

AEEMA MEETING - JUNE 2, 2023: COMMUNICATIONS

Emergence of the epizootic haemorrhagic disease in Europe

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Epizootic haemorrhagic disease virus (EHDV) is an orbivirus belonging to the Sedoreoviridae family that poses a serious threat to the European cattle herd. In white-tailed deer, it causes a fatal infection with a mortality rate of up to 90% (2,000 deer died in 2022 in New Jersey). The virus was first identified in the United States of America in 1955. Since then, EHDV strains have been isolated in Japan, Canada, Australia, Africa and China. There are now seven serotypes (EHDV1-2, 4-8). This virus is transmitted by blood-sucking arthropods, the Culicoides. This infection is included in the list of notifiable diseases of the World Organization for Animal Health and is classified as a DE under the new European animal health law.

This virus was detected in Tunisia in 2021. After determination of the nucleotide sequence of segment 2 and comparison with homologous sequences present on GenBank, phylogenetic analyses showed that the VP2 of this virus showed a similarity with an EHDV of serotype 8 isolated in Australia in 1982. By virus neutralization test, our laboratory was able to confirm that this virus belonged to serotype 8. Unexpectedly, this virus was detected in Sardinia and then in Sicily in cattle and in a deer. Finally, it was detected in Andalusia where it caused ten outbreaks. Global warming (high temperatures in October and November) combined with southern air currents are probably responsible for this first emergence in Southern European countries. No vaccine against this serotype is currently available. This is therefore another emergence of an arbovirolosis in Europe that is as worrying and unexpected as that of the Bluetongue virus in 2006 or the Schmallenberg virus in 2011.

Estimating the date of the first infection by highly pathogenic avian influenza in poultry to optimise contact tracing

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Since 2014, Europe and France in particular, have been affected by several devastating epidemics of highly pathogenic avian influenza viruses (HPAI). During such epidemics, characterizing disease transmission dynamics is crucial for efficient contact-tracing and the timely identification of new outbreaks. The aim of our study was to estimate the time of first infection for various HPAI outbreaks, in order to focus contact tracing on the relevant period for each case.

By fitting a mechanistic model of within-flock transmission dynamics to daily mortality data recorded in 59 HPAI-infected flocks from France and the Netherlands between 2014 and 2022, we estimated times of first infection that ranged between 3.3 days (95% credible interval: 1.6, 5.6) and 14.1 days (8.2, 24.3). Our results suggest that efficient modelling pipelines fed with daily mortality data in outbreak farms could provide real-time support to veterinary services by estimating realistic ranges of dates of first infections to inform contact tracing.

Toxoplasmosis in the peri-urban area of Ouagadougou in Burkina Faso: seroprevalence in dairy cows, knowledge and behaviours at risk of zoonotic transmission of this zoonosis

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The general objective of this study was to estimate the seroprevalence of toxoplasmosis in dairy cows, the knowledge and behaviours at risk of zoonotic transmission of this zoonosis in herds in the peri-urban area of Ouagadougou in Burkina Faso. To do this, a blood sample was taken from 600 dairy cows. The indirect ELISA test was performed. An epidemiological questionnaire has been used for the farmers to better understand the knowledge and behaviours at risk of zoonotic transmission of the disease. Individual apparent seroprevalence and herd prevalence were 62% and 80% respectively. Only 13% of breeders were aware of bovine toxoplasmosis and know that it can be transmitted to humans and other animal species, 95% attended birth and abortion, and 97% consumed raw milk. Since toxoplasmosis is a major zoonosis, research into the disease in humans and an efficient control strategy are necessary to improve public health.

Development of scenario tree model to determine the probability of introducing *Dirofilaria immitis* in mainland France by military working dogs returning from overseas mission

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Dirofilaria immitis is a vector-borne nematode responsible for cardio-respiratory damage in infected dogs. It is also a zoonotic disease. This parasitic infection is widely distributed worldwide and is already established in mainland France. As such, this parasite is associated with animal and public health concerns. Military dogs appear to be particularly vulnerable to vector-borne diseases and, due to their overseas missions, they can influence the dynamics of these diseases. To assess the risk of introducing the *Dirofilaria immitis* parasite into mainland France through military working dogs returning from foreign missions, a quantitative risk analysis approach was chosen.

In this context, scenario trees were developed to describe the sequence of events necessary for the entry of the parasite into French territory. These event sequences consider the pathophysiology of infestation, prophylactic measures implemented in military dog populations, as well as the associated level of compliance. Parameterizing this scenario tree model involves determining a distribution for the probability of each event in the model, requires specific data on canine dirofilariasis and military dogs, which can be challenging as sources of data are sometimes scarce. Various sources of data were used, such as scientific literature, and a specific survey was conducted within military dog populations to gather information on their lifestyle and level of exposure to vector-borne diseases.

Field observations (conducted in Ivory Coast) were also used to provide some necessary data for parameterization of the model. This type of approach is particularly interesting for combining various sources of data and could provide decision support to animal health managers within the armed forces to optimize the management of this parasitic infection. This type of model could also be extrapolated to other pathogens of interest.

Monitoring the risk of entry of African swine fever at the farm level in Catalonia (Spain) in English

Alba-Casals Ana, Pailler Lola, Sánchez Carlos, Vilalta Carles, Colomer Joana, Ciria Natalia & Napp Sebastián

The spread of African swine fever (ASF) poses a serious threat to the pig industry of Catalonia (north-eastern Spain). The official veterinary authorities routinely collect a huge volume of data of different nature from commercial swine farms. The monitoring of some of that data might serve to assist in identifying specific farms and subpopulations with a higher risk of ASF entry.

With this goal, we created an algorithm that allowed the integration of these data into a decision tree analysis, and compared the risk of entry of ASF among commercial pig farms in the region through several ways that we can quantify. The system assessed the following pathways:

- 1. entry of live animals from international or national origin;*
- 2. contamination from vehicles that transport animals between farms,*
- 3. vehicles that transport pigs from farms to slaughterhouses,*
- 4. rendering trucks,*
- 5. indirect contact with neighbouring farms, and*
- 6. contact with wild boars.*

The initial assumption was that during a user-defined study period ASF had entered a single pig farm in Catalonia through one of these routes. The algorithm calculated the likelihood that each farm of the population had of being this first affected considering various risk and protection factors. The algorithm was fed on demographic and management data from the swine farms, surveys of biosecurity, national and international movements of live pigs, ASF outbreaks in Europe, and maps of wild boar density in Catalonia. Pathways that could not be assessed using official data were not considered.

This tool provides periodic information in reproducible reports, interactive maps, and Excel files on the risk of each farm taking in account each pathway independently and jointly.

Modelling of the probabilities of favourable areas of *Aedes albopictus* in Auvergne-Rhône-Alpes, France

Lebrun Jean, Rey Delphine, Besnard Gilles, Foussadier Rémi, Rome Sandra & Bicout Dominique]

*A vector of arboviruses responsible for human diseases including dengue fever, chikungunya and Zika, *Aedes albopictus* is the subject of national surveillance plans in mainland France. Since 2013, *Ae. albopictus* is considered to be present and active in five departments of the Auvergne-Rhône-Alpes region (Ardèche, Drôme, Isère, Rhône and Savoie). On January 1, 2021, only Allier and Haute-Loire*

were considered not yet colonized by *Ae. albopictus*. In a context of climate change, it is crucial for surveillance to identify areas favourable to the presence of these mosquitoes and to analyse the evolution of colonizable areas over the years. In this work, an ecological niche approach to determine the susceptibility of the presence of *Ae. albopictus* as a function of climatic and environmental variables was developed and probability maps of the areas of presence of *Ae. albopictus* were generated over the period 2000 -2020 in the 12 departments of the Auvergne-Rhône-Alpes region.

Exploring modelling methods to monitor mortality indicators in dairy farms. Case study: Catalonia (Spain) in English

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The authors propose a strategy for monitoring dairy cattle in Catalonia, in order to obtain reliable mortality indicators over time. The proposed strategy is divided into three parts: data preparation, clustering, and modelling. The data preparation part includes the integration, selection, cleansing, and transformation of various data sources of different nature. In the clustering part, mortality patterns are found and grouped using hierarchical clustering with Dynamic Time Warping.

In the modelling part, the most representative time series of dairy cattle mortality rates are modelled using the PSF and ARIMA logit models. Finally, the results of the PSF modelling are compared with those of the ARIMA logit model to evaluate the accuracy of PSF, which simplifies the calculations and automates the modelling processes.

Analysis of risk factors associated with bovine brucellosis in a region of Paraguay

Avalos Amaias, Durand Benoît & Zanella Gina

In Paraguay, where the primary economic activity is cattle farming, bovine brucellosis is an endemic disease. Between May 2019 and October 2020, a national prevalence survey was conducted by Paraguayan veterinary services.

As part of this survey, a cross-sectional study was carried out in the eastern region of Paraguay to estimate the seroprevalence of bovine brucellosis, assess farmers' awareness of the disease, and identify factors associated with positive brucellosis outcomes in farms. A questionnaire was administered to farmers to collect data on factors related to bovine brucellosis and awareness of the disease. A logistic regression model was used to identify factors associated with a positive brucellosis status in a farm. Blood samples were collected from 2,551 cattle in the 133 farms selected for the study.

The overall apparent seroprevalence at the farm level was 27.8% (95% CI: 20.4%-36.3%), and at the animal level, it was 5.5% (95% CI: 4.7%-6.5%). Among the 17 potential factors, four were associated with a positive brucellosis status at the farm level. Farm size was associated with a higher risk of positive status in medium-sized farms (20-80 cows) and large farms (>80 cows) compared to small farms (<20 cows). Stable disinfection was associated with a reduced risk of positive status, while the presence of dogs and non-incineration/burial of aborted materials was associated with an increased risk.

Although 89% of farmers acknowledged being aware of the transmission of bovine brucellosis to humans, only 46% of these farmers reported using protective gloves during calving or handling of abortions. The results of this study emphasize the importance of implementing biosecurity measures and proper disposal of aborted materials to control the disease. Therefore, to control the disease in Paraguay, vaccination campaigns should be accompanied by awareness campaigns promoting good farm management practices to minimize the risk of introducing and maintaining brucellosis, as well as the risk of human infection.

Modelling the spread of bovine brucellosis in Paraguay through the cow trade

Avalos Amaias, Zanella Gina & Durand Benoît

*Bovine brucellosis (BB), primarily caused by *Brucella abortus*, predominantly affects pregnant cows, which can lead to abortion. In Paraguay, BB is an endemic disease and poses a significant problem not only due to its economic impact on the livestock industry but also its implications for public health. A mathematical model of brucellosis transmission in Paraguay can help to understand the dynamics of its spread and be used to explore different control scenarios.*

We developed a stochastic compartmental model for BB transmission within a single farm and used this model to simulate the disease's spread between farms through the trade of female cattle. We considered two geographical regions in Paraguay: the eastern region with low farm density, a high number of cattle,

and extensive production, and the western region with high farm density and intensive production. Three categories of farm sizes were defined based on the number of cows: small family farms, medium-sized commercial farms, and large commercial operations.

Various scenarios involving the basic reproduction number (R_0 , the average number of infected animals originating from one infected animal introduced into a disease-free population) were explored through simulations to represent disease spread within a farm. The scenarios that best fit the BB seroprevalence data for the years 2019-2020 were selected and used to simulate disease transmission between farms through the trade of replacement heifers, based on the national animal movement database.

The model's predicted actual prevalences were higher in farms with many cows, namely, large and medium-sized farms in the eastern region and large farms in the western region of the country. Furthermore, the results indicated that considering the trade of breeding females as the sole mode of transmission between farms allowed for the generation of a global prevalence equilibrium of BB in Paraguay, consistent with the endemic disease situation in the absence of control measures.

Spatial distribution and phylogeny of Borrelia garinii found in common birds in France

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Lyme disease is transmitted to humans via the bite of a tick. It is caused by bacteria of the *Borrelia* genus belonging to the *Borrelia burgdorferi sensu lato (Bbsl)* complex. *Borrelia garinii*, a member of this complex and the main cause of neuroborreliosis in humans in Europe, has birds as its reservoir. The aim of our study was to investigate the genetic diversity and spatial distribution of *Bbsl* detected in gorged larvae collected from 70 birds belonging to 15 species during the breeding season in France, focusing mainly on *B. garinii*. To do this, we used the genetic sequences of 96 *Bbsl* (including 74 *B. garinii*), corresponding to a fragment of the *flaB* gene. *B. garinii* has been identified throughout France. The sequences studied were genetically close. The phylogenetic tree constructed using the maximum parsimony method did not reveal any clades specific to any bird species. No relationship between the clades identified in the phylogenetic tree and spatial distribution could be demonstrated. The gene sequenced (*flaB*) is a gene conserved within *Bbsl* species, which explains the low genetic diversity observed for the *Bbsl* sequences studied. As a result, the genetic diversity observed in this study for the *flaB* gene does not reflect the genetic diversity that exists in the *Bbsl* genome, as a whole. More discriminating sequencing methods should be used to study the phylogeny of *Bbsl*.

ARTICLE ANALYSIS

Viral zoonosis and "Machine learning": looking for genomic signatures to predict the zoonotic potential of viruses

Gondard Mathilde, Benfrid Souheyla and Dheilly Nolwenn

The rapid progress in metagenomics and meta transcriptomics studies revolutionized modern virology with the discovery of an extraordinary viral diversity which was largely unknown and underestimated.

The ongoing production of new viral genomic sequences, ever higher thanks to the advances in sequencing technologies, currently exceeds our capacity to characterize the biology of these viruses. Due to a lack of time and resources, very little epidemiological and virological data are available. In a context of (re)emergence of viral zoonosis, our ability to estimate and then rapidly determine the capacity of a virus to infect humans is becoming a global public health issue.

The work of Mollentze et al., published in 2021 in *PLOS Biology*, proposes the use of machine learning models, based on the search for genomic signatures, as an innovative way to predict the zoonotic potential of a virus and to help in research prioritization. In this article, after a brief presentation of the method, we decided to highlight and discuss what we believe to be the strengths (and possibilities for improvement) of the study by Mollentze et al.