

2018, ISSUE 74 - Abstracts

COVER

On the cover' first page, a picture of a male grown Alpine Ibex, taken in the Bargy massif by M. Jean Hars (ONCFS), illustration of the May, 31st meeting of year 2018, which enable the research carried out in this area to be reviewed about the outbreak of brucellosis, find in 2012 on this species in this region.

AEEMA MEETING, MAY 30th, 2018: BRUCELLOSIS UPDATE IN THE BARGY MASSIF

Heterogeneity in the excretion of *Brucella melitensis* in Alpine ibex

Gilot-Fromont Emmanuelle, Freycon Pauline, Rossi Sophie *et al.*

The transmission' dynamics of *Brucella melitensis* in the Alpine ibex was mostly unknown in 2012. The discovery of a reservoir in the population of the Bargy massif raised the need to identify the factors that allowed the persistence of infection at a high level in this population. In order to determine the transmission routes and to identify which classes of individuals were more at risk to excrete bacteria, we necropsied 88 seropositive ibexes between 2012 and 2017. Bacteriological cultures were undertaken in 1 to 15 samples for each individual. The bacteria was detected in 51 (58%) of the necropsied ibexes. In 45 individuals, the bacteria was detected, at least, in one sample issued from the genital tract or a lymph node from the pelvic area, thus these individuals were potentially at risk of excreting the bacteria in the future. Among these, 26 (58%, or 30% of all necropsied animals) had at least one positive culture from an organ of the urogenital sphere and were thus considered as actually at risk of excreting the bacteria at the time of capture. The bacteriological results were heterogeneous among age and sex classes: the bacteria was most often detected in seropositive females aged less than five years old. This was possibly due to a primary infection that would include a possible abortion event during the first pregnancy, as it is described in domestic ruminants. Moreover, the bacteriological result was related to the serological response in females, suggesting that the serological response may help identify females having a high risk of excretion. The high shedding potential in young females may have contributed to the long-term maintenance of infection in this population, the males may be the vector of transmission to other areas. This heterogeneity should be considered to evaluate management scenarios, in this and other situations.

Ibex's brucellosis infection in the Bargy range: What's new from genetic?

Quéméré Erwan, Rossi Sophie, Game Yvette *et al.*

To understand the mechanisms of a wild population's infection by a pathogen and how transmission works inside, we need knowledge on the genetic and immunogenetic background of this population. Indeed, genetic diversity is a prerequisite for population's adaptation to multi-pathogen pressures. The genetic diversity of a population is a reflection of his demographic and evolutive history. When Alpine ibex (*Capra ibex*) has been reintroduced, populations had undergone several successive bottlenecks that considerably

eroded their adaptive genetic variability. Here, we tested the hypothesis that intrinsic sensitivity to brucellosis of ibex in the Bargy Massif results from a particular high level of inbreeding and low genetic diversity, notably for immunity-related genes. To assess the risk of spreading pathogen/infection, we also evaluated the historic and contemporary gene flow between the different social-spatial units of the Bargy Massif and with the neighbouring populations of *Leschaux-Andey* and *Aravis*. Our results suggested a low level of neutral and adaptive genetic diversity in Bargy Massif but very similar to levels observed in the source populations and many other recently reintroduced populations in the Alps. However, we observed a very small effective population size ($NE < 50$) that predict a strong decrease of the genetic diversity in the mid-term without migration/reinforcement. Overall, immunity-related genes showed a weak polymorphism but some rare variants (of the gene *SLC11A1* and to a lesser extent *Tlr1*) are associated with a lower rate of infection to Brucellosis, hence suggesting a better resistance of individuals carrying these variants. Lastly, gene flows between Bargy and the neighbouring populations are historically limited, but we detected many recent movements (particularly between *Bargy* and *Aravis*) that indicate a risk of spreading disease.

Alpine ibex' vaccination against brucellosis, an option to sanitize the *Bargy* Massif? Comparison of safety and effectiveness level of Rev.1 vaccine between Alpine ibex and goats
Ponsart Claire, Garin-Bastuji Bruno, Riou Mickaël *et al.*

Rev.1 is a stable live attenuated vaccine, which has significantly contributed to reduce the incidence of brucellosis due to *Brucella melitensis* in many countries, provided a sufficient coverage of sheep and goat populations was achieved. As regards the control of the brucellosis outbreak in Alpine ibex, an experiment to compare the safety of conjunctival Rev.1 vaccination between domestic goats and Alpine ibex was undertaken in spring 2017. Twenty-four adult animals were included in the study, divided into two batches of 6 males and two batches of 6 non-pregnant females of each species, for a period of 45 or 90 days. The Rev.1 vaccine resulted in a humoral response in all vaccinated animals, with a higher intensity in ibex compared to goats, regardless of age and sex. The risk resulted in the Rev.1 transmission from vaccinated ibex to one control animal. Despite what the genetic proximity between goat and ibex might suggest, the distribution of Rev.1 in organs and the risk of urogenital excretion were much more marked in ibex than in goats, all ages and sexes combined. These results highlight a reduced ability of Alpine ibex to contain the spread, multiplication and excretion of Rev.1 vaccine, suggesting a risk of spread of the vaccine strain in the ibex population. In nature, the uncontrolled diffusion of the vaccine strain may impair surveillance and management of this outbreak, inducing seroconversions of animals, without difference between animals infected from wild and vaccine strains.

Insights of modelling in the understanding of the brucellosis-ibex system in the *Bargy* Massif
Lambert Sébastien, Gilot-Fromont Emmanuelle, Toïgo Carole *et al.*

Dynamic modelling is a complementary tool to observational and experimental data on complex systems, such as *Brucella melitensis* infection in Alpine ibex in the *Bargy* Massif (French Alps). In such a case, the first step of the modelling approach was to formally represent the system and summarize the available knowledge. This step can already provide valuable insights and qualitative conclusions on key mechanisms of the system. The second step is

analytical. The aim is to identify key parameters and to estimate them, so as to reduce uncertainty and assess the most important processes. Here, parameters related to major transmission routes of brucellosis (abortion and venereal) as well as the capacity of the environment to affect the ibex population dynamics, appear to be key factors in brucellosis transmission. Finally, the last step consists in predicting the effects of wild outbreak management scenarios. Numerical simulations allow comparing several scenarios, which is not feasible in field or laboratory experiments. An important aspect of the modelling approach is that field data and biological knowledge are both used to formulate model assumptions and to estimate parameters. In return, model results can predict dynamics of future situations, and therefore lead to new research questions and can help to prioritize future experimental or field research. Despite the complexity of the system, available knowledge on ibex ecology and on brucellosis epidemiology of domestic ruminants allowed us to accurately model this unique situation and to better understand the possible interactions between the host and the pathogen.

Brucellosis update in the *Bargy* Massif: the contribution of collective expertise

Dunoyer Charlotte and Ganière Jean-Pierre

Since the discovery of the outbreak of brucellosis in a cattle farm in *Haute-Savoie* (France) in 2012 and the demonstration of a reservoir in the population of ibex of the *Bargy* Massif, the French Agency for Food, Environmental and Occupational Health & Safety (Anses) has received several mandates from risk managers, to shed scientific light on the various management scenarios, at the interface between wildlife and domestic animals. The collective appraisal methods, adopted by Anses to answer the questions, have shown their importance regarding an issue that has all the characteristics of a public debate, involving actors with different interests, questioning scientific knowledge and surveillance data very deficient, which could only be completed little by little and, on the opposite, an urgent expectation of decision-making by the authorities. Anses Working Groups faced many challenges in this context, especially multidisciplinary and the challenge of active dialogue and cooperation! A comprehensive approach, providing different insights, at the crossroads of epidemiology and ecology, has allowed experts, despite many uncertainties, to give some management conclusions. This approach calls to mind the importance of the One Health concept, which aims to take into account health, in a comprehensive approach of Man-Animal-Environment compartments.

AEEMA MEETING, JUNE 1st, 2018: COMMUNICATIONS

Contribution of four contact networks to *Mycobacterium bovis*'s transmission between cattle farms in "*Pyrénées-atlantiques*" and "*Landes*" areas, 2007-2015

Bouchez-Zacria Malika, Courcoul Aurélie and Durand Benoît

In the French *départements* of *Pyrénées-Atlantiques* and *Landes*, bovine tuberculosis (bTB) due to *Mycobacterium bovis* is detected within cattle farms through prophylactic measures and within wild populations through a devoted surveillance system. Within the infected area at the border of these two departments, we analysed a contact network between cattle farms as nodes, with known infectious status and molecular typing in case of detected infection, for

the 2007-2015 period. The 1946 cattle farms were linked through trade (T type) and/or neighbouring pastures (P type) and/or badger-mediated neighbourhood: cattle farms (their pastures) could neighbour the same badger home range (B type), and/or two distinct but neighbouring badger home ranges (D type). The analysis of components showed networks complementarity for *M. bovis* transmission. A non-parametric test showed a significant association between the network structure and the distribution of infected farms. Using a logistic regression model, we found that T-edges (OR=7.4 [3.5-15.5]95%), B-edges (OR=1.9 [1.4-2.9]95%) and D-edges (OR=10.1 [4.3-25.6]95%) were significantly associated to the probability for an edge starting from an infected farm to join another infected farm with the same molecular type.

Reconstitution of *Mycobacterium bovis*' transmission chain between cattle and wild animals

Michelet Lorraine, Courcoul Aurélie, Durand Benoît and Boschioli Maria Laura

The genotyping of *Mycobacterium bovis* using conventional techniques (spoligotyping and MLVA), allows to trace the origin of the infection of a very large number of outbreaks of bovine tuberculosis and to highlight a possible inter-species transmission. However, in areas with the highest incidence of the disease, dominant genotype patterns are shared by almost all isolates, making reconstitution of the transmission chain impossible. The use of whole genome sequencing, as a very fine resolution typing method, can make possible to differentiate clonal strains of the same genotype in a zone of high incidence and to rebuild transmission scenarios. This method has been used in the case of the French "*Département de Côte-d'Or*", area where endemic tuberculosis is noticed during last years. The use of a mathematical model will integrate epidemiological parameters combined with typing and genomic data to better understand the transmission network of bovine tuberculosis in *Côte-d'Or*.

A simple method to estimate the number of doses to be included in a vaccine bank: example of lumpy skin disease in France?

Casal Jordi, Saegerman Claude, Bertagnoli Séphane *et al.*

The lumpy skin disease (LSD) virus is a DNA virus belonging to the family Poxviridae and the genus Capripoxvirus. LSD is a highly contagious transboundary disease in cattle that causes significant economic losses. The disease was reported for the first time during the year 2014 in the European Union, (Cyprus, and next year in Greece. In 2016, it spread to different Balkan countries. A simple stochastic method for estimating the size of a vaccine bank is presented. It was applied to the hypothetical introduction of an epizootic of the LSD in France. The size of the vaccine bank was calculated taking into account three parameters which are the spatial spread of the disease, the time needed to obtain a good vaccination coverage of the population of interest and the density of the livestock in the region where the epizootic starts. The results were compared to a more refined and validated model, used as a reference method. The differences between the simplified model and the refined model in different scenarios considered vary from 7.0% to 10.5% more vaccines in the simple method compared to the refined method to cover 90% of the simulations and 9.0% to 13.8% for 75% of the simulations. Assuming a necessary 7 weeks' period to vaccinate all animals, and a disease spread of 7.3 km/week, the number of cattle would be 740,716 heads or less for 90% of the

simulations (608,196 for 75% simulations). The simplified model is easy to use and adapt to different diseases and countries and does not require many data to work.

Outbreaks of acute cryptosporidiosis inside a military camp during year 2017: thinking on the crisis's management

Watier-Grillot Stéphanie, Biletorte David, Petit Cédric *et al.*

In June 2017, two successive outbreaks of acute gastroenteritis were reported to the Center for Epidemiology and Public Health of Armed Forces (CESPA). They occurred in a military camp in southwestern France. The same strain of the parasite *Cryptosporidium hominis* was found among the affected military population and in the civilian water resource, which was responsible for the contamination of the public and military water systems. These epidemics of water-borne cryptosporidiosis have led to a real health crisis. This has been managed in several stages: Alert, Immediate measures to protect the health of civilian and military populations (water restrictions) and to rapidly restore normal conditions of supply in quality water compliant with regulatory requirements, Medium and long-term actions (enhanced monitoring of the water quality of the resource, monitoring of the military population exposed, modification of the water treatment plant, continuation of the environmental investigation, etc.). From the moment of the alert, an interdepartmental crisis cell, including civilian and military actors, was quickly organized. It made it possible to set up interfaces facilitating exchanges between the various stakeholders and thus to coordinate effectively the actions carried out, with a very positive assessment.

Risk of introduction of Lumpy Skin Disease in France by the import of cattle

Étoré Florence, Bertagnoli Stéphane, Casal Jordi *et al.*

In order to estimate the threat for France, a quantitative import risk assessment (QIRA) model was developed to assess the risk of Lumpy Skin Disease (LSD) introduction in France by imports of cattle. Based on available information and using a stochastic model, the probability of a first outbreak of LSD in France following the import of batches of infected live cattle was estimated to be between 4×10^{-5} and 3.3×10^{-3} (in 95% of cases). This model can easily be adapted to different countries and to other diseases.

Execution of biosecurity plan for bovine cattle in Belgium and farmers' perception of constraints

Renault Véronique, Damiaans Bert, Sarrazin Steven *et al.*

Farmers' perception regarding the main constraints linked to the implementation of various biosecurity measures in cattle farming. Biosecurity is a strategic and integrated approach aiming at preventing the introduction and spread of infectious diseases. The objective of the study was to evaluate the level of implementation of biosecurity measures by cattle farmers as well as the different constraints and opinions of the farmers. The finality was to assess the relevance and global feasibility of the recommended measures in order to better promote the adoption of new practices. A field survey has been done in 100 cattle farms in Belgium. The survey confirmed the generally low level of implementation of biosecurity measures with the feasibility or relevance of the measures regarding the low perception of the risk or impact expressed as the main constraints. In the future, joined reflexions between biosecurity

experts, decision makers and cattle farmers are necessary in order to jointly identify relevant, realistic, feasible and acceptable control measures. This step is necessary to improve the eradication and control programs of infectious diseases in cattle farms.

Tuberculosis in wild boar (*Sus scrofa*) in the western Liguria Region

Bona Maria Cristina, Mignone Walter, Ballardini Marco *et al.*

Mycobacterium bovis, the causative agent of bovine tuberculosis, can infect a wide range of domestic and wild animals. The infection has been described in wild boars (*Sus scrofa*) as well. In the Western Liguria Region (Northern Italy) the first case of tuberculosis in a wild boar was observed in 1989. To understand the relationship between mycobacterial infections' existence in livestock vs wildlife, a surveillance activity, targeting hunted animals, has been carried out over the last 25 years. The aim of this work is to show the local evolution of the disease within the wild boar population based on 2002-2016 data. During the study period, about 48,000 animals were submitted to anatomopathological examination. The majority of affected wild boars were caught during hunting seasons, in territories located nearby infected livestock or pastures where cattle from infected livestock used to graze. The observed decreasing trend in wild boars is likely associated with the progressive fading out of tuberculosis in the local cattle (last outbreak in 2012) that led in 2014 to the recognition of official free status of the province. A different trend has been observed for infections associated to *M. microti*, a microorganism unrelated to cattle. Our data suggest that wild boar could be considered as a sentinel of *M. bovis* in an area without necessarily acting as a reservoir or a vector of infection.

Risk of introduction of Lumpy Skin Disease in France by vectors in animal trucks

Saegerman Claude, Bertagnoli Séphane, Meyer Gilles *et al.*

The lumpy skin disease virus (VDNC) is a dsDNA virus belonging to the *Poxviridae* family and the *Capripoxvirus* genus. Lumpy skin disease (DNC) is a highly contagious transboundary disease in cattle producing major economic losses. In 2014, the disease was first reported in the European Union (in Cyprus); it was then reported in 2015 (in Greece) and has spread through different Balkan countries in 2016. Indirect vector transmission is predominant at small distances, but transmission between distant herds and between countries usually occurs through movements of infected cattle or through vectors found mainly in animal trucks. In order to estimate the threat for France due to the introduction of vectors found in animal trucks (cattle or horses) from at-risk countries (Balkans and neighbours), a quantitative import risk analysis (QIRA) model was developed according to the international standard [OIE, 2004]. Using stochastic QIRA modelling and combining experimental/field data and expert opinion, the yearly risk of VDNC being introduced by stable flies [*Stomoxys calcitrans*], that travel in trucks transporting animals was between 2×10^{-5} and $4,4 \times 10^{-3}$ with a median value of 53×10^{-5} ; it was mainly due to the risk related to insects entering farms in France from vehicles transporting cattle from the at-risk area. The risk related to the transport of cattle going to slaughterhouses or the transport of horses was much lower (between 1×10^{-7} and $2,7 \times 10^{-5}$ and between 1×10^{-8} and $1,67 \times 10^{-6}$ for cattle and horses, respectively). The disinfection of trucks transporting live animals was important to reduce this risk. The development of a stochastic QIRA made it possible to quantify the risk of DNC being introduced in France through the import of vectors that travel in trucks transporting animals. This tool is of prime

importance because the DNC situation in the Balkans is continuously changing. Indeed, this model can be updated to process new information on vectors and the changing health situation, in addition to new data from the TRAdE Control and Expert System (TRACES, EU database). This model is easy to adapt to different countries and to other vectors and diseases.

EPIDEMIOLOGICAL PAPERS

Sero-epidemiology of the bovine and swine brucellosis to Bobo-Dioulasso, Burkina Faso

Tialla Dieudonné, Zio Anaïse Carène, Yaméogo Ina Gwladys *et al.*

The objective of this study was to evaluate the seroprevalence of the bovine and swine brucellosis in intra-urban and sub-urban circles of Bobo-Dioulasso in Burkina Faso. So, the individual serological status of 600 cattle and 600 pigs was determined by the EAT and iELISA tests used in parallel. The farm prevalence of the brucellosis was estimated at 95% for the cattle and 60% for the pigs.