

2022, issue 79 – ABSTRACTS

About the definition of veterinary public health

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Following the publication of a new definition of "Veterinary public health" by the French Veterinary Academy in June 2021, the AEEMA revised the definitions of the word "Health" and the phrases Public health and Veterinary public health present on its website. The new definitions are explained within an inventory of definitions available over time and commented on.

AEEMA MEETING - MAY 13^{en}, 2022: COMMUNICATIONS

Hypothesis on the re-emergence of BTV-8 in 2015 in France

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Bluetongue virus serotype 8 (BTV-8), a midge-transmitted arbovirus, emerged in northern Europe in 2006 and spread to most European countries until 2010. Although the outbreak was successfully controlled by vaccination in early 2010, the BTV-8 strain re-emerged in France in 2015, triggering a second epizootic that continues today. The origin of this virus and the mechanism of its re-emergence were unknown.

In this study and in collaboration with European partners, we performed phylogenetic analyses of 164 complete BTV-8 genomes sequenced directly from blood samples of naturally infected ruminants during the two epizootics from 2006 to 2010 and from 2015 to 2018.

A consistent and linear genetic evolution of the virus is demonstrated during each epizootic and reflects the average rate at which BTV-8 accumulates mutations. However, the sequence of the strain at the origin of the 2015 wave is similar to a virus from the first wave (2006-2010), which abruptly interrupted its evolution around March 2008. The use of contaminated semen, kept during several years, for insemination of cattle herds, so-called private breeding, could explain the re-emergence of BTV8 in 2015.

External evaluation and recommendations for improvement of the epidemiological surveillance of amphibians in French metropolitan National Parks

Palumbo Loïc, Miaud Claude, Durand Thierry, Le Loc'h Guillaume, Hendrikx Pascal and Larrat Sylvain

This study aimed to evaluate the surveillance network of amphibian mortality' events in French National Parks, using the OASIS method. The main strengths of the network were revealed by the evaluation, as well as limitations that narrow the surveillance's efficiency. The limitations encompass structural and functional parts of the network, which decrease its sustainability. Those observations lead to recommendations and a proposition for updating surveillance protocols in National Parks.

- *These include mobilizing experts and organizing work sessions in existing steering committees (locally and nationally),*
- *The reinforcement of laboratory capacity, including the setting-up of macroscopic pathology and histology techniques, and*
- *Strengthened monitoring of dedicated endangered species.*

This study also compared the specific amphibian surveillance network to the wider "Health strategy for wildlife" of the National Parks.

Investigation about the influence of the duck farms' density on the poultry sector's resistance to highly pathogenic avian influenza H5N8

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Managing sanitary crises linked to avian influenza viruses has become a crucial challenge for the long-term sustainability of the European poultry sector. The southwestern region of France, characterized by

a very high density of duck farms for the production of foie gras, has been highly impacted by each of the epizootics of the last six years.

Previous studies have shown that duck farms play a key role in the epidemiology of highly pathogenic avian influenza (HPAI). In this study, we analysed the impact of reducing duck farm density on the resilience of the poultry sector to the spread of HPAI H5N8. To do so, we used a mechanistic model fitted to the observed spatiotemporal distribution of outbreaks in France during the 2016-17 HPAI H5N8 epidemic. We considered six scenarios in which we decreased the density of duck farms in the communes with the highest density of duck farms. For each scenario, we calculated the basic reproduction number (R_0), i.e., the average number of secondary cases produced by an infectious farm in a population where every farm is susceptible. These scenarios were then investigated in conjunction with the management measures that were implemented during the outbreak. By running stochastic simulations of the model with the same initial conditions and keeping track of who infected whom, we calculated the effective reproduction number (R_e) during the epidemic, i.e., the average number of farms that an infectious farm has infected in a population that contains both susceptible and non-susceptible farms.

Our results show that reducing the density of duck farms in the densest communes would have had a strong impact on the epidemic, but would have not been sufficient to prevent the spread of the epizootic. In order to improve the resilience of the poultry sector to HPAI epizootics, it is now essential to further investigate the effect that complementary strategies may have on virus dynamics. This work will be extended to study the impact of other approaches, including reducing the size of duck flocks on site, the impact of confinement of ducks in farm buildings during risk periods, and strengthening biosecurity measures.

Modelling Mycobacterium bovis's transmission between domestic and wild animals: comparison of three endemic areas

Canini Laetitia, Durand Benoît, Duault Hélène, Boschioli Maria Laura and Michelet Lorraine

Genotyping of Mycobacterium bovis using classical techniques (spoligotyping and MIRU-VNTR) allows to trace the origin of infection of a very large number of bovine tuberculosis outbreaks, but does not make it possible to reconstruct transmission scenarios, particularly in areas where the incidence of the disease is high and where dominant genotypes are shared by cattle and wildlife. The use of whole genome sequencing provides very fine resolution data to overcome this problem. We therefore sequenced M. bovis strains in three endemic areas for bovine tuberculosis (Côte-d'Or, Dordogne/Haute-Vienne and Pyrénées-Atlantiques/Landes). The genomic data, combined with epidemiological data were integrated into Bayesian models. These studies highlighted transmission systems that appear to be specific to each zone. Intervention measures adapted to each context could be considered to interrupt these transmission cycles locally.

Biosecurity challenges in poultry farms from local food systems: semi-structured interviews

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Avian influenza is a worldwide sanitary issue threatening the poultry sector. The recent outbreaks of avian influenza in France have led to the implementation of new regulatory standards regarding biosecurity for the poultry sector (decree of February 8, 2016). This study aims at investigating biosecurity practices in poultry farms belonging to local food systems. It was based on the analysis of 20 semi-structured interviews conducted with poultry farmers from local food systems in South-West France.

Results showed that the farmers shared several core values about their production methods, including close interactions with occasional visitors. Farmers described several issues regarding the implementation of biosecurity measures on their farms. They stressed challenges associated with economic, space and time management, as well as constraints due to the management of multiple flocks and various types of productions. On-farm visits by customers was also identified as a critical point. Risk awareness about the pathways of avian influenza spread was heterogeneous among the interviewees.

The perceived effectiveness and usefulness of biosecurity measures also varied. Some farm owners described biosecurity policies as too vague or equivocal, resulting in uncertainties and difficulties during official inspections. These policies were also judged as unfair and disadvantageous for farms from local food systems, in comparison with farms from conventional systems. Further studies in other areas of France and various actors of the poultry sector are still needed to better document biosecurity in local food systems.

Monitoring of the vaccination cover and immunity of peste des petits ruminants in Niger (2019-2021)

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Peste des petits ruminants (PPR) is a viral disease responsible for heavy losses in sheep and goat flocks. It is found in several continents, including a large part of Africa, and is under a global eradication campaign, since 2015. The International Committee of the Red Cross (ICRC) has been supporting for several years in Niger the national annual vaccination campaign against PPR, implemented by the ministry of livestock on a free and mandatory basis for livestock keepers. This support occurs in three border regions suffering from insecurity linked to the presence of armed groups: Tahoua and Tillabéri regions at the West, close to Mali, and Diffa region at the East, in the Lake Chad area. In these three regions, 2 to 2.5 million small ruminants are vaccinated annually with the support of ICRC by the state services and private veterinary.

In order to evaluate the vaccination cover, a seroprevalence survey is implemented each year after the vaccination campaign in the ICRC's intervention zones. Sera were tested by a commercial ELISA (IDVet). The sampling plan consisted of a proportional cluster sampling in villages selected at random within the three regions, with a total of approximately 1 800 small ruminant sera collected each year. This study was done in close collaboration with the Central livestock laboratory of Niger (Laboratoire central de l'élevage du Niger - LABOCEL).

Results from the three previous years (2019, 2020, 2021) show that the individual seroprevalence for the three regions shifted from 86% to 73% despite an increase in the number of vaccinated animals, suggesting a decrease of immunity linked to vaccination. However, this trend was statistically significant both in 2020 and 2021 only in the Tillabéri region where it decreased from 90% in 2019 to 66% in 2021. In 2020 the seroprevalence also significantly decreased in Diffa compared to 2019, but it was stable in the Tahoua region, while in 2021 it was stable in Diffa and increased in Tahoua. Several hypotheses could explain the observed decrease or stagnation of the seroprevalence, despite an increase in the number of vaccinated animals: movements of vaccinated animals due to transhumance, a lower quality of the vaccines (default of the cold-chain), a vaccination protocol not strictly implemented, difficulty to reach small ruminant flocks due to insecurity. To maintain a good vaccine immunity (seroprevalence 70-80%), it is recommended to reinforce the supervision of vaccination teams during the campaign, control the vaccine quality along the cold chain, implement a systematic ear tagging of vaccinated animals and implement an annual sero-monitoring of PPR.

Q fever 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

Tialla Dieudonné, Sondo Ives and Sebou Dah Jean-Baptiste

The general aim of this study was the seroprevalence of Q fever in dairy cows estimate, and the knowledge and behaviors 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 registered with farmers to better understand the knowledge and behaviors at risk of zoonotic transmission of the disease. Individual apparent seroprevalence and herd prevalence were 26.2% and 60% respectively. Only 10% of breeders are aware of bovine Q fever and know that it can be transmitted to humans and other animal species, 95% attend birth and abortion, and 98% consume raw milk. Since Q fever is a major zoonosis, search for the disease in humans and an efficient control strategy are required to improve public health.

Animal and zoonotic schistosomiasis in Northern Senegal: A mixed of three cross-sectional studies combined with a slaughterhouse follow-up in 2016, 2017 and 2018

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Animal schistosomiasis is a waterborne disease caused mainly by Schistosoma bovis or S. curassoni that affects livestock living in the wetlands of the Senegal River delta and Ferlo with serious consequences for the economy of livestock farmers in northern Senegal. Its zoonotic character linked to the possible

hybridization between different species of schistosomes complicates efforts to effectively control bilharziasis in humans generally caused by *Schistosoma haematobium* or *S. mansoni* in Senegal. Indeed, hybrids of *S. haematobium* x *S. bovis* and/or *S. curassoni* x *S. bovis* have a zoonotic potential that allows them to cross the species barrier. Schistosomiasis is now a major public health concern, which justifies its place on the World Health Organization (WHO) roadmap for neglected tropical diseases.

The aim of the study was to determine the prevalence of schistosomiasis in cattle in the field and at slaughter and to identify hybrids of parasite species that can infect humans. This study was conducted in northern Senegal between November 2015 and December 2018, involving 2,490 live animals including 804 cattle, 874 sheep and 812 goats. Faeces samples were collected to detect schistosome eggs while adult worms were collected from the liver and mesenteric vessels from other animals in the same area at slaughterhouses. The miracidia hatching technique was performed for eggs and DNA extraction from adult worms for molecular analysis was done. In 2018, daily monitoring was carried out for one year at St-Louis slaughterhouse.

The overall prevalence rate of animal schistosomiasis was 72% in slaughtered cattle compared to 14.4% in live cattle, 13.1% in slaughtered goats compared to 2.6% in live goats and 19.9% in slaughtered sheep compared to 19.5% in live sheep. Molecular analysis of 440 miracidia collected from live and slaughtered animals showed that 52% were infected with *S. bovis* only, 46% with *S. curassoni* only and 2% with *S. curassoni* x *S. bovis* hybrids. In Barkedji area, 86% of animals were infested with *S. curassoni* only, while in the Richard-Toll area, 93% of animals were infested with *S. bovis* only. Analysis of 371 adult worms showed that 62.8% of animals were infested with *S. bovis* only, 35.6% with *S. curassoni* only and 1.6% with *S. curassoni* x *S. bovis* hybrids. These results reveal the presence of hybrids, which may challenge efforts to eliminate bilharzia from the human population in northern Senegal.

Microbial world realities from small ruminant breeders: anthropologic investigations based on the example of Q fever

Ramillien Emilie, Cayre Patrice, Fourt Xavier, Rousset Elodie and Jourdain Elsa

This study, performed in 2019 as part of the EXPAIRCOX project, aims at describing how small ruminant farmers perceive sanitary risks, including sanitary risks related to Q fever. Socio-anthropological surveys were conducted and interpreted by seriously considering the opinion of the surveyed stakeholders and revealing their relationships with the microbial world. The results show that farmers perceive themselves as standing at the frontier between two worlds: a « naturalist » world, made of long time-frames and complex interactions; and a « non-naturalist » world, defined by rationality, short time frames and poorly complex interactions. This polarity is particularly significant regarding the management of sanitary risks, for which a high level of delegation is frequently associated with ill-being and lack of meaning. Q fever is more, or less, perceived as an elusive and threatening disease depending on how much the farmers delegate sanitary risk management.