web of Science (2014): Impact factor 2.944
  - Web of Science (2014): Indexed yes
  - BFI (2013): BFI-level 1
  - Scopus rating (2013): CiteScore 2.33 SJR 0.975 SNIP 1.123
  - Web of Science (2013): Impact factor 3.116
  - ISI indexed (2013): ISI indexed yes
  - Web of Science (2013): Indexed yes
  - BFI (2012): BFI-level 1
  - Scopus rating (2012): CiteScore 2.04 SJR 0.847 SNIP 1.178
  - Web of Science (2012): Impact factor 2.096
  - ISI indexed (2012): ISI indexed yes
  - Web of Science (2012): Indexed yes
  - BFI (2011): BFI-level 1
  - Scopus rating (2011): CiteScore 2.05 SJR 0.939 SNIP 1.124
  - Web of Science (2011): Impact factor 1.809
  - ISI indexed (2011): ISI indexed yes
  - BFI (2010): BFI-level 1
  - Scopus rating (2010): SJR 0.761 SNIP 0.983
  - Web of Science (2010): Impact factor 2.448
  - Web of Science (2010): Indexed yes
  - BFI (2009): BFI-level 1
Dynamic changes in antibody levels as an early warning of Salmonella Dublin in bovine dairy herds

Salmonella Dublin is a bacterium that causes disease and production losses in cattle herds. In Denmark, a surveillance and control program was initiated in 2002 to monitor and reduce the prevalence of Salmonella Dublin. In dairy herds, the surveillance includes herd classification based on bulk tank milk measurements of antibodies directed against Salmonella Dublin at 3-mo intervals. In this study, an “alarm herd” concept, based on the dynamic progression of these repeated measurements, was formulated such that it contains predictive power for Salmonella Dublin herd classification change from “likely free of infection” to “likely infected” in the following quarter of the year, thus warning the farmer 3 mo earlier than the present system. The alarm herd concept was defined through aberrations from a stable development over time of antibody levels. For suitable parameter choices, alarm herd status was a positive predictor for Salmonella Dublin status change in dairy herds, in that alarm herds had a higher risk of changing status in the following quarter compared with nonalarm herds. This was despite the fact that both alarm and nonalarm herds had antibody levels that did not indicate the herds being “likely infected” according to the existing classification system in the present quarter. The alarm herd concept can be used as a new early warning element in the existing surveillance program. Additionally, to improve accuracy of herd classification, the alarm herd concept could be incorporated into a model including other known risk factors for change in herd classification. Furthermore, the model could be extended to other diseases monitored in similar ways.

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Statistics and Data Analysis, National Veterinary Institute, Section for Epidemiology, University of Copenhagen
Contributors: Stockmarr, A., Bødker, R., Nielsen, L. R.
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Web of Science (2019): Indexed yes
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.84 SJR 1.35 SNIP 1.491
Web of Science (2017): Impact factor 2.749
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.66 SJR 1.331 SNIP 1.484
Occurrence of Schmallenberg virus in Danish biting midges (Culicoides spp.)

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Epidemiology
Contributors: Rasmussen, L. D., Kirkeby, C., Kristensen, B., Rasmussen, T. B., Belsham, G., Bødker, R., Bøtner, A.
Number of pages: 1
Publication date: 2013
Peer-reviewed: Yes
Event: Poster session presented at EDENext Annual Meeting, Barcelona, Spain.
Electronic versions:
prod2136337499956.poster2_stor.pdf
Source: dtu
Source-ID: u::7276
Research output: Research - peer-review > Poster – Annual report year: 2013

Optimal vaccination scenarios against vector-borne diseases
Using a process oriented semi-agent based model we simulated the spread of Bluetongue virus in Denmark. We evaluated the efficiency and minimum vaccination cover for eight different preventive vaccination strategies in Denmark.

The simulation model replicates both passive and active flight of Culicoides between hosts on pasture and stables in Denmark. Seasonal abundance of midges and temperature dependence on biological processes were included in the model. The eight vaccination scenarios comprised of: All holdings vaccinated to a given percentage, random holdings selected for vaccination, two scenarios based on the size of holdings, mosaic vaccination of nearest neighbor farms, vaccination of hosts on pasture, regional vaccination, and trench vaccination from the border to Germany. These eight scenarios were investigated under normal grazing conditions and under a forced housing scenario.

The most robust vaccination scenarios were all holdings vaccinated and the mandatory vaccination of hosts on pasture. Regional vaccination and trench vaccination display better results under some conditions, but are very sensitive to the incursion route.

With this study we intended to test scenarios that would increase distance between infectious and susceptible hosts. This can be done very efficiently on a regional scale if the incursion route is well specified. However as the long-range spread of midge borne disease is still poorly quantified, more robust national vaccination schemes seems preferable.

Results in this presentation were obtained building upon the model presented in: Simulating spread of Bluetongue Virus by flying vectors between hosts on pasture. Kaare Græsbøll et al. Scientific Reports. 2:863 (2012).

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science , Dynamical Systems, National Veterinary Institute, Section for Epidemiology
Contributors: Græsbøll, K., Enæe, C., Bødker, R., Christiansen, L. E.
Publication date: 2013
Peer-reviewed: Yes
Source: dtu
Source-ID: u::8525
Research output: Research - peer-review > Conference abstract for conference – Annual report year: 2013

Quantifying Dispersal of European Culicoides (Diptera: Ceratopogonidae) Vectors between Farms Using a Novel Mark-Release-Recapture Technique
Studying the dispersal of small flying insects such as Culicoides constitutes a great challenge due to huge population sizes and lack of a method to efficiently mark and objectively detect many specimens at a time. We here describe a novel mark-release-recapture method for Culicoides in the field using fluorescein isothiocyanate (FITC) as marking agent without anaesthesia. Using a plate scanner, this detection technique can be used to analyse thousands of individual Culicoides specimens per day at a reasonable cost. We marked and released an estimated 853 specimens of the Pulicaris group and 607 specimens of the Obsoletus group on a cattle farm in Denmark. An estimated 9,090 (8,918–9,260) Obsoletus group specimens and 14,272 (14,194–14,448) Pulicaris group specimens were captured in the surroundings
and subsequently analysed. Two (0.3%) Obsoletus group specimens and 28 (4.6%) Pulicaris group specimens were recaptured. The two recaptured Obsoletus group specimens were caught at the release point on the night following release. Eight (29%) of the recaptured Pulicaris group specimens were caught at a pig farm 1,750 m upwind from the release point. Five of these were recaptured on the night following release and the three other were recaptured on the second night after release. This is the first time that movement of Culicoides vectors between farms in Europe has been directly quantified. The findings suggest an extensive and rapid exchange of disease vectors between farms. Rapid movement of vectors between neighboring farms may explain the high rate of spatial spread of Schmallenberg and bluetongue virus (BTV) in northern Europe.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Department of Applied Mathematics and Computer Science, Statistics and Data Analysis, Section for Immunology and Vaccinology
Contributors: Kirkeby, C., Bødker, R., Stockmarr, A., Lind, P., Heegaard, P. M. H.
Number of pages: 7
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- Web of Science (2019): Indexed yes
- BFI (2018): BFI-level 1
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 1
- Scopus rating (2017): CiteScore 3.01 SJR 1.164 SNIP 1.111
- Web of Science (2017): Indexed yes
- BFI (2016): BFI-level 1
- Scopus rating (2016): CiteScore 3.11 SJR 1.236 SNIP 1.101
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 1
- Scopus rating (2015): CiteScore 3.32 SJR 1.427 SNIP 1.136
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 1
- Scopus rating (2014): CiteScore 3.54 SJR 1.559 SNIP 1.148
- Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 1
- Scopus rating (2013): CiteScore 3.94 SJR 1.772 SNIP 1.153
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 1
- Scopus rating (2012): CiteScore 4.15 SJR 1.982 SNIP 1.156
- Web of Science (2012): Impact factor 3.73
- ISI indexed (2012): ISI indexed yes
- Web of Science (2012): Indexed yes
- BFI (2011): BFI-level 1
- Scopus rating (2011): CiteScore 4.58 SJR 2.425 SNIP 1.233
- Web of Science (2011): Impact factor 4.092
- ISI indexed (2011): ISI indexed no
- Web of Science (2011): Indexed yes
- BFI (2010): BFI-level 1
- Scopus rating (2010): SJR 2.705 SNIP 1.178
Spatial abundance and clustering of Culicoides (Diptera: Ceratopogonidae) on a local scale

Background
Biting midges, Culicoides, of the Obsoletus group and the Pulicaris group have been involved in recent outbreaks of bluetongue virus and the former was also involved in the Schmallenberg virus outbreak in northern Europe.

Methods
For the first time, here we investigate the local abundance pattern of these two species groups in the field by intensive sampling with a grid of light traps on 16 catch nights. Neighboring trap catches can be spatially dependent on each other, hence we developed a conditional autoregressive (CAR) model framework to test a number of spatial and non-spatial covariates expected to affect Culicoides abundance.

Results
The distance to sheep penned in the corner of the study field significantly increased the abundance level up to 200 meters away from the sheep. Spatial clustering was found to be significant but could not be explained by any known factors, and cluster locations shifted between catch nights. No significant temporal autocorrelation was detected. CAR models for both species groups identified a significant positive impact of humidity and significant negative impacts of precipitation and wind turbulence. Temperature was also found to be significant with a peak at just below 16 degrees Celsius. Surprisingly, there was a significant positive impact of wind speed. The CAR model for the Pulicaris group also identified a significant attraction to the smaller groups of sheep placed in the field. Furthermore, a large number of spatial covariates which were incorrectly found to be significant in ordinary regression models were not significant in the CAR models. The 95% C.I. on the prediction estimates ranged from 20.4% to 304.8%, underlining the difficulties of predicting the abundance of Culicoides.

Conclusions
We found that significant spatial clusters of Culicoides moved around in a dynamic pattern varying between catch nights. This conforms with the modeling but was not explained by any of the tested covariates. The mean abundance within these clusters was up to 11 times higher for the Obsoletus group and 4 times higher for the Pulicaris group compared to the rest of the field.
Spatio-temporal abundance of Culicoides on a local scale

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Department of Applied Mathematics and Computer Science, Statistics and Data Analysis
Contributors: Kirkeby, C., Bødker, R., Stockmarr, A., Lind, P.
Number of pages: 15
Publication date: 2013
Peer-reviewed: Yes
Event: Abstract from EDENext Annual Meeting, Barcelona, Spain.
Electronic versions:
Spatio_temporal_abundance.pdf

Bibliographical note
The presentation won 3rd prize (300 Euro) among 27 other contributions at the conference.

Spatio-temporal optimization of sampling for bluetongue vectors (Culicoides) near grazing livestock

BACKGROUND: Estimating the abundance of Culicoides using light traps is influenced by a large variation in abundance in time and place. This study investigates the optimal trapping strategy to estimate the abundance or presence/absence of Culicoides on a field with grazing animals. We used 45 light traps to sample specimens from the Culicoides obsoletus species complex on a 14 hectare field during 16 nights in 2009.

FINDINGS: The large number of traps and catch nights enabled us to simulate a series of samples consisting of different numbers of traps (1-15) on each night. We also varied the number of catch nights when simulating the sampling, and sampled with increasing minimum distances between traps. We used resampling to generate a distribution of different mean and median abundance in each sample. Finally, we used the hypergeometric distribution to estimate the probability of falsely detecting absence of vectors on the field. The variation in the estimated abundance decreased steeply when using up to six traps, and was less pronounced when using more traps, although no clear cutoff was found.

CONCLUSIONS: Despite spatial clustering in vector abundance, we found no effect of increasing the distance between traps. We found that 18 traps were generally required to reach 90% probability of a true positive catch when sampling just one night. But when sampling over two nights the same probability level was obtained with just three traps per night. The results are useful for the design of vector monitoring programmes on fields with grazing animals.
The range of attraction for light traps catching Culicoides biting midges

**General information**

State: Published
Organisations: Department of Applied Mathematics and Computer Science, Cryptology, Dynamical Systems, National Veterinary Institute, Section for Epidemiology, Statistics and Data Analysis
Contributors: Græsbøll, K., Kirkeby, C., Bødker, R., Stockmarr, A., Christiansen, L. E., Lind, P.
Number of pages: 1
Publication date: 2013

**Bibliographical note**

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Source: dtu
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Research output: Research - peer-review ; Journal article – Annual report year: 2013
The range of attraction for light traps catching Culicoides biting midges

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Dynamical Systems, National Veterinary Institute, Section for Epidemiology, Statistics and Data Analysis
Contributors: Græsbøll, K., Kirkeby, C., Bødker, R., Stockmarr, A., Christiansen, L. E., Lind, P.
Number of pages: 1
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Electronic versions:
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Source-ID: u::7293
Research output: Research - peer-review › Poster – Annual report year: 2013

Background
Culicoides are vectors of e.g. bluetongue virus and Schmallenberg virus in northern Europe. Light trapping is an important tool for detecting the presence and quantifying the abundance of vectors in the field. Until now, few studies have investigated the range of attraction of light traps.

Methods
Here we test a previously described mathematical model (Model I) and two novel models for the attraction of vectors to light traps (Model II and III). In Model I, Culicoides fly to the nearest trap from within a fixed range of attraction. In Model II Culicoides fly towards areas with greater light intensity, and in Model III Culicoides evaluate light sources in the field of view and fly towards the strongest. Model II and III incorporated the directionally dependent light field created around light traps with fluorescent light tubes. All three models were fitted to light trap collections obtained from two novel experimental setups in the field where traps were placed in different configurations.

Results
Results showed that overlapping ranges of attraction of neighboring traps extended the shared range of attraction. Model I did not fit data from any of the experimental setups. Model II could only fit data from one of the setups, while Model III fitted data from both experimental setups.

Conclusions
The model with the best fit, Model III, indicates that Culicoides continuously evaluate the light source direction and intensity. The maximum range of attraction of a single 4W CDC light trap was estimated to be approximately 15.25 meters. The attraction towards light traps is different from the attraction to host animals and thus light trap catches may not represent the vector species and numbers attracted to hosts.

The range of attraction for light traps catching Culicoides biting midges (Diptera: Ceratopogonidae)

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Department of Applied Mathematics and Computer Science, Cryptology, Dynamical Systems, Statistics and Data Analysis
Contributors: Kirkeby, C., Græsbøll, K., Stockmarr, A., Christiansen, L. E., Bødker, R.
Number of pages: 19
Publication date: 2013
Peer-reviewed: Yes
Electronic versions:
prod21377679734408.geove13.pdf
Source: dtu
Source-ID: u::8524
Research output: Research - peer-review › Poster – Annual report year: 2013

Background
Culicoides are vectors of e.g. bluetongue virus and Schmallenberg virus in northern Europe. Light trapping is an important tool for detecting the presence and quantifying the abundance of vectors in the field. Until now, few studies have investigated the range of attraction of light traps.

Methods
Here we test a previously described mathematical model (Model I) and two novel models for the attraction of vectors to light traps (Model II and III). In Model I, Culicoides fly to the nearest trap from within a fixed range of attraction. In Model II Culicoides fly towards areas with greater light intensity, and in Model III Culicoides evaluate light sources in the field of view and fly towards the strongest. Model II and III incorporated the directionally dependent light field created around light traps with fluorescent light tubes. All three models were fitted to light trap collections obtained from two novel experimental setups in the field where traps were placed in different configurations.

Results
Results showed that overlapping ranges of attraction of neighboring traps extended the shared range of attraction. Model I did not fit data from any of the experimental setups. Model II could only fit data from one of the setups, while Model III fitted data from both experimental setups.

Conclusions
The model with the best fit, Model III, indicates that Culicoides continuously evaluate the light source direction and intensity. The maximum range of attraction of a single 4W CDC light trap was estimated to be approximately 15.25 meters. The attraction towards light traps is different from the attraction to host animals and thus light trap catches may not represent the vector species and numbers attracted to hosts.
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BFI (2018): BFI-level 1
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Scopus rating (2017): CiteScore 3.29 SJR 1.702 SNIP 1.295
Web of Science (2017): Impact factor 3.163
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.23 SJR 1.534 SNIP 1.313
Web of Science (2016): Impact factor 3.035
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.61 SJR 1.72 SNIP 1.396
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.31 SJR 1.568 SNIP 1.595
Web of Science (2014): Impact factor 3.43
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.52 SJR 1.56 SNIP 1.474
Web of Science (2013): Impact factor 3.251
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 3.43 SJR 1.224 SNIP 1.354
Web of Science (2012): Impact factor 3.246
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 3.06 SJR 1.071 SNIP 1.302
Web of Science (2011): Impact factor 2.937
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.98 SNIP 1.015
Web of Science (2010): Impact factor 2.13
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.872 SNIP 0.815
Web of Science (2009): Indexed yes
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Electronic versions:
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Source: dtu
Source-ID: u::7314
Research output: Research - peer-review › Journal article – Annual report year: 2013
Vector-borne Infections: risk based and Cost Effective surveillance systems

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Central Veterinary Institute, National Institute for Agronomic Research, National Veterinary Institute, Centrum voor Onderzoek in Diergeneeskunde en Agrochemie, Universität Bern, National Veterinary Institute, Friedrich-Loeffler-Institute, University of Oldenburg
Number of pages: 1
Publication date: 2013
Peer-reviewed: Yes
Event: Poster session presented at EMIDA-Funded Project Review Meeting and Networking Event, Brussels, Belgium.

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Oral presentation.
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Source-ID: u::9293
Research output: Research - peer-review › Poster – Annual report year: 2013

Culicoids as Vectors of Schmallenberg Virus

General information
State: Published
Organisations: National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy
Contributors: Rasmussen, L. D., Kristensen, B., Kirkeby, C., Rasmussen, T. B., Beilsham, G., Bødker, R., Bøtner, A.
Detection of Dairy Herds at risk for changing Salmonella Dublin status

General information
State: Published
Organisations: DTU Data Analysis, Department of Informatics and Mathematical Modeling, Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute, University of Copenhagen
Contributors: Stockmarr, A., Bødker, R., Nielsen, L.
Publication date: 2012

Event information
Event: 34th Symposium i Anvendt Statistik 2012
Location: Copenhagen, Denmark
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Symposium.pdf
URLs:
http://www.statistiksymposium.dk/
Source: orbit
Source-ID: 317622
Research output: Research › Sound/Visual production (digital) – Annual report year: 2012

Detection of Dairy Herds at Risk for Changing Salmonella Dublin status
Salmonella Dublin (S. Dublin) is a costly infection for dairy cows, potentially lethal to humans. Surveillance is based on bulk tank milk (BTM) antibody measurements, taken each quarter of the year. Herds are classified as Status 1- likely free of S. Dublin, or Status 2 – likely infected with S. Dublin, based on present/recent characteristics, but not actual S. Dublin detection. We develop a predictive model based on characteristics from last quarter, using on registry data for 2001-2007 for 9387 herds in Denmark. Only 2004-2007 data modeled due to data contamination.

General Information
State: Published
Organisations: Department of Informatics and Mathematical Modeling, DTU Data Analysis, National Veterinary Institute, Section for Epidemiology, University of Copenhagen
Contributors: Stockmarr, A., Bedker, R., Nielsen, L. R.
Number of pages: 1
Publication date: 2012
Peer-reviewed: Yes
Electronic versions:
Emerging Schmallenberg and Bluetongue virus in Europe – what should we expect next?

Evidence for Culicoides obsoletus group as vector for Schmallenberg virus in Denmark

Schmallenberg virus (SBV) was first identified in Germany in late 2011 by the Friedrich Loeffler Institute and has now been found in several European countries including Holland, France, Belgium, U.K. and Spain. The disease, which affects sheep, cattle and goats, was first recognized due to transient clinical symptoms including fever, diarrhea and loss of milk production. However, a more significant consequence of infection in pregnant animals is the production of severe congenital malformations in newborn animals, especially lambs. The virus is a member of the Orthobunyavirus genus within the Bunyaviridae family and is closely related to Shamonda and Akabane viruses. These viruses are transmitted by insect vectors (including biting midges (Culicoides sp.) and mosquitoes). To determine whether these insects may act as vectors for SBV, biting midges (Culicoides spp.) caught in October 2011, in the south-west of Denmark (close to the German border), were sorted into pools and tested for the presence of Schmallenberg virus RNA by RT-qPCR. From 18 pools of 5 midges from the C. obsoletus group, 2 pools were both found positive in two separate assays, targeting the L- and S- segments of the SBV RNA. However, 4 pools of C. punctatus s.str were negative. The sequence of 80bp (excluding the primer sequences) from the amplicons (ca. 145bp) was identical to that published for the expected region of the SBV L-segment. The levels of SBV RNA detected in the biting midges were much higher than could be accounted for due to the residue of a blood meal and no ruminant actin mRNA could be detected either. These results strongly suggest that SBV has replicated within specimens of the C. obsoletus group and indicates that these biting midges can act as vectors for this virus. To date (end of March), no cases of disease due to SBV have been detected in sheep, cattle or goats in Denmark.

First detection of tick-borne "Candidatus Neoehrlichia mikurensis" in Denmark 2011

This is the first reporting of the tick-borne zoonotic bacterium "Candidatus Neoehrlichia mikurensis" in Denmark. A total of 2,625 xodes ricinus ticks from 58 locations in Denmark were collected and analysed for "Ca. Neoehrlichia mikurensis". A nested PCR revealed the presence of the bacterium at three geographically separate locations, which indicates that it is widely established in ticks.
Increased temperatures and changes in rainfall pattern are likely to facilitate the spread and establishment of new vector borne diseases in the Baltic Sea Region. There are a large number of potential vector borne threats to the area. Existing endemic vector borne diseases are likely to increase and new exotic diseases like Usutu and West Nile Virus may lead to outbreaks in the region. In the worst case the combined effect of climate change and globalization may potentially lead to European outbreaks of important zoonotic mosquito borne infections like Rift Valley Fever in cattle and Japanese Encephalitis in swine. Being able to model the impact of climate and environmental change on the transmission intensity of vector borne diseases is potentially a powerful tool to both monitor and prevent outbreaks in a cost effective way.

The recent unexpected outbreaks of bluetongue and Schmallenberg virus in ruminants have been attributed an increase in European temperatures. Mathematical models clearly demonstrate the potential for increased virus transmission at elevated temperatures. However there is little evidence to support the idea that the spread of these tropical viruses in northern Europe is the direct result of climate change. The potential for virus transmission by biting midges was here modeled monthly for the Baltic Sea Region and the rest of Europe. The results showed that Baltic Sea Region has a lower transmission potential than most other areas in Europe. And the model identified an increasing trend in transmission potential over the last 25 years. However the model suggested that the climate in the Baltic Sea Region has always permitted transmission of these diseases. The model therefore suggests that a presently unknown factor until recently prevented introduction and spread in Northern Europe.

This model approach may be used as a basis for risk based surveillance. In risk based surveillance limited resources for surveillance are targeted at geographical areas most at risk and only when the risk is high. This makes risk based surveillance a cost effective alternative to the present surveillance strategies based on random samples.

We still don’t understand the mechanisms underlying the recent outbreaks of bluetongue, Schmallenberg, Usutu virus, tick borne encephalitis or dirofilarial worms in the Baltic Sea Region. It is therefore not possible to use mathematical models to pinpoint the next outbreak of an exotic vector borne disease. A new outbreak will most likely be detected by a veterinarian deciding to submit a sample based on a subjective clinical suspicion. But the question is how far the epidemic will progress before a veterinarian decides to submit this crucial sample to a diagnostic laboratory. Risk based surveillance models may reduce this delay. An important feature of risk based surveillance models is their ability to continuously communicate the level of risk to veterinarians and hence increase awareness when risk is high. This is essential for submission of samples and hence early detection of outbreaks. Models for vector borne diseases in Denmark have demonstrated dramatic variation in outbreak risk during the season and between years. The Danish VetMap project aims to make these risk based surveillance estimates available on the veterinarians smart phones, thus allowing easy access to risk estimates when in the field. Knowing when and where the potential risk for transmission of a specific vector borne disease is high is likely to help veterinarians decide when and when not to submit a sample to a diagnostic laboratory. This may both increase sensitivity of national surveillance and reduce the cost.
"Schmallenberg" virus: Analysis of the Epidemiological Data and Assessment of Impact: EFSA-Q-2012-00305

This scientific report provides an overall assessment of the impact of the infection on animal health, animal production and animal welfare of the provisionally named "Schmallenberg" virus (SBV) first detected in Germany. In Europe, 3745 holdings have been reported with SBV cases confirmed by laboratory testing across several Member States, mid May 2012. EFSA reviewed the epidemiological reports noting that SBV has been detected in cattle, sheep, goats and a bison. SBV antibodies have been detected in deer and no other species are known to be affected. EFSA also confirms that new studies support the initial assessment undertaken by the European Center for Disease Control and Prevention, that it is very unlikely that SBV poses a risk to humans. In terms of transmission routes, recent entomological investigations have identified SBV in field samples of biting midges of the Culicoides obsoletus group. Currently there is no evidence of any other route of transmission other than transplacental or vector borne routes. EFSA coordinated the collation of SBV epidemiological data during 2011-2012 in order to obtain comparable data for Europe. The maximum proportion of reported sheep holdings with SBV confirmed was 4% per country and 7.6% per region while for cattle less than 1.3 % of holdings were reported as SBV confirmed at both country and regional level. In order to assess the impact of SBV (spatial and temporal spread, proportion of affected holding and potential projection of arthrogryposis hydranencephaly syndrome cases) three models were used. In regions with SBV confirmed holdings, assuming a high prevalence of infection and post infection immunity, impact in the 2012-2013 calving and lambing season should be low. However, assuming SBV survived the winter of 2011, the models suggest that in unaffected regions with suitable temperatures for within herd transmission by vectors and high density of susceptible species (cattle and sheep) SBV infection is likely to spread. EFSA puts forward a number of recommendations to fill the knowledge gaps, these include but are not limited to: continuing serological investigations in affected regions and regions neighbouring affected areas, within herd and animal level impact investigation, monitoring putative vector population, setting SBV host vector transmission parameters, investigating other routes of transmission, host susceptibility, virulence and vulnerable period during gestation. Furthermore, the possible origins of the virus should be investigated as more information becomes available on the virus characteristics and infection epidemiology.

General information

State: Published
Organisations: National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy, Division of Virology, Sektion for Eksotiske Virussygdomme, European Food Safety Authority
Number of pages: 89
Publication date: 2012

Publication information

Publisher: European Food Safety Authority
Original language: English
(EFSA Journal; No. 2768, Vol. 10(6)).
DOIs: 10.2903/j.efsa.2012.2768
URLs: http://www.efsa.europa.eu/efsajournal.htm
Research output: Research - peer-review \ Report – Annual report year: 2012

Schmallenberg virus fundet i mitter i Danmark

General information

State: Published
Organisations: National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy
Contributors: Rasmussen, L. D., Kristensen, B., Kirkbye, C., Rasmussen, T. B., Belsham, G., Bødker, R., Bøtner, A.
Pages: 45
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Journal: Dansk Veterinaertidsskrift
Volume: 5
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Ratings:
BFI (2019): BFI-level 1
Simulating spread of Bluetongue Virus by flying vectors between hosts on pasture

Bluetongue is a disease of ruminants which reached Denmark in 2007. We present a process-based stochastic simulation model of vector-borne diseases, where host animals are not confined to a central geographic farm coordinate, but can be distributed onto pasture areas. Furthermore vectors fly freely and display search behavior to locate areas with hosts. We also include wind spread of vectors, host movements, and vector seasonality. Results show that temperature and seasonality of vectors determines the period in which an incursion of Bluetongue may lead to epidemic spread in Denmark. Within this period of risk the number of infected hosts is affected by temperature, vector abundance, vector behavior, vectors’ ability to locate hosts, and use of pasture. These results indicate that restricted grazing during outbreaks can reduce the number of infected hosts and the size of the affected area. The model can be implemented on other vector-borne diseases of grazing animals.

General information
State: Published
Organisations: Department of Informatics and Mathematical Modeling, Mathematical Statistics, National Veterinary Institute, Section for Epidemiology
Contributors: Græsbøll, K., Bødker, R., Enøe, C., Christiansen, L. E.
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Peer-reviewed: Yes

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Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.36 SJR 1.533 SNIP 1.245
Web of Science (2017): Impact factor 4.122
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.63 SJR 1.692 SNIP 1.354
The impact of climate environment and control on Culicoides borne Schmallenberg virus

General information
State: Published
Organisations: National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy, Department of Informatics and Mathematical Modeling, Mathematical Statistics, Aalborg University, Roskilde University
Contributors: Bødker, R., Kristensen, B., Græsbøll, K., Kirkeby, C., Skovgaard, H., Nielsen, S. A.
Publication date: 2012
Peer-reviewed: Yes
Source: dtu
Source-ID: u::3883
Research output: Research - peer-review › Paper – Annual report year: 2012

Vektorers betydning for smitsomme sygdomme - kan vi vente andre sygdomme end bluetongue og schmallenberg i nær fremtid?

General information
State: Published
Organisations: National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy
Contributors: Bødker, R.
Publication date: 2012
Peer-reviewed: Yes
Event: Abstract from Kvægkonference 2012, Bredsten, Denmark.
Electronic versions:
A mathematical model for optimising prophylactic deworming strategies of companion pets moving from Echinococcus multilocularis endemic areas to countries free of infection

Echinococcus multilocularis (Em) is a minute tapeworm residing in the small intestine of carnivores like foxes and dogs. The eggs produced forms cysts in the intermediate mice hosts and develop into the adult worms when ingested by a suitable carnivore. However, cysts may also develop in accidental intermediate hosts such as humans. The disease, human alveolar echinococcosis, is fatal in untreated patients and results in reduced survival rates in continuously treated patients. Finland, Ireland, Malta, UK and mainland Norway consider themselves free from Em. The first case of Em was reported in Sweden in 2011. These countries therefore require dogs, cats and ferrets to be treated with an appropriate drug to prevent accidental introductions. Ireland, UK and Malta requires dogs to be treated 24-48 hours before entry, while Sweden and Finland allow treatment up to 10 and 30 days respectively prior to entry. Such national legislations are however under pressure from the EU Commission who wants to abandon national rules to insure free movement of goods between the member states. There is thus a need to objectively assess the risk of introducing Em to free areas in order to optimise preventive strategies while insuring national legislations does not cause unnecessary or irrational trade barriers. A qualitative import risk assessment model has been presented by EFSA. The EFSA model estimates the annual risk of importing infected dogs from an endemic area to a specific free country when taking into account the number of dogs imported, the risk of infection in the countries of origin, treatment efficacy and reinfection risk after treatment. The EFSA model identified relatively high risk of reinfection in the Swedish and Finnish prophylactic treatment strategies. These strategies allow Praziquantel to be administrated 10 and 30 days prior to entering Sweden and Finland respectively. Because the drug is only effective 24 hours after oral intake, these strategies leaves 9 and 29 days for the dogs to be reinfected in endemic areas. The lifespan of the worms is only 90 days and the maximum prevalence is therefore reached after 90 days exposure. A reinfection period of e.g. 9 days will thus allow for 10% of the maximum prevalence to be reached in the period between treatment and crossing the border. In the worst case the Swedish and the Finnish strategies only reduce the probability of importing an infected dog with 90% and 68% respectively. EFSA therefore recommended that pet animals are treated with a single dose of Praziquantel 24 to 48 hours prior to departure. The EFSA risk assessment model defines risk as the probability of introducing a dog with an Em infection. However, I suggest Em may not be so contagious that a single infected animal crossing the border necessarily will result in the successful establishment of the parasite. A worm will produce a large number of eggs in its lifetime. But on average only very few of these eggs will result in a new adult tapeworm. And because the real concern is establishing the parasite in a free area rather than the risk of importing an infected dog, I propose risk should be defined as the number of eggs excreted in a non-endemic area. Furthermore I suggested that the probability of establishing the parasite in a free area is linearly proportional to the number of eggs excreted in this area, and that this is a better measure of risk than the number of infected dogs crossing the border. An import risk assessment model do not differentiate between dogs with many or few worms, between long or short stays in the free area, whether the worms are egg producing or still in the immature stage or whether the worm are young or old and thus likely to have a long or short remaining lifespan. I here present an alternative deterministic mathematical model which calculates the average number of eggs excreted in a free country by a dog exposed in an endemic area. The model quantifies the risk as the cumulative number of eggs excreted by a dog in the free country. In order to calculate the number of eggs excreted, the model calculates the probability that a dog is infected in the endemic area of exposure, and also the number of worms the dog is carrying as well as the duration each of these worms remaining lifespan together with the number of days the dog will spend in the non-endemic country. The model also takes into account that the worms undergo a 30 days immature stage before developing into a mature egg producing stage. The model allows for a comparison of the relative risk in individual dogs with different durations of exposure in endemic areas and various durations of visits to a free country, ranging from a few hours to permanent import. These import scenarios are then combined with various treatment strategies e.g. treatment 10 or 30 days prior to import, and even treatment several days after entering the non-endemic area. The model calculated that the number of eggs deposited in a free country was reduced the closer the treatment took place to the time of entering the free country. But the model calculated the risk resulting from reinfection under the Swedish and Finnish treatment strategies to be relatively higher than did the EFSA model. This is because the worms potentially reinfesting the dogs after prophylactic treatment were all young and thus were expected to have a relatively long egg producing lifespan in the free country compared to the worms acquired before treatment. While both the EFSA model and this model calculated a 90% reduction in the risk of infections in dogs when treating the dogs 10 days prior to import, this model calculated that the actual number of eggs deposited in Sweden was only reduced by 85% because the reinfesting worms produced more eggs. Somewhat counter intuitively and contrary to the EFSA risk assessment model, this model predicted that delaying treatment until arriving in free country may sometimes be highly advantageous. Delaying treatment of Swedish dogs returning from a visit in an endemic area resulted in fewer eggs being deposited in Sweden. The shorter the duration of the stay in an endemic area the greater was the relative advantage of delaying the treatment. The benefit was very high when the stay in the endemic area was less than 30 days. This was because returning dogs only carried the immature worm stage and therefore could not excrete eggs after returning to Sweden as long as the dogs were treated in Sweden before the worms matured to the egg excreting stage. The model suggested that e.g. a dog permanently imported from Central Europe and treated 10 days prior to entering Sweden using a 99.6% efficient drug on average would deposit 400 million times as many eggs and hence constitute a 400 million times higher risk than a treated Danish dog passing Sweden in four hours transit. This is a much higher difference than would be estimated by a traditional import risk assessment model. This is because import risk assessment focus on the difference in infection incidence in the two endemic areas of exposure, but ignores that infected dogs from high risk areas also have higher worm burdens and ignores that dogs in transit have much shorter time in the
free country to deposit eggs than dogs permanently imported, and finally ignores that reinfecting worms remains in the immature stage during transit while they will eventually mature and excrete eggs in permanently imported dogs. The only eggs that dogs in transit may deposit will therefore originate from the few worms surviving treatment due to treatment failure. Because we do not know the actual risk of establishing the infection caused by each deposited egg the model cannot quantify the risk. But the model allows for relative quantitative comparisons of different import scenarios, endemicity levels, drug efficiencies and treatment strategies, and can thus be useful for optimising national preventive measures in an objective and transparent way.

**General information**

**State:** Published

**Organisations:** Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute

**Contributors:** Bødker, R.

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**Peer-reviewed:** Yes

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Source: orbit

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Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2011

**Årsrapport for Center for vildtsundhed 2011**

**General information**

**State:** Published

**Organisations:** National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Epidemiology, Technical University of Denmark, Aarhus University

**Contributors:** Chriél, M., Enemark, H., Stensgaard, M., Bødker, R., Therkildsen, O. R., Eimeros, M., Winding, A., Sonne, C., Dietz, R.

**Number of pages:** 61

**Publication date:** 2011

**Publication information**

Original language: Danish

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**Disease-modeling as a tool for surveillance, foresight and control of exotic vector borne diseases in the Nordic countries**

Modeling the potential transmission intensity of insect borne diseases with climate driven R0 process models is frequently used to assess the potential for veterinary and human infections to become established in non endemic areas. Models are often based on mean temperatures of an arbitrary time period e.g. a monthly temperature mean. Average monthly temperatures are likely to be suitable for predicting permanent establishment of presently exotic diseases. But mean temperatures may not predict the true potential for local spread or limited outbreaks resulting from accidental introductions in years with temporary periods of warm weather. This is particular true for the relatively cool Nordic countries where periods of suitable temperatures, the ‘windows of opportunity for transmission’, may be very short and only appear in odd years.

DTU-Veterinary Institute is developing a system for continuous risk assessment of the potential for local spread of exotic insect borne diseases of veterinary and human importance. In this system R0-models for various vector borne diseases are continuously updated with spatial temperature data to quantify the present risk of autochthonous cases (R0>0) and the present risk of epidemics (R0>1) should an infected vector or host be introduced to the area. The continuously updated risk assessment maps function as an early warning system allowing authorities and industry to increase awareness and preventive measures when R0 raises above the level of ‘no possible transmission’ and target costly active serological surveillance to these limited periods of potential risk, thus dramatically reducing the number of samples collected and analysed. The risk estimated from the R0 modelling may be combined with the risk of introduction from neighbouring countries and trading partners to generate a truly risk based surveillance system for insect borne diseases. We have also used the R0 models to predict the potential impact of climate change on four selected vector borne disease: Bluetongue in cattle, African Horse Sickness in horses, Dirofilariasis in dogs and Vivax-malaria in humans.

Both the presently very restricted potential spatial and seasonal distribution was predicted to increase in the coming 50 years. While the predicted new areas potentially affected by vector borne diseases are relatively small they closely follow the spatial distribution of human habitation and agriculture. The practical impact of climate change on human health and agriculture may therefore be greater than simple distribution maps suggest. This presentation will demonstrate the system for selected vector borne diseases, compare the predicted R0 with the actual spread of bluetongue in Scandinavia i 2008, and discuss the level of preventive measures needed to prevent large scale epidemics in the future.

**General information**
Dynnect's overview of the Culicoides surveillance systems in the EU and distribution maps of key species

One of the aims of the DynVect project was to set up a network of European entomologists working on Culicoides, the vectors of bluetongue virus, to create a platform for discussion, data sharing and data analysis. The first task consisted in describing the surveillance systems in place in each country. For this, a questionnaire was sent to 9 countries: Belgium, Denmark, England, France, Germany, Italy, Spain, Sweden and The Netherlands. Between 1 and 9 institutes per country were involved in the surveillance. The first country to set up a surveillance system was Spain (in 2000), followed by other southern countries (Italy and France). A second wave of countries set up surveillance systems in 2006, with the arrival of bluetongue in northern Europe. All countries currently continue the surveillance except Germany (which stopped the surveillance in mid 2008). All countries shared common aims: defining “vector-free” periods and describing the diversity and dynamics of species. Except in Italy, all surveillance protocols evolved over the years, for example from covering specific regions to the entire country, and/or with an increasing number of traps. Surveillance systems vary between countries in terms of i) number of traps per country (5 - 300), ii) types of traps used (OVI, CDC, BG, Rieb, Rothamsted suction trap), although currently all countries use OVI traps except for Spain, iii) trapping frequency (day and night, weekly, fortnightly or monthly), iv) number of collection nights (mainly 1 night trapping, except Belgium with 2 consecutive nights and Germany with 7 consecutive days), v) trap location within farm (inside or outside buildings or both according to the season), vi) the level to which species are identified (Group, Complex or species) and vii) the definition of the vector-free period. Following this descriptive phase, participants discussed the data which could be shared and the associated aims as well as the database structure which should be used. This was fruitful and lead to the sharing of Culicoides data from 7 countries (Belgium, Denmark, France, Germany, Spain, Sweden, England), thus allowing, for the first time ever at that scale, to map Culicoides distribution, and to further analyze and model the dynamics and distribution of Culicoides in Europe.

General information
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Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute
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Peer-reviewed: Yes
Electronic versions:
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http://www.epizone-eu.net/annual-meetings/4th-annual-meeting.aspx
Source: orbit
Source-ID: 277787
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2011

How does increasing immunity change spread kernel parameters in subsequent outbreaks? – A simulation study on Bluetongue Virus

Modelling the spatial spread of vector borne diseases, one may choose methods ranging from statistic to process oriented. One often used statistic tool is the empirical spread kernel. An empirical spread kernel fitted to outbreak data provides hints on the spread mechanisms, and may provide a good estimate on how future epidemics could proceed under similar conditions. However, a number of variables influence the spread of vector borne diseases. If one of these changes significantly after an outbreak, it needs to be incorporated into the model to improve the prediction on future
outbreaks. Examples of such changes are: vaccinations, acquired immunity, vector density and control, meteorological variations, wind pattern, and so on. Including more and more variables leads to a more process oriented model. A full process oriented approach simulates the movement of virus between vectors and host, describing density and motion of vectors/hosets, climatic variables, and so on will theoretically be able to describe an outbreak under any circumstances. It will most likely contain parameters not very well established, and is also very heavy in computer time. Nevertheless, we have tried to create a relatively detailed simulation spread model. And by using empirical spread kernels from past outbreaks we have fitted some of the more uncertain parameters for this case study. A stochastic simulation model was developed for the spread of bluetongue virus. In the model hosts (cattle) and vectors (Culicoides) are distributed onto a grid representing farm/field quadrants of 1 hectare. Each quadrant has a host SEIR model (Susceptible Exposed Infectious Recovered) and a vector SEI model attached. Transmission of virus between hosts and vectors depend on many parameters most of which are temperature dependent. Spatial movement of virus between quadrants is modelled by local flight and wind spread of vectors. The simulated spatial spread rate of virus is very dependent on movement parameters, but also the distribution and total numbers of hosts and vectors influenced the spread of virus. With empirical spread kernels from past outbreaks and known distributions of host animals, it was possible to fit parameter values of vector movement. The final model including the fitted process based movement parameters is used to simulate e.g. 50% of cattle protected by acquired immunity after a first epidemic outbreak. We can then demonstrate how this changes the spread kernel for future outbreaks.

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Mathematical Statistics, Department of Informatics and Mathematical Modeling, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Græsbøll, K., Bødker, R., Enøe, C., Christiansen, L. E.
Publication date: 2011
Peer-reviewed: Yes
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Source: orbit
Source-ID: 277822
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2011

Nordic climate change: data for modeling vector borne diseases
The distribution of vector species is generally restricted by a range of different climatic and geographical factors, while the development and spread of the vector-borne diseases (veterinary and zoonotic) is often primarily temperature driven. Thus temperature and its derivatives are key factors in the modelling of vector-borne diseases. This puts a high demand on the quality and accuracy of the temperature data to be used as input in such models. In order to best capture the local temporal and spatial variation in the temperature surfaces, accurate daily temperature data were used in the present project. Temperature data for a 30 year period (1980-2009) were obtained directly from the Meteorological stations in the five Nordic countries. The temperature data consisted of daily min and max measurements from 200 climate stations, adding up to more than two million measurements. Temperature point-data were interpolated to daily climate surfaces, using a squared IDW method. In the absence of a more local lapse rate the generally accepted lapse rate of -0.006 C˚/m was used to account for the relationship between temperature and altitude. The interpolation was carried out on temperatures at sea-level and subsequently adjusted for the altitude. As a spherical adjustment, the min and max temperature was interpolated on a grid with a spherical surface geometry. This ensures a more accurate estimate of the temperature isolines in the northernmost areas (above the Arctic Circle) of Scandinavia. Various temperature derivatives were calculated in order to assess the geographical and seasonal variation in the area. In order to evaluate the response of vector borne diseases to possible future climate changes and the subsequent potential spread into new areas, daily temperature predictions (mean, min and max) for three 20-year periods and 7 different prediction models were obtained from the Danish Meteorological Institute (DMI). Predicted temperature scenarios for year 2040 and 2060 were calculated and the data were incorporated in various models. Additionally, major geographical, topographical, husbandry and biological spatial parameters relevant to the distribution of vectors were included in the database and used as input in various distribution models. All collected datasets were assembled in a gridded climate database and presented at the website, www.nordrisk.dk. The website was created with the purpose of presenting the data to the public and making the data available to research projects in the Nordic countries. The website consists of an interactive web-application linked to a summarized climatic database. This allows for interactive selection of summary data for display. Detailed data files are available for research projects on request.

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Kristensen, B., Bødker, R.
R0-modeling as a tool for early warning and surveillance of exotic vector borne diseases in Denmark

Modeling the potential transmission intensity of insect borne diseases with climate driven R0 process models is frequently used to assess the potential for veterinary and human infections to become established in non endemic areas. Models are often based on mean temperatures of an arbitrary time period e.g. a monthly temperature mean. Temperature decreases with latitude, and in the Nordic countries periods of suitable temperatures, the windows of opportunity for transmission, may be very short and only appear in odd years. While average monthly temperatures are likely to be suitable for predicting permanent establishment of presently exotic diseases, mean temperatures may not predict the true potential for local spread and limited outbreaks resulting from accidental introductions in years with temporary periods of warm weather. We present a system for continuous risk assessment of potential local spread of exotic insect borne diseases of veterinary and human importance. R0 models for various vector borne diseases are continuously updated with spatial temperature data to quantify the present risk of autochthonous cases (R0>0) and the present risk of epidemics (R0>1) in case an infected vector or host are introduced to the area. The continuously updated risk assessment maps functions as an early warning system allowing authorities and industry to increase awareness and preventive measures when R0 raises above the level of ‘no possible transmission’ and target active serological surveillance to these limited periods of potential risk, thus dramatically reducing the number of samples collected and analysed. The risk estimated from the R0 modelling may be combined with the risk of introduction from neighbouring countries and trading partners to generate a truly risk based surveillance system for insect borne diseases. R0 models for many vector borne diseases are simple and the available estimates of model parameters like vector densities and survival rates may be uncertain. The quantitative value of R0 estimated from such models is therefore likely to deviate from the true R0. However assuming the models are qualitatively able to rank the estimated R0 correctly, a period resulting in a relatively high estimated R0 will also be a period with a relatively high true R0. This allows the estimated R0 to be used for targeted surveillance by focussing the surveillance on periods and areas with high R0 estimates even if the actual value of these estimates are difficult to interpret. Furthermore running R0 models on historic outbreaks in Europe may be used to fit estimates for R0 for these data. When comparing the model R0 to the observed value of R0 a correction factor is obtained that may be used to adjust the model estimates in Denmark, and thus allowing a more quantitative interpretation of the estimated R0. We here demonstrate the system for bluetongue using 2008 climate data and compare the predicted R0 with the actual spread of bluetongue in Scandinavia in 2008.

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Bødker, R., Kristensen, B., Græsbøll, K., Kirkeby, C., Stockmarr, A.
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Peer-reviewed: Yes
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R0-modeling as a tool for early warning and surveillance of exotic vector borne diseases in Denmark

Modeling the potential transmission intensity of insect borne diseases with climate driven R0 process models is frequently used to assess the potential for veterinary and human infections to become established in non endemic areas. Models are often based on mean temperatures of an arbitrary time period e.g. a monthly temperature mean. Temperature decreases with latitude, and in the Nordic countries periods of suitable temperatures, the windows of opportunity for transmission, may be very short and only appear in odd years. While average monthly temperatures are likely to be suitable for predicting permanent establishment of presently exotic diseases, mean temperatures may not predict the true potential for local spread and limited outbreaks resulting from accidental introductions in years with temporary periods of warm weather.
DTU-Veterinary Institute is developing a system for continuous risk assessment of potential local spread of exotic insect borne diseases of veterinary and human importance. R0 models for various vector borne diseases are continuously updated with spatial temperature data to quantify the present risk of autochthonous cases (R0>0) and the present risk of epidemics (R0>1) in case an infected vector or host are introduced to the area. The continuously updated risk assessment maps functions as an early warning system allowing authorities and industry to increase awareness and preventive measures when R0 raises above the level of “no possible transmission” and target active serological surveillance to these limited periods of potential risk, thus dramatically reducing the number of samples collected and analysed. The risk estimated from the R0 modelling may be combined with the risk of introduction from neighboring countries and trading partners to generate a truly risk based surveillance system for insect borne diseases. R0 models for many vector borne diseases are simple and the available estimates of model parameters like vector densities and survival rates may be uncertain. The quantitative value of R0 estimated from such models is therefore likely to deviate from the true R0. However assuming the models are qualitatively able to rank the estimated R0 correctly, a period resulting in a relatively high estimated R0 will also be a period with a relatively high true R0. This allows the estimated R0 to be used for targeted surveillance by focusing the surveillance on periods and areas with high R0 estimates even if the actual value of these estimates are difficult to interpret. Furthermore running R0 models on historic outbreaks in Europe may be used to fit estimates for R0 for these data. When comparing the model R0 to the observed value of R0 a correction factor is obtained that may be used to adjust the model estimates in Denmark, and thus allowing a more quantitative interpretation of the estimated R0. This presentation will demonstrate the system for selected vector borne diseases and compare the predicted R0 with the actual spread of bluetongue in Scandinavia in 2008.
Wildlife as reservoirs for vector borne diseases in a warmer Scandinavian climate

The distribution of vector borne diseases is highly determined by environmental and climatic parameters. As the climate becomes warmer the potential for spread of exotic vector borne diseases may therefore increase in the Nordic countries. But this does not mean that all new outbreaks of diseases can be attributed global warming. Some of these new infections have important reservoirs in wild animals and this may affect prevention and control of outbreaks in humans and domestic animals. This may also put wild animals at risk of not just infections but also of control efforts targeted at eliminating reservoirs. Insect borne Blue tongue, Black tongue, West Nile Virus, Usutu, avian malaria, Dirofilarial worms and Tick Borne Encephalitis are spreading and pose an increasing threat to people and animals in Northern Europe. Climate driven mathematical models may provide quantitative estimates of the future risk of outbreaks in the Nordic countries. DTU Veterinary Institute is developing a system for continuous risk assessment of potential spread of exotic insect borne diseases of veterinary and human importance. Mathematical models for selected vector borne diseases are continuously updated with spatial temperature data and vector data to quantify the present risk of outbreaks in case an infected vector or host is introduced to the area.
A mathematical model for optimising prophylactic treatment strategies of companion pets moving from *Echinococcus multilocularis* endemic areas to countries free of infection

**General information**
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Bødker, R.
Publication date: 2010
Peer-reviewed: Yes
Source: orbit
Source-ID: 272159
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2010

An atlas of climatic and environmental determinants of present and future veterinary and zoonotic diseases in the Nordic area

**General information**
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Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Bødker, R., Kirkeby, C.
Publication date: 2010
Peer-reviewed: Yes
Event: Poster session presented at NKVet Symposium: Databases in veterinary medicine – Validation, harmonisation and application.
Source: orbit
Source-ID: 272169
Research output: Research - peer-review › Poster – Annual report year: 2010

Et nyt flavivirus er dukket op i baghaven

**General information**
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Statens Serum Institut, Copenhagen University Hospital
Contributors: Christiansen, C. B., Fomsgaard, A., Bødker, R.
Pages: 3-6
Publication date: 2010
Peer-reviewed: Yes

**Publication information**
Journal: Dansk Selskab for Rejsemedicin
Volume: 15
Original language: English
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Source-ID: 272065
Research output: Research - peer-review › Journal article – Annual report year: 2010

Geo-locating cattle using EU databases

**General information**
Increasing the resolution of Bluetongue spatial modelling - from cattle farms to cattle in fields

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Mathematical Statistics, Department of Informatics and Mathematical Modeling
Contributors: Græsbøll, K., Bødker, R., Enøe, C., Christiansen, L. E.
Publication date: 2010
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Event: Poster session presented at NKVet Symposium, Databases in veterinary medicine – Validation, harmonisation and application, Copenhagen, Denmark.
Source: orbit
Source-ID: 272161
Research output: Research - peer-review › Poster – Annual report year: 2010

Modeling the density of bluetongue vectors in a field

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Kirkeby, C., Bødker, R., Stockmarr, A.
Publication date: 2010
Peer-reviewed: Yes
Event: Poster session presented at Bluetongue in the Nordic countries, Oslo, Norway.
Source: orbit
Source-ID: 272068
Research output: Research - peer-review › Poster – Annual report year: 2010

Modelling the seasonal variation in the basic reproduction ratio for bluetongue – a model incorporating Culicoides biology to quantify the vaccination cover needed to prevent outbreaks in the Nordic countries

General information
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Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Bødker, R., Græsbøll, K., Kristensen, B., Kirkeby, C., Stockmarr, A.
Publication date: 2010
Peer-reviewed: Yes
Event: Abstract from Bluetongue in the Nordic countries, Oslo, Norway.
Source: orbit
Source-ID: 272060
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2010

Simple spatial distribution models for vector density in a field: Bloodsucking creatures from dusk to dawn

General information
State: Published
Organisations: National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy
Contributors: Kirkeby, C., Bødker, R., Stockmarr, A., Lind, P., Græsbøll, K.
Number of pages: 13
Simulating the spread of Bluetongue virus – Focused on the effects of spatial distribution of cattle

General information
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Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Mathematical Statistics, Department of Informatics and Mathematical Modeling
Contributors: Græsbøll, K., Bødker, R., Christiansen, L. E., Enøe, C., Kirkeby, C.
Publication date: 2010
Peer-reviewed: Yes
Event: Abstract from GEOFET 2010, Sydney, Australia.
Electronic versions:
Simple_spatial_distribution_models.pdf
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2010

Association between land cover and Culicoides (Diptera: Ceratopogonidae) breeding sites on four Danish cattle farms

Biting midges of the genus Culicoides are vectors of bluetongue virus. Their larval habitats are poorly known in Northern Europe. Three classes of the CORINE land cover index, found within 300 m of four farms in Denmark, were used to stratify sampling sites for a total of 360 soil core samples from 30 sampling points. Soil samples were set up in emergence chambers for hatching adult Culicoides. Two species of Culicoides (C. punctatus and C. pulicaris) emerged from nine of 12 soil samples from a wet, grazed field with manure. Seventy-two other samples from similar land cover on the three other farms were negative. Seven sampling points from pastures were incorrectly classified by CORINE. The remaining 23 sampling points were classified correctly. The visually observed land use was not sufficiently detailed to adequately predict Culicoides breeding sites in this study. The CORINE index failed to identify pastures in which Culicoides breeding sites were found.

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Kirkeby, C., Bødker, R., Stockmarr, A., Enøe, C.
Pages: 228-232
Publication date: 2009
Peer-reviewed: Yes
Event: Abstract from Bluetongue in the Nordic countries, Oslo, Norway.
Source: orbit
Source-ID: 272269
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2010

Publication information
Journal: Entomologica Fennica
Volume: 20
Issue number: 4
ISSN (Print): 0785-8760
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 0.39 SJR 0.184 SNIP 0.335
Web of Science (2017): Impact factor 0.256
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 0.31 SJR 0.181 SNIP 0.305
Web of Science (2016): Impact factor 0.3
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 0.31 SJR 0.201 SNIP 0.299
Web of Science (2015): Impact factor 0.353
First identification of tick-borne encephalitis in Denmark outside of Bornholm, August 2009

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Fomsgaard, A., Christiansen, C. B., Bødker, R.
Pages: 2-3
Publication date: 2009
Peer-reviewed: Yes

Publication information
Journal: Eurosurveillance (Online Edition)
Volume: 14
Issue number: 36
ISSN (Print): 1025-496X
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1

Original language: English
Source: orbit
Source-ID: 253906
Research output: Research - peer-review : Journal article – Annual report year: 2009
Future animal health in Denmark

State: Published
Geographical cluster analyses of human salmonella cases in 25 European countries over a 6 year period using two complementary spatial methods

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Bødker, R., Pedersen, A., Tenhagen, B., Fisher, I., Ethelberg, S.
Publication date: 2009
Peer-reviewed: Yes
Keywords: GIS Salmonella
Source: orbit
Source-ID: 254923
Research output: Research - peer-review › Poster – Annual report year: 2009

Geographical pattern of Q fever in Danish dairy cattle farms

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Christoffersen, A., Bødker, R.
Publication date: 2009
Peer-reviewed: No
Electronic versions:
Geograpical pattern of Q fever in Danish Dairy cattle farms.ppt
Source: orbit
Source-ID: 244547
Research output: Research › Poster – Annual report year: 2009

Klimaændringer, zoonoser og dyresundhed: Hvad er på vej til Danmark, hvad gør vi ved det og hvor er dyrlægerne?

General information
State: Published
Organisations: National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy
Contributors: Bødker, R.
Publication date: 2009

Event information
Event: Klimaændringer, zoonoser og dyresundhed: Hvad er på vej til Danmark, hvad gør vi ved det og hvor er dyrlægerne?
Source: orbit
Source-ID: 254938
Research output: Research › Sound/Visual production (digital) – Annual report year: 2009

Spatial patterns and trends in the Salmonella atlas

General information
Spatial scan statistics to assess sampling strategy of antimicrobial resistance monitoring programme

Pie collection and analysis of data on antimicrobial resistance in human and animal populations are important for establishing a baseline of the occurrence of resistance and for determining trends over time. In animals, targeted monitoring with a stratified sampling plan is normally used. However, to our knowledge it has not previously been analyzed whether animals have a random chance of being sampled by these programs, regardless of their spatial distribution. In this study, we used spatial scan statistics, based on a Poisson model, as a tool to evaluate the geographical distribution of animals sampled by the Danish Integrated Antimicrobial Resistance Monitoring and Research Programme (DANMAP), by identifying spatial clusters of samples and detecting areas with significantly high or low sampling rates. These analyses were performed for each year and for the total 5-year study period for all collected and susceptibility tested pig samples in Denmark between 2002 and 2006. For the yearly analysis, both high and low sampling rates areas were significant, with two clusters in 2002 (relative risk [RR]: 2.91, p <0.01 and RR: 0.06, p <0.01) and one in 2005 RR: <0.01, p <0.01). For the 5-year analysis, one high sampling rate cluster was detected (RR: 2.56, p = 0.01). These findings allowed subsequent investigation to clarify the source of the sampling clusters. Overall, the detected clusters presented different spatial locations over the years and we can conclude that they were more associated to temporary sampling problems than to a failure in the sampling strategy adopted by the monitoring program. Spatial scan statistics proved to be a useful tool for assessment of the randomness of the sampling distribution, which is important when evaluating the validity of the results obtained by an antimicrobial monitoring program.
Status and ongoing research on vector borne diseases in Denmark: Developing a pragmatic adaptive strategy to climate change

General information
State: Published
Organisations: National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy
Contributors: Bødker, R.
Publication date: 2009

Event information
Event: Status and ongoing research on vector borne diseases in Denmark: Developing a pragmatic adaptive strategy to climate change
Location: Riga
Source: orbit
Source-ID: 254942
Research output: Communication › Sound/Visual production (digital) – Annual report year: 2009
TBE påvist i Nordsjælland

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Fomsgaard, A., Mølbak, K., Christiansen, C. B., Bødker, R.
Publication date: 2009
Peer-reviewed: No

Publication information
Journal: EPI-NYT
Issue number: Uge 35
ISSN (Print): 1602-4184
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
URLs:
http://www.ssi.dk/sw68937.asp
Source: orbit
Source-ID: 254916
Research output: Research › Journal article – Annual report year: 2009

Vectors of importance to animal health in the Nordic Baltic region: Present situation and possible future trends

General information
State: Published
Organisations: National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy
Contributors: Bødker, R.
Publication date: 2009

Host publication information
Title of host publication: Nordic Baltic seminar on the importance of vectors in the spread of animal diseases today and in the future
Source: orbit
Source-ID: 254941
Research output: Research › Article in proceedings – Annual report year: 2009

Danske aktiviteter vedr. mitteovervågning og forskning

General information
State: Published
Organisations: National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology, Section for Veterinary Epidemiology and public sector consultancy
Contributors: Larsen, L. E., Bødker, R.
Publication date: 2008
Peer-reviewed: No
Event: Poster session presented at RUFF-møde om klimaændringer, Krogerup Avlsgård, Humlebæk, .
Source: orbit
Source-ID: 222701
Research output: Research › Poster – Annual report year: 2008

Screening for spatial and temporal trends across Europe among registered cases of human salmonellosis, 1994-2006

General information
State: Published
Organisations: National Veterinary Institute, Bundesinstitut für Risikobewertung, Health Protection Agency, National Institute of Hygiene, Statens Serum Institut
Contributors: Bødker, R., Ethelberg, S., Tenhagen, B., Fisher, I., Sadkowska-Todys, M.
Publication date: 2008
Små myg overvåges fra rummet

General information
State: Published
Organisations: Division of Food Production Engineering, National Food Institute, Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Jørgensen, S. B. (ed.), Bødker, R.
Publication date: 2008
Peer-reviewed: Unknown

Publication information
Journal: FoodDTU Midt i Ugen
Original language: Danish
Source: orbit
Source-ID: 258511
Research output: Communication › Journal article – Annual report year: 2008

Udbredelse af den bakterielle zoonose Q-feber i danske kvægbesætninger.: En epidemiologisk analyse af laboratoriedata fra 2007

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics
Contributors: Bødker, R., Christoffersen, A.
Publication date: 2008

Publication information
Publisher: Dansk Veterinærtidsskrift
Edition: 91
Original language: Danish
Source: orbit
Source-ID: 240699
Research output: Research › Report – Annual report year: 2008

Udbredelse af den baktielle zoonose i danske kvægbesætninger: - En epidemiologisk analyse af laboratoriedata fra 2007

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics
Contributors: Bødker, R., Christoffersen, A.
Pages: 16 - 17
Publication date: 2008
Peer-reviewed: Yes

Publication information
Journal: Dansk VeterinærTidsskrift
Issue number: 14
ISSN (Print): 1902-3715
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
Vektorbårne sygdomme: Nye teknologier til overvågning og kontrol

General information
State: Published
Organisations: National Veterinary Institute
Contributors: Bødker, R.
Publication date: 2008
Peer-reviewed: No
Source: orbit
Source-ID: 222670
Research output: Research - peer-review › Journal article – Annual report year: 2008

Growth inhibitory factors in bovine faeces impair detection of Salmonella Dublin by conventional culture procedure

Aims: To analyse the relative importance of different biological and technical factors on the analytical sensitivity of conventional culture methods for detection of Salmonella Dublin in cattle faeces. Methods and Results: Faeces samples collected from six adult bovines from different salmonella-negative herds were split into subpools and spiked with three strains of S. Dublin at a concentration level of c. 10 CFU g(-1) faeces. Each of the 18 strain-pools was divided into two sets of triplicates of four volumes of faecal matter (1, 5, 10 and 25 g). The two sets were pre-enriched with and without novobiocin, followed by combinations of culture media (three types) and selective media (two types). The sensitivity of each combination and sources of variation in detection were determined by a generalized linear mixed model using a split-plot design. Conclusions: Biological factors, such as faecal origin and S. Dublin strain influenced the sensitivity more than technical factors. Overall, the modified semisolid Rappaport Vassiliadis (MSRV)-culture medium had the most reliable detection capability, whereas detection with selenite cystine broth and Mueller Kauffman tetrationionate broth combinations varied more in sensitivity and rarely reached the same level of detection as MSRV in this experiment. Significance and Impact of the Study: The study showed that for MSRV-culture medium and xylose lysine decarboxylase agar as the indicative medium, the sensitivity of the faecal culture method may be improved by focusing on the strain variations and the ecology of the faecal sample. Detailed investigation of the faecal flora (pathogens and normal flora) and the interaction with chemical factors may result in developing an improved method for detection of S. Dublin.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Baggesen, D. L., Nielsen, L., Sørensen, G., Bødker, R., Ersboll, A.
Pages: 650-656
Publication date: 2007
Peer-reviewed: Yes

Publication information
Journal: Journal of Applied Microbiology
Volume: 103
Issue number: 3
ISSN (Print): 1364-5072
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.41
Web of Science (2017): Impact factor 1.471
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.41
Web of Science (2016): Impact factor 1.575
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.57
Web of Science (2015): Impact factor 1.579
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.56
Web of Science (2014): Impact factor 1.659
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.69
Web of Science (2013): Impact factor 1.749
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.51
Web of Science (2012): Impact factor 1.629
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.55
Web of Science (2011): Impact factor 1.622
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Web of Science (2010): Impact factor 1.647
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Web of Science (2006): Indexed yes
Web of Science (2005): Indexed yes
Web of Science (2004): Indexed yes
Web of Science (2003): Indexed yes
Web of Science (2002): Indexed yes
Web of Science (2001): Indexed yes
Web of Science (2000): Indexed yes

Original language: English
Keywords: bacterial culture, analytical sensitivity, Salmonella Dublin, biological factors, technical, cattle
DOIs:
10.1111/j.1365-2672.2007.03292.x
Evaluation of the risk of spread of Echinococcus multilocularis from Denmark to Sweden: DFVF Risk Assessment Report

General information
State: Published
Organisations: National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research
Contributors: Maddox-Hyttel, C., Vigre, H., Bødker, R.
Publication date: 2006

Publication information
Volume: 55017-0005
Original language: English
Source: orbit
Source-ID: 240703
Research output: Research › Report – Annual report year: 2006

Relationship between the intensity of exposure to malaria parasites and infection in the Usambara Mountains, Tanzania

The relationship between exposure to Plasmodium falciparum malaria and parasite density and prevalence was studied in six communities along an altitude transect. Prevalence of parasitemia in children decreased by 5% for every 100 meter increase in altitude from 82% in the lowlands at 300 meters to 12% in the highlands at 1,700 meters. This decrease in prevalence corresponded to a 1,000-fold reduction in transmission intensity. The ability to suppress parasite density and prevalence with age increased proportionally with increasing transmission intensity when transmission rates were higher than 0.1 infective bites per year, but developed after 2-3 years of age, regardless of transmission intensity. However, at transmission rates less than 0.1 infective bites per year, prevalence remained similar in all age groups. We propose that both exposure-dependent acquired immunity and age-dependent acquired immunity regulate parasite prevalence and density and suggest that transmission control will not hinder the development of protective anti-parasite immunity.

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Bødker, R., Msangeni, H., Kisinza, W., Lindsay, S.
Pages: 716-723
Publication date: 2006
Peer-reviewed: Yes

Publication information
Journal: American Journal of Tropical Medicine and Hygiene
Volume: 74
Issue number: 5
ISSN (Print): 0002-9637
Ratings:
BFI (2019): BFI-level 2
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.42 SJR 1.43 SNIP 0.99
Web of Science (2017): Impact factor 2.564
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.57 SJR 1.556 SNIP 1.138
Web of Science (2016): Impact factor 2.549
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.48 SJR 1.473 SNIP 1.107
Web of Science (2015): Impact factor 2.453
BFI (2014): BFI-level 2
Risikovurdering gennemført af Danmarks Fødevareforskning vedr. effekten af at fjerne loftet på 500 dyreenheder pr. landbrugsejendom

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Section for Poultry Diseases, Division of Poultry, Fish and Fur Animals, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy
Publication date: 2006

Publication information
Publisher: Danmarks Fødevareforskning
Original language: Danish
Source: orbit
Source-ID: 230115
Research output: Research - peer-review › Journal article – Annual report year: 2006
Addition of novobiocin in pre-enrichment step can improve Salmonella culture protocol of modified semisolid Rappaport-Vassiliadis

The aim was to investigate the effect of addition of Novobiocin to the non-selective buffered peptone water (BPW) for pre-enrichment of Salmonella in connection with plating on modified semisolid Rappaport-Vassiliadis (MSRV). In a semi-quantitative study, the level of Salmonella following pre-enrichment of 32 presumably naturally contaminated swine fecal samples were assessed for BPW with and without addition of Novobiocin (22 mug/ml). In another experiment, a total of 400 swine fecal samples were screened for the presence of Salmonella spp., in order to compare the performance of the nonselective pre-enrichment broth with BPW made semi-selective by addition of Novobiocin. The semi-quantitative assessment of the Salmonella level showed that addition of Novobiocin in the pre-enrichment step on average increased the level of Salmonella 1.2 log dilution steps. When growth was scored at five levels, 90 samples opposed to 50 yielded a strong positive reading (+++) when Novobiocin was applied. Growth was on average 0.3 scores higher when pre-enriched with Novobiocin. The difference in growth score medians of the two methods was highly significant (Sign test; p <0.001). Despite the increased sensitivity, 13 culture-positive samples were missed when using the Novobiocin-containing BPW. In conclusion, a simple addition of Novobiocin in the BPW pre-enrichment step of fecal samples may facilitate reading and thereby detection of Salmonella on MSRV. The increase of Salmonella in the semi-quantitative study may be caused by a reduction in the number of competitive microorganisms.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Jensen, A. N., Sørensen, G., Baggesen, D. L., Bødker, R., Hoofar, J.
Pages: 249-255
Publication date: 2003
Peer-reviewed: Yes

Publication information
Journal: Journal of Microbiological Methods
Volume: 55
Issue number: 1
ISSN (Print): 0167-7012
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.95 SJR 0.696 SNIP 0.781
Web of Science (2017): Impact factor 1.701
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.05 SJR 0.742 SNIP 0.817
Web of Science (2016): Impact factor 1.79
Relationship between altitude and intensity of malaria transmission in the Usambara Mountains, Tanzania

There is a consensus that malaria is a growing problem in African highlands. This is because many parts of the highlands were considered too cold to support transmission. In this report, we examined how transmission of Plasmodium falciparum in six villages changed along an altitude transect in the Usambara Mountains, Tanzania, from 300 m to 1700 m. Routine entomological collections were made using spray catches and light traps for 15 mo. Direct estimates of entomological inoculation rates and indirect estimates of vectorial capacity suggested a >1000-fold reduction in transmission intensity between the holoendemic lowland and the hypoendemic highland plateau. Lowland transmission was perennial with a significant peak in the cool season after the long rains in May, when vectors densities were high. In the highlands, low temperatures prevented parasite development in mosquitoes during the cool season rains, and highland transmission was therefore limited to the warm dry season when vector densities were low. The primary effect of increasing altitude was a log-linear reduction in vector abundance and, to a lesser extent, a reduction in the proportion of infective mosquitoes. Highland malaria transmission was maintained at extraordinarily low vector densities. We discuss herein the implications of these findings for modeling malaria and suggest that process-based models of malaria transmission risk should be improved by considering the direct effect of temperature on vector densities. Our findings suggest that variation in the short rains in November and changes in agricultural practices are likely to be important generators of epidemics in the Usambaras.

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Bødker, R., Akida, J., Shayo, D., Kisinza, W., Msangeni, H., Pedersen, E., Lindsay, S.
Pages: 706-717
Publication date: 2003
Peer-reviewed: Yes

Publication information
Journal: Journal of Medical Entomology
Volume: 40
Issue number: 5
ISSN (Print): 0022-2585
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.78 SJR 0.962 SNIP 0.844
Web of Science (2017): Impact factor 1.968
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.82 SJR 0.883 SNIP 0.959
Web of Science (2016): Impact factor 1.65
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.93 SJR 0.953 SNIP 0.935
Web of Science (2015): Impact factor 1.712
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.87 SJR 1.063 SNIP 0.99
Web of Science (2014): Impact factor 1.953
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.02 SJR 1.003 SNIP 1.034
Web of Science (2013): Impact factor 1.815
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.18 SJR 1.016 SNIP 1.091
Web of Science (2012): Impact factor 1.857
Diversity of Plasmodium falciparum populations and complexity of infections in relation to transmission intensity and host age: a study from the Usambara Mountains, Tanzania

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Bendixen, M., Msangeni, H. A., Pedersen, B. V., Shayo, D., Bødker, R.
Pages: 143-148
Publication date: 2001
Peer-reviewed: Yes

Publication information
Journal: Transactions of the Royal Society of Tropical Medicine and Hygiene
Volume: 95
Issue number: 2
ISSN (Print): 0035-9203
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.12
Web of Science (2017): Impact factor 2.82
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.85 SJR 1.03 SNIP 0.811
Web of Science (2016): Impact factor 2.279
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.65 SJR 0.939 SNIP 0.728
Web of Science (2015): Impact factor 1.631
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.01 SJR 1.009 SNIP 1.036
Web of Science (2014): Impact factor 1.839
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.12 SJR 0.982 SNIP 1.153
Web of Science (2013): Impact factor 1.931
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.15 SJR 1.01 SNIP 1.165
Web of Science (2012): Impact factor 1.823
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.34 SJR 1.089 SNIP 1.24
Web of Science (2011): Impact factor 2.162
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.252 SNIP 1.148
Web of Science (2010): Impact factor 2.832
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.09 SNIP 1.113
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.02 SNIP 1.053
Scopus rating (2007): SJR 1.084 SNIP 1.206
Scopus rating (2006): SJR 1.047 SNIP 1.077
Scopus rating (2005): SJR 0.876 SNIP 0.924
Scopus rating (2004): SJR 0.98 SNIP 0.926
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.085 SNIP 1.33
Scopus rating (2002): SJR 1.282 SNIP 1.278
Scopus rating (2001): SJR 1.157 SNIP 1.302
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.977 SNIP 1.047
Scopus rating (1999): SJR 1.07 SNIP 1.37
Original language: English
DOIs:
Effect of 1997-98 El Nino on highland malaria in Tanzania

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Lindsay, S. W., Bødker, R., Malima, R., Msangeni, H. A., Kisinza, W.
Publication date: 2000
Peer-reviewed: Yes

Publication information
Journal: Lancet
Volume: Mar 18
Original language: English
Source: orbit
Source-ID: 240692
Research output: Research - peer-review » Journal article – Annual report year: 2000

Resurgence of malaria in the Usambara mountains, Tanzania, an epidemic of drug-resistant parasites

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Bødker, R., Kisinza, W., Malima, R., Msangeni, H. A., Lindsay, S. W.
Pages: 134-153
Publication date: 2000
Peer-reviewed: Yes

Publication information
Journal: Global Change & Human Health
Volume: Dec;1(2)
ISSN (Print): 1389-5702
Original language: English
Source: orbit
Source-ID: 240690
Research output: Research - peer-review » Journal article – Annual report year: 2000

Variation in malaria risk in the Usambara Mountains, Tanzania

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Bødker, R.
Publication date: 2000

Publication information
Original language: English
Source: orbit
Source-ID: 240711

Aminopropeptide of human procollagen type I: a marker for the identification of blood from children in the mosquito blood meal

General information
State: Published
Projects:

**Novel methods for applied spatio-temporal risk assessment models of endemic and emerging vector borne diseases**
Cuellar, A. C., PhD Student, National Veterinary Institute
Bedker, R., Main Supervisor, National Veterinary Institute
Kjær, L. J., Supervisor, National Veterinary Institute
Toft, N., Supervisor, National Veterinary Institute
Christiansen, L. E., Examiner, Department of Applied Mathematics and Computer Science
Konradsen, F., Examiner
Purse, B., Examiner
Institut stipendie (DTU)
15/02/2015 → 15/01/2019
Award relations: Novel methods for applied spatio-temporal risk assessment models of endemic and emerging vector borne diseases
Project: PhD

**Veterinary Epidemiology - biological models of vector borne diseases**
Haider, N., PhD Student, National Veterinary Institute
Bedker, R., Main Supervisor, National Veterinary Institute
Kjær, L. J., Supervisor, National Veterinary Institute
Toft, N., Supervisor, National Veterinary Institute
Vigre, H., Examiner, National Food Institute
Mortensen, S., Examiner
Offentlig finansiering
15/02/2015 → 11/12/2018
Award relations: Veterinary Epidemiology - biological models of vector borne diseases
Project: PhD

**Short range modelling of Culicoides dispersal**
Kirkeby, C. T., PhD Student, National Veterinary Institute
Lind, P., Main Supervisor, National Veterinary Institute
Bedker, R., Supervisor, National Veterinary Institute
Stockmarr, A., Supervisor, Risø National Laboratory for Sustainable Energy
Ersbøll, B. K., Examiner, Department of Informatics and Mathematical Modeling
Chirico, J. C. F., Examiner
Institut stipendie (DTU) Samf.
01/02/2010 → 29/05/2013
Award relations: Short range modelling of Culicoides dispersal
Project: PhD

**VICE: Vector-borne infections: risk based and cost effective surveillance systems**
EMIDA ERA-Net Application
The overall aim is to develop a fully functional framework for a dynamic risk-based surveillance for VBD according to EMIDAs specific topic A5. The potential risk of outbreaks of VBD and consequently the spread within the population at risk will be continuously estimated. This will permit 1) active surveillance to be focused on specific periods and areas of elevated risk and 2) active surveillance activities to be fitted to the available resources at EU and national level. The proposed surveillance system will be based on computer models scanning and interpreting risk parameters already collected for other purposes (weather data, environmental data, import data, syndromes) and costs may therefore be very low. Only during time periods and in areas of elevated risk will costly active surveillance activities
gradually be suggested based on cost-effectiveness estimates and the desired sensitivity. This framework for continuous risk based surveillance will be based on three independent pillars: (1) risk of introduction, (2) potential for spread if introduced and (3) syndrome surveillance. The sensitivity of the system will be evaluated with scenario trees. The surveillance system will be built on present knowledge of disease biology and vector ecology. The surveillance system will be modular allowing for easy and continuous updating of the underlying models whenever new or more precise information becomes available. Using selected VBD we will demonstrate how risk and hence the need for active surveillance can be communicated as dynamic maps of risk displayed on the internet at a weekly resolution. We will also demonstrate the surveillance system on historic data for a 30-year period to determine the average risk and hence cost of surveillance. This will assist decision makers at national and EU level to estimate long-term expenses for surveillance in various regions. Furthermore we will make spatially specific 50-year prognoses based on existing climate change predictions.

Bødker, R., Project Applicant, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy
Project ID: 22525
01/04/2012 → 31/03/2015
Keywords: VICE
Collaborators: FLI, National Veterinary Institute, Oldenburg, Wageningen University & Research, CODA-SERVA, CVI Lelystad, NVI, VPHi, Switzerland, National Institute for Agronomic Research
Project: Research

Multiple detections of epizootic and zoonotic pathogens in ticks. Development of low density DNA microarrays used as new epidemiologic investigative tools
Club 5 project A third of tick-borne pathogens (bacteria, parasites, virus) are the causative agents of zoonosis. A better understanding of their epidemiologies, requires multiplex of pathogens in one sample (tick or pool of ticks). To this end, we propose to develop low density DNA microarrays that will be used as new epidemiologic investigative tools. Based on chip technology called BioMarkTM dynamic arrays, we will detect 48 pathogens in 48 samples with few nanoliters of sample. Besides to save money and time, these arrays will permit to perform large scale studies on epidemiology of tick-borne pathogens.

Bødker, R., Project Participant, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy
Project ID: 11/04545
01/10/2011 → 31/03/2013
Keywords: Club 5 Flåter
Collaborators: National Veterinary Institute, CVI Lelystad, Agence nationale de la sécurité sanitaire, alimentation, environnement et travail
Project: Research

EDENext: Biology and control of vector-borne infections in Europe
The EDENext project (Biology and control of vector-borne diseases in Europe) builds on the concepts, methods, tools and results of the FP6 EDEN project (Emerging diseases in a changing European environment). We adopt here the same general approach of understanding and explaining the biological, ecological and epidemiological processes in order to develop a set of state-of-the-art methods and tools to improve prevention, surveillance and control of vector populations, and vector-borne diseases (VBD). The EDEN project has been focusing on the effects of environmental changes on the emergence of VBD. Here, we want to explain and model the processes leading to the introduction, establishment, and spread of vectors and/or vector-borne diseases, and assess the possible control strategies to break the epidemiological cycles of vector-borne diseases. The project structure follows that of EDEN that was so conspicuously successful, with a set of vertical disease related activities linked by horizontal themes providing integrated technical input to all vertical groups, thereby minimising duplication and ensuring a coordinated approach throughout the project.

Bødker, R., Project Participant, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy
FP7 Contract ID: 261504
Project ID: 22484
01/01/2011 → 31/12/2015
Keywords: EDENext
Documents:
Ansøgning_EDENext Biology and control of vector-borne infections in Europe
Project: Research

Opbygning af et Dansk veterinært beredskab for Bluetongue
En række sygdomme, der overføres af blodsugende insekter og mider, og som smitter husdyr og mennesker, spredes i disse år nordpå som følge af ændringer i klima og miljø. Senest er virussygdommen Bluetongue, der rammer drøvtyggere for første gang brudt ud nord for Alperne i Holland, Belgien og Tyskland. Sygdommen overføres af to millimeter lange mitter, der kan være særdeles talrige i Danmark. For at kortlægge hvor mitterne findes i Danmark vil dette forskningsprojekt udvikle en metode, der vil kunne forudsige mitternes forekomst ud fra satellitdata, vejrdata og nogle få

Bødker, R., Project Manager, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy
Stockmarr, A., Project Participant, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy
Jensen, K. V., Project Manager, Aarhus University
Skovgård, H., Project Participant, Aarhus University
Jensen, K. V., Project Participant, Aarhus University
Nielsen, S. A., Project Manager, Roskilde University
Balstrøm, T., Project Manager, Københavns Universitet, Institut for Geografi og Geologi

Bluetongue distribution and the impact of climate change in the Nordic countries

The project will use climate driven mathematical models to predict the potential spread of bluetongue and other vector borne diseases. The project is supplemented with a detailed analysis of bluetongue which emerged in the Nordic area in 2007. This detailed analysis involves joint Nordic field work. The project: • will identify and rank the vector borne zoonoses and vector borne infections in domestic animals most likely to emerge in the Nordic countries as a result of climate change. • will model the geographical distribution in the Nordic countries for the diseases that are most likely to emerge in the area. These models will be based on internationally recognised climatic scenarios for the coming 20 years (2030). • will facilitate Nordic exchange of entomological bluetongue surveillance data. • will facilitate joint presentations and interpretations of bluetongue surveillance data. • will analyse climatic determinants of bluetongue vector free periods in the Scandinavian region. • model bluetongue transmission in various parts of Scandinavia. • model potential impact on bluetongue of exceptional warm periods in the very near future. • model the risk that biting midges may become established on Iceland. • the project will hold a Nordic workshop to communicate the results, identify important gaps in present knowledge and discuss future Nordic veterinary surveillance and control strategies.

Bødker, R., Project Manager, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy

Climate change, globalisation and vector borne diseases in the Nordic countries. The future distribution of vector borne diseases.

1. The project will identify and rank the vector borne zoonoses and vector borne infections in domestic animals most likely to emerge in the Nordic countries as a result of climate change. 2. The project will model the geographical distribution in the Nordic countries for the diseases that are most likely to emerge in the area. These models will be based on internationally recognised climatic scenarios for the coming 20 years (2030). 3. The project will hold a workshop to communicate the results, identify important gaps in present knowledge and discuss future Nordic veterinary surveillance and control strategies.

Bødker, R., Project Manager, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy

Climate change, globalisation and vector borne diseases in the Nordic countries. The future distribution of vector borne diseases.
Nordic Climate Change Atlas. An atlas of climatic and environmental determinants of present and future veterinary and zoonotic diseases in the Nordic area

Develop a geographical information system (GIS) which includes major geographical, husbandry and biological spatial parameters relevant to the distribution of veterinary and zoonotic diseases, temperature and rainfall from the last 10 years and future temperature and rainfall based on internationally recognised climate scenarios. • Make the GIS available to Nordic researchers or alternatively describe data and provide scripts which will allow users to transform data obtained directly from data owners into the chosen GIS format. This will allow joint Nordic analysis of the impact of climate and environmental change on climate and environment driven disease e.g. vector borne diseases.

Bedker, R., Project Manager, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy

Project ID: 22437
Forsk. Andre offentlige og private - Nordiske: DKK300,000.00
01/01/2010 → 31/12/2010
Award relations: Nordic Climate Change Atlas. An atlas of climatic and environmental determinants of present and future veterinary and zoonotic diseases in the Nordic area

Opbygning af et Dansk veterinært beredskab for Bluetongue


Bedker, R., Project Manager, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy
Jensen, K. V., Project Participant, Aarhus University
Nielsen, S. A., Project Participant, Roskilde Universitetscenter, Department of Environmental, Social and Spatial Change, Balstrøm, T., Project Participant, Københavns Universitet, Institut for Geografi og Geologi,

Project ID: 23331
Forskningsprojekter - Fødevareministeriet: DKK678,000.00
01/01/2008 → 31/07/2011
Collaborators: Aarhus University, University of Copenhagen, Roskilde Universitetscenter, Department of Environmental, Social and Spatial Change, Roskilde University, Københavns Universitet, Institut for Geografi og Geologi,
Award relations: Opbygning af et Dansk veterinært beredskab for Bluetongue

Activities:

Vektorbårne infektioner
Period: 3 Jun 2014
Rene Bedker (Invited speaker)
National Veterinary Institute
Section for Epidemiology

Description
Kortlægning af risiko for vektorbårne infektioner
Documents:
Akademisk dag

Related event

Vektorbårne infektioner
The need to measure and predict vector abundance and biting rate
Period: 1 Nov 2012
Rene Bødker (Speaker)
National Veterinary Institute
Section for Epidemiology

Description
Presentation at half-day seminar about arthropods as vectors of diseases at the Swedish National Veterinary Institute (SVA).
Links:
http://www.sva.se/en/

Related event
Arthropods as vectors of diseases
01/11/2012 → …
Uppsala, Sweden
Activity: Talks and presentations › Conference presentations

Risk based surveillance for vector borne diseases
Period: 30 Oct 2012
Rene Bødker (Keynote speaker)
National Veterinary Institute
Section for Epidemiology

Related event
NJF seminar 457: Sustainable Agriculture in The Baltic Sea Region with focus on climate change
30/10/2012 → 31/10/2012
Uppsala, Sweden
Activity: Talks and presentations › Conference presentations

Dyrlægernes dag (DDD): Vektorbårne sygdomme - hvilken vej blæser vinden
Period: 3 Oct 2008
Rene Bødker (Speaker)
Division of Veterinary Diagnostics and Research
Section for Veterinary Epidemiology and public sector consultancy
National Veterinary Institute

Description
Place: SAS Radison, Silkeborg
Degree of recognition: National

Related event
Dyrlægernes dag (DDD)
03/10/2008 → …
Silkeborg, Denmark
Activity: Talks and presentations › Conference presentations

Early detection of Salmonella Dublin herds at risk for changing test status in the Danish surveillance program
Period: 22 May 2008
Rene Bødker (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Epidemiology and public sector consultancy

**Description**
Place: D4, Nordre Sti, KU LIFE

**Related external organisation**

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

**Aftagerkonference: FoodDTU - konference 27. maj 2008**
Period: 9 Jan 2008 → 27 May 2008
Rene Bødker (Speaker)

National Veterinary Institute

**Description**
Place: Lyngby

**Related external organisation**

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

**Evaluation of factors affecting the analytical sensitivity of bacteriological methods for investigation of S. Dublin in bovine faecal samples**
Period: 10 May 2006 → 12 May 2006
Rene Bødker (Speaker)

National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Epidemiology and public sector consultancy

**Description**
Place: The I3S International Symposium Salmonella and Salmonellosis, Saint-Malo, France

**Related external organisation**

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations