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The sub-network “Acute Respiratory Syndrome” of RESPE: epidemiological analysis of data collected from 2006 to 2013

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In the sub-network “SRA-Gourme” (Acute Respiratory Syndrome) of the RESPE (“Réseau d’Epidémiologie-Surveillance en Pathologie Equine”), in charge of surveillance on a voluntary basis, of Equine Influenza, EHV-1, EHV-4, equine viral arteritis and *Streptococcus equi equi* infections, the sentry veterinarians may declare one or more cases of acute respiratory syndrome. Any declaration is based on clinical suspicion. Clinical signs include hyperthermia along with either nasal discharge or cough. The objectives of the present study were to review the cases reported from 2006 to 2013 and to characterize the confirmed cases of equine influenza and EHV-1, EHV4 infections compared to other cases. 1368 horses were reported to RESPE during the study period and among the 911 horses included in the statistical analysis, 8.8% were confirmed cases of equine influenza and 10.1% confirmed cases of EHV-1, EHV-4 infections. The absence of cough may be a valuable clinical criterion for characterizing confirmed cases of EHV-1, EHV-4 infections compared with other cases of acute respiratory syndrome.

Relationship between clinical forms of tularemia and transmission cycles of *Francisella tularensis*

Masson Claire, Maurin Max, Caspar Yvan & Bicout Dominique J.

Tularemia is a zoonosis typical of the Northern hemisphere. It is regarded as a re-emerging disease worldwide, and an emerging disease in some countries. A number of wild animal species, several arthropod vectors and terrestrial and aquatic environments are involved in the natural life cycle of *F. tularensis*, but the natural reservoirs of this pathogen remain partially unknown. The objective of this study was to construct a relationship matrix between the clinical forms of human cases of tularemia in France and risk exposures of the corresponding patients, in order to identify environmental determinants of these infections. This research project is designed to construct risk maps of transmission and identify the transmission cycles of *F. tularensis* involved in each department in France.

Modelling the spread of the Porcine Epidemic Diarrhoea virus in case of introduction into a densely populated area, with no prior immunity

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The consequences of introducing in a densely pig populated area (French Brittany) a new variant of Porcine Epidemic Diarrhea virus (PEDV) with epidemiological characteristics of hyper-pathogenic strains circulating in the US were assessed using a modelling approach. A stochastic, individual-based model of spatio-temporal spread of the virus was used to simulate the propagation of the virus in the area. Data on geographical location, farm type and size, animal movements between herds and frequency of contacts was developed using the North American Disease Spread Model (NAADSM) interface. The structure of the infectious model is based on a compartmental SEIRS model with transition probabilities derived from literature data and recent reports from the US or Canada focusing on hyper-virulent strains. The impact

of various combinations of control measures was also investigated (suppression of animal movements for farms located in a 2 km radius area around the infected case, increase of external biosecurity measures, stamping out of infected units). The simulations show that, in the absence of control measures, a large epidemic would occur with characteristics in terms of propagation rate and persistence similar to those recorded in the US. The representation of the introduction of milder strains less persisting within infected farms (15 days on average) led to only sporadic cases with no epidemic. The most efficient control measures were fast stamping out of infected units (within 10 days of infection) of first identified cases and early restriction of animal movements. The increase in external biosecurity would enhance the efficacy of control measures. In every case, the rapidity in implementation of the control measures appeared as a key factor in the control of the epidemic.

Importance of quantitative data quality assessment in epidemiology: Case of the "Résabeille" network

Quéré Pauline, Bronner Anne, Meziani Fayçal & Hendrikx Pascal

The "Résabeille", pilot epidemiological surveillance program, is the French component of the European Epilobee surveillance system. It was implemented during two consecutive seasons (2012-2013 and 2013-2014) in six areas (French "*départements*") in the country. The objectives of this active surveillance system were to estimate the winter and in-season mortality as well as the prevalence of certain infectious and parasitic diseases of honey bees. Our study was specifically designed to evaluate quantitatively the quality of the data collected under the French surveillance program and to identify the difficulties experienced in the collection and compilation of data. Several dimensions of data quality (completeness, format, plausibility and consistency) were analysed quantitatively. Furthermore, in order to assess the quality of entries into the visit forms and the quality of their recording into the database, 60 Spring 2014 visits forms were thoroughly analysed and double entered into the database. In the evaluation of winter mortality data, plausibility varied between 98 and 100% depending on the variable considered and the consistency was 82%. In a random sample of 60 visit forms, between 77 and 97% of the expected data were recorded. The recording was feasible for all the items to be filled in the visit form, but between 12 and 27% of the data required an interpretation prior to the recoding (such as finding the correct value by crossing with other data in the visit form). Comparing the entry of data into the forms made by actors in the field with our double entry, led us to estimate that between 36 and 73% of the data in the visit forms were improperly recorded at the time of data entry (mostly in cases where the estimation of the correct value required crossing with other information from the visit form), which led to misinterpretation. Between 0 and 2% of data properly entered into the visit forms were incorrectly entered into the compilation. The results of this investigation led us to propose various improvements for future campaigns, in the design of the visit forms, in the training of actors, in coordination and assistance and in data verification prior to entry into the database.

Evaluation of the surveillance system for equine infectious anaemia in France and recommendations for improvement

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Equine infectious anaemia (EIA) is an equine viral disease. Since 1980, its prevalence has significantly decreased in France. However, sporadic outbreaks are still declared nowadays.

The French EIA surveillance network includes several independent passive or active surveillance components. The objective of this study was to assess the surveillance network for EIA in France using the OASIS method (“flash” variant) in order to identify improvements. The main strengths of the system are the quality of laboratory diagnosis, the simplicity and the timeliness of the reporting procedures. Recommendations are mainly related to a better definition of the objectives (that could lead to the modification of surveillance procedures), the improvement of the connection between components and the reinforcement of the central institutional organizations: management unit, steering committee and scientific and technical committee. Moreover, data management should be improved, especially data sharing, epidemiological analysis and generalization of automated data transfers regarding the diagnostic tests results. The OASIS “flash” method used in this study was well-received by the members of the surveillance network. This approach has readily highlighted the main weaknesses and the possible improvements and its cost-effectiveness is satisfactory.

Congenital jaundice in bovine aborted fetuses: an emerging syndrome in Southern Belgium

Delooz Laurent, Mori Marcella, Petitjean Thierry, Evrard Julien, Czaplicki Guy & Saegerman Claude

Southern Belgium faced recently an unusual increase in icteric bovine aborted fetuses. In the necropsy room, the majority of fetuses presented jaundice and splenomegaly. Despite a wide range of investigations, no definitive cause of abortion has yet been identified but leptospirosis was suspected. Lately, his suspicion has received confirmation. Further studies are in progress. This first description may help veterinary practitioners to identify more cases and encourage them to send appropriate samples to the laboratory for further study.

Development of new strategies to model bovine fallen stock data from large and small subpopulations for syndromic surveillance use

Alba-Casals Ana, Fernández-Fontelo Amanda, Revie Crawford, Dórea Fernanda, Sánchez Javier, Romero Luis, Cáceres Germán, Pérez Andrés & Puig Pèrre

The continuous monitoring of fallen stock mortality in bovine farms has been demonstrated in different studies to have potential as an important component of veterinary syndromic surveillance. However, as far as we know, the usefulness of these systems to detect abnormal events in near real-time in the field has not been assessed. To implement this type of system, a number of challenges must be faced. The main difficulties are associated with the non-specific nature of fallen stock data, since multiple events may cause bovine mortality at farm level. Moreover, these data are originated from heterogeneous subpopulations that can be clustered and studied in accordance with different traits (e.g. production type, type of farm and/or individuals, husbandry and environmental conditions, or administrative level). In this study, we present the main pillars of a syndromic system to collect continuous fallen stock data from a specific region and to model time series and detect abnormal events at large and small scale.

Modelling Presence Probability Maps of *Aedes albopictus* in the Rhône-Alpes area, France

Moyne Oriane, Cardoso Élodie, Rey Delphine, Besnard Gilles, Foussadier Rémi & Bicout Dominique J.

Unknown outside the Asian jungles almost forty years ago, the tiger mosquito *Aedes albopictus*, vector of several human pathogens, is now established across the 5 continents, including in urban areas. In France, a national plan for surveillance of dengue and chikungunya

is active, and some autochthonous cases of transmission have been reported recently, underlying the present risk of transmission in areas where the mosquito is present. Probably first introduced in the Rhône-Alpes area via road transport, *Ae. albopictus* is since 2013 considered present and active in 5 on 8 departments. For the surveillance purposes, it is now a question of identifying areas suitable for this mosquito and how these areas could be colonized. Thus, the aim of this study is to build maps of susceptibility of *Ae. albopictus* presence in the Rhône-Alpes area by a modelling approach combining knowledge on both the climatic and environmental determinants for establishment.

Using Bayes' rule to define the value of evidence from syndromic surveillance

Faverjon Céline, Andersson Mats Gunnar, Vial Flavie, Legrand Loïc & Leblond Agnès

In this work we propose the adoption of a statistical framework to be used in the evaluation of forensic evidence as a tool for evaluating and presenting circumstantial "evidence" of a disease outbreak from syndromic surveillance. The basic idea is to exploit the predicted distributions of reported cases to calculate the ratio of the likelihood of observing n cases given an ongoing outbreak over the likelihood of observing n cases given no outbreak. The likelihood ratio defines the Value of Evidence. Using Bayes' rule, the prior odds for an ongoing outbreak are multiplied with V to obtain the posterior odds. This approach was applied to time series on the number of horses showing nervous symptoms. The separation between prior beliefs about the probability of an outbreak and the strength of evidence from syndromic surveillance offers a transparent rational process suitable for supporting decision making. Furthermore, a Bayesian approach makes it possible to combine data from syndromic surveillance with results from predictive modelling and with information from other sources such as assessments of risks of disease introduction.

Schmallenberg virus: analysis of clinical suspicions reported by French veterinary practitioners in 2012

Maitia Fabienne, Dufour Barbara, Dominguez Morgane, Sailleau Corinne, Bréard Emmanuel, Millemann Yves & Zanella Gina

The clinical surveillance of congenital infection of lambs, calves and kids by the Schmallenberg virus (SBV) was introduced in France starting January 4, 2012. It was based on information sheets sent by veterinary practitioners together with biological samples collected for of SBV virus diagnosis. The information sheets were analysed in order to record clinical suspicions. The objective was to study the relationship between the RT-PCR results and the data recorded in the information sheets. A total of 1 589 clinical suspicions were reviewed. Three conclusions were drawn from this study. The best type of sample for SBV detection was the brain. Sheep were more frequently affected than cattle or goats and positive results for SBV were strongly associated with malformations of the head, spine or limbs, especially when two or three of them occurred together.

Towards an integrated approach to epidemiological surveillance of exotic health hazards

Calavas Didier, Bronner Anne, Marcé Clément, Fediaevsky Alexandre & Hendrikx Pascal

The overall health status of livestock in continental France is most encouraging with regard to a number of Category I health hazards, most of which are currently non-existent in the country. Surveillance programs have been set up and implemented for some of these hazards. There is a sound health monitoring system in operation which involves players in the field and centralised operations. Since October 2011, this system has been reinforced by the National

epidemiological surveillance platform for animal health. However, the overall surveillance organisation suffers from a certain number of limitations and flaws. To remedy these, it has been suggested that an integrated surveillance of exotic health hazards be set up by production sector, with four components: outbreak surveillance, programmed surveillance, clinical surveillance for detection of emerging diseases, and surveillance of non-specific signals, also known as syndromic surveillance. These four components should either be developed based on what already exists, or be created ex novo. They should be combined in order to find the most efficient means of organising them.

Identification of a new Bluetongue virus in goats in Corsica in 2014

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Since 2000, four serotypes of the bluetongue virus (BTV) were detected in Corsica, France. At the end of 2013, BTV-1 was detected in Corsica and a compulsory BTV-1 vaccination program for domestic ruminants was initiated. Apart from this vaccination program, biological samples were collected from Corsican goat farms. The laboratory diagnosis confirmed BTV-1 infection in goats in the Island but also evidenced another BTV serotype. The genome of this new serotype was entirely sequenced. Comparisons of nucleotide sequences suggested that this was a new BTV serotype never described earlier.

Ten years of sanitary monitoring on the chamois population (*Rupicapra rupicapra*) in the Ligurian Alps

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In recent years, the alpine chamois (*Rupicapra rupicapra*) population of the Province of Imperia, NW Italy, underwent sanitary monitoring. The monitoring plan was set up to investigate the effects of coexistence between free-range livestock and wildlife in the area, at the provincial and regional scale. Alpine chamois in the Ligurian Alps represents the westernmost and southernmost population of this species in the Alps, demographically distinct from the others and of particular interest from an ecological point of view, as its habitat is influenced by the Mediterranean climate. Our study refers to the results of the sanitary monitoring in the period 2002-2012, based on descriptive epidemiology (distribution of pathologies by place, time and features of the affected individuals).

POSTERS

Risk factors analysis for honeybee colony mortality in North Western Italy (Piedmont, Liguria and Valle d'Aosta regions)

Irico Lara, Vitale Nicoletta, Radaelli Maria Cristina, Chiavacci Laura & Possidente Rosaria

In recent years, large-scale losses of colonies and a high mortality in bees were reported in all countries. In 2012 the French Agency for Food, Environmental and Occupational Health Safety (ANSES) published a pilot project with an active epidemiological surveillance protocol for honeybee colony mortality in 17 European member states, including Italy. Data for North Western Italy (NWI) were collected and analysed in order to study colony mortality and apiary management. The colony mortality rate in NWI amounted to 5.8 (CI95% 3.8-7.8). Every region presented an over winter colony mortality rate: 6.2% in Liguria, 3.2% in Piedmont and 11.8%

in Valle d'Aosta, respectively. The difference between regions was not statistically significant (χ^2 : 4.54, $p = 0.10$). At apiarian level, the highest mortality rate was observed in the spring, as 41.6% of observed apiaries showed at least one dead colony, while in the summer the apiaries with at least one dead colony were only 12.5%. The difference was statistically significant (Mc Nemar test: 3.90 $p = 0.0482$). No statistically significant association was found between bee colony mortality rate and various factors considered in the questionnaire.

Four years investigation on *Trichinella spp.* larvae in wild and domestic animals in North-Western Italy

Bellio Alberto, Bianchi Daniela Manila, Adriano Daniela, Gallina Silvia, Zuccon Fabio, Delvento Paola, Possidente Rosaria, Chiavacci Laura & Decastelli Lucia

The results of analyses performed from 2011 to 2014 in Piedmont region for the detection of muscle larvae of *Trichinella spp.* are reported. A total of 212.997 meat samples (61.177 in 2011, 53.709 in 2012, 61.493 in 2013 and 36.618 in 2014) were analysed. All samples were analysed according to the methods described in Regulation CE 2075/2005. Four fox (*Vulpes vulpes*) samples resulted positive for *Trichinella spp.* in 2011; one fox muscle in 2012 and two wild boar (*Sus scrofa*) samples in 2013 tested positive. No samples of reared animals were found to be infected with *Trichinella spp.* confirming that herd system is able to avoid contact between wild and domestic animals protecting herds from this type of infection.

Serologic evidence of Crimean-Congo haemorrhagic fever infection in small ruminants in South-Eastern Romania

Răileanu Cristian, Aniță Adriana, Porea Daniela & Savuța Gheorghe

Crimean-Congo haemorrhagic fever (CCHF) is a widespread zoonotic disease caused by a tick-borne virus (Nairovirus) of the Bunyaviridae family. Small ruminants with CCHF undergo a mild infection, sometimes with transient viraemia. Serum samples to test for CCHFV antibodies were collected from 90 small ruminants in various sites in Tulcea and Constanța Counties. All serum samples were tested for the presence of specific IgG antibodies against CCHFV by a commercial ELISA kit (Vectorbest, Novosibirsk, Russia), slightly modified. The serological examination of serum samples for anti - CCHFV infection evidenced CCHF IgG antibodies in the blood of 16 out of 29 goats (55%) and in 51 out of 61 (85%) sheep. These results suggest that the CCHF virus may be widespread in traditionally reared small ruminant livestock in Tulcea and Constanța Counties. CCHF infected animals also represent a potential threat to abattoir workers and to public health.