AEEMA MEETING, MAY 30st, 2013: FROM ERADICATION TO RE-EMERGENCE OF ANIMAL INFECTIOUS DISEASES

From eradication to re-emergence of animal infectious diseases: background and definitions of the major concepts

B. Toma & J-P. Ganière

As stated by Charles Nicolle, an animal infectious disease is a live entity resulting from exposure to an infectious agent of a receptive population. In view of the diversity of potential situations, in terms of population and infectious agents, a distinction can be made (both in time and space), between several steps in the disappearance of this entity: Control of a disease: Reduction in the incidence of a disease to a level regarded as acceptable; Elimination of a disease: Reduction to zero in the case/outbreak incidence of a disease; Elimination of an infection: Reduction to zero in the incidence of an infection; Eradication of a disease (the ultimate step): Sum of all actions leading to the complete elimination of a disease based on the suppression of its cause in a country, a group of countries or the whole world, over a period of time regarded as sufficient, and the resulting situation. The magnitude of technical problems to be solved to obtain the eradication of an animal infectious disease in a given country may vary, particularly due to the nature of its reservoir (strictly in domestic animals or in wild animals as well), the duration and frequency of silent carriage of the pathogen, as well as available control means, such as an efficacious vaccine. Whereas the difficulties are limited when there is no reservoir among wild animals and when the disease appears largely as an acute condition, without major carriage (e.g. foot-and-mouth disease), they increase substantially with chronic diseases with limited and uncertain expression in terms of symptoms or lesions (e.g. bovine tuberculosis) or in diseases with a reservoir in wild animals against which a vaccine is available (fox rabies). The problem become insurmountable for diseases with a wild reservoir against which no efficacious vaccine easily administered to wild animals is available (tuberculosis with a wild reservoir). An infectious disease may re-appear after its eradication either by way of re-emergence (but the eradication was not as complete as anticipated) or by introduction of the infectious agent through various mechanisms.

Difficulties and uncertainties of eradication: example of Bluetongue in France

P. Hendrikx & S. Zientara

Bluetongue hit the headlines for Animal Health in France since 2000 in Corsica (serotypes 2, 4 and 11) and between 2006 and 2010 in mainland France (serotypes 8 and 1). Difficulties and uncertainties of eradication in mainland France were of four types: (i) evolution of control objectives, (ii) knowledge gaps related to the disease and its epidemiology in temperate climate and (iii) practical difficulties in the implementation of control measures that explain (iv) difficulties in defining strategies as a whole. Finally, specific difficulties in proving the absence of the disease were also sources of uncertainty even if the surveillance results confirm eradication and allow us to draw lessons for the future.

Re-occurrence of an infectious disease: origin and detection; example of bovine brucellosis in France

B. Garin-Bastuji, Séverine Rautureau, J. Hars, Virginie Mick & Marine Jaÿ

France has been officially free from bovine brucellosis since 2005. This status implies that no case of abortion due to Brucella infection and no isolation of Brucella have been recorded for

at least three years and, at least 99.8 % of herds have achieved the officially brucellosis-free status each year for five consecutive years. Due to the absence of brucellosis in cattle - as well as in sheep and goats - since 2003 in France, it appeared desirable to modify the surveillance strategy. The main objective was to limit unwarranted suspicions generated by false- positive reactions (FPSR) in serological tests; their positive predictive value has logically decreased to close to zero as a result of eradication. Therefore, the annual control of dairy herds on bulk tank milk was adopted. As far as meat cattle are concerned, EU regulations provide the possibility of testing, in 20 % of the herds, only animals over the age of 24 months, since these are less subject to FPSR than younger animals. Nevertheless, France has preferred to maintain the annual surveillance of all such bovine herds, but testing only 20 % of these animals. Surveillance remains also based on notification of abortions, regarded as the most efficient tool to early detect the reintroduction of Brucella infection in a free country. Two outbreaks of bovine brucellosis were confirmed in 2012 in France, while no case had been reported since 2003. The first outbreak, located in the Nord-Pas-de-Calais northern region of France, where *Brucella abortus* biovar 3 was identified, was due to the import of an animal issued from a Belgian confirmed outbreak. The French outbreak was not identified by the surveillance system, but through the notification by the Belgian authorities to the French counterpart of recent movements towards France of animals from the first outbreak identified in Belgium in 2012. The disease did not spread in France since the introduction was quite recent when discovered. However, in Belgium, 6 outbreaks due to the same strain were reported and confirmed as related, but the source of the index outbreak was not identified. The same MLVA 16 genotype was identified in all Belgian and French outbreaks. The second French outbreak was confirmed in a mountain dairy farm in Haute-Savoie (French Northern Alps), through the notification of an abortion. A human case connected to this outbreak had been identified a few weeks before. It was later confirmed as due to the consumption of fresh cheese produced in the same farm. The origin of this bovine outbreak remains unexplained since all investigations carried out in all domestic ruminants of the mountain range were negative. However, investigations performed in local wild ruminants during fall 2012 evidenced the presence of the Brucella infection in two wild species (one case in Chamois [*Rupicapra rupicapra*] and several cases in Alpine ibex [*Capra ibex*]. Again, the strains isolated from the human case, that from cattle, as well as those from Chamois and Ibex all belonged to the same species and biovar (*B. melitensis* biovar 3) as well as to the same MLVA 16 cluster. The epidemiological mechanisms that allowed the silent persistence and spread of the disease in the local wildlife, presumably over the 10 previous years, (the last domestic outbreak in the area occurred in 1999) are still under study. Several measures are being considered to limit or eradicate the risk of contamination of domestic herds from what seems to be a real primary wild reservoir. The control of this risk is a real challenge for public health and for the local economy, based in part on production of raw milk cheese. Two major difficulties are anticipated: How to control a severe sanitary problem in a protected wild species like the Ibex in an open mountain area, How to reinforce the surveillance of domestic ruminants in order to early detect infection, and prevent human contamination, without damaging the raw-milk cheese economy. These two recent cases highlight the importance of maintaining appropriate surveillance and expertise, in France as well as in the EU, even when eradication has been reached, as this was the case in France and in Eastern, Central and Northern Europe for over 10 years.

Emergence and re-emergence of West-Nile Virus: origin and detection
Sylvie Lecollinet, Sophie Pradier, Cécile Beck, B. Durand, Agnès Leblond & S. Zientara
Infection by the West Nile virus (WNV) is an ancient arboviral disease described since the 60s in Europe and in the Mediterranean basin. It is associated with many emergences (the most

famous being the introduction on the East coast of the U.S. of a new viral strain in 1999 as well as the introduction and spread of a new strain of lineage 2 in Central Europe since 2004) or re-emergences (with outbreaks caused by lineage 1 strains), characterized by the reporting of human cases and/or equine infections. In this review, we propose to describe and analyze the methods of detection of WNV outbreaks. For virus infections with complex epidemiological cycles like WNV, it is difficult at the moment to predict the emergence of clinical disease and it is of upmost importance to minimize introduction risks and sources, as well as to ensure appropriate monitoring and effective prophylaxis.

How should we perform disease surveillance in a low prevalence context? The example of brucellosis by the surveillance of bovine abortions in France.

Anne Bronner, Emilie Gay, Viviane Hénaux & D. Calavas

The bovine abortion surveillance system in France is based since 1965 on mandatory notification of abortions It is nowadays the main tool to survey brucellosis. It was designed to detect as early as possible any resurgence of bovine brucellosis and to ensure the officially brucellosis free status of France (obtained in 2005). However, several studies questioned the capacity of the current abortion surveillance and brucellosis surveillance system to meet these objectives. Brucellosis surveillance may be reinforced by improving the mandatory bovine abortion notification system, developing a complementary syndromic surveillance system (based on calving intervals), and resorting to an active surveillance based on a risk-based sampling.

From eradication to re-emergence of animal infectious diseases. The hazards of wildlife: context and management

J. Hars, B. Garin-Bastuji, Céline Richomme, Ariane Payne & Sophie Rossi

Wildlife species may act as preserving hosts for infectious diseases including zoonotic diseases such as Aujeszky's disease and classical swine fever in swine, tuberculosis, brucellosis or bluetongue in ruminants or avian influenza in birds. So, wildlife reservoirs have become a real issue in terms of public and animal health, because they hamper efforts made to control major infections in livestock. Surveillance and control of infectious diseases in wildlife is complex because it is based on the voluntary participation of stakeholders in the field (hunters, naturalists). It is costly and not always sufficiently effective to make the wild population healthier. Drug treatments cannot be used on a population scale. Mass vaccination is a valuable tool but it is difficult to implement and oral vaccines are not always available. Control measures include forbidding artificial feeding and reducing population' densities. The latter is often necessary to prevent the persistence or the spread of diseases but is difficult to carry out on the long term. Besides, it can lead to adverse effects such as post-culling demographic recovery or spread of the infection due to the dispersion of wild animals. Biosecurity measures on farms designed to reduce contact between wildlife and livestock are also needed (often the only recourse to reduce the risk of contamination), but they do not guarantee the total absence of contact between wild and domestic animals and thus the risk of transmission.

From eradication of bovine tuberculosis in France to its recurrence: Illustration of the complexity factors

Barbara Dufour & J-J. Bénet

Bovine Tuberculosis due to *Mycobacterium bovis* (bTb) is a good example of an eradication process undergone in France since the 1950's. After an initial phase of relatively rapid decline in the number of infected farms in 50 years from an annual prevalence of about 25 % to less than 0.02 %, France was able to claim the status of country officially bTb free in 2000, delivered by the European Union. However, shortly thereafter, several signals announced that the fight

against bTb was not quite won. Thus, in the Dordogne department, from the 2000s a small but constant and then, from 2004, increasing number of outbreaks of bTb in livestock was recorded each year. In the Côte-d'Or department, until 2006 the situation appeared stable but from 2007 the number of new cases also increased. Moreover, it was in 2001 that was reported *in Brotonne-Mauny* forest (Normandy) the first outbreak of *M. bovis* identified on a wild animal (a deer Elaphe). Since then, investigations in the areas of bTb showed a worrying situation as boars, badgers and some deer have consistently been found to be infected with *M. bovis*. Causes, of what appears to be a resurgence of the infection, are complexes and should probably be sought in the analysis of changes since the beginning of the fight. Elements of change can be grouped into three main groups: the terms of the fight (changes to a legitimate reduction controls frequency to limit non-specific reactions and blockages caused), the evolution of farming practices (increased herd size and farming practices including suckling animals) and increased densities of receptive wild populations. All of these developments has radically changed the complex pattern of contamination and persistence of *M. bovis* in herds and have now led to consider bTb as a host-pathogen ecosystem for which nowadays available tools are less suitable than in the past.

AEEMA MEETING, MAY 31st, 2013: COMMUNICATIONS

Atypical mycobacteriosis of wild fish in north-west of Italy
Maria Cristina Bona, G. Ru, Elena Pavoletti, Marzia Righetti, T. Scanzio & M. Prearo
Atypical Mycobacteriosis is a chronic and progressive disease of fish affecting all species (freshwater, brackish water and saltwater); the disease has been documented in more than 160 species worldwide [Chinabut, 1999]. *Mycobacterium marinum*, *M. fortuitum* and *M. chelonae* are the most commonly isolated bacterial species Apart from the mortality it induces in fish, Mycobacteriosis represents a potential hazard of human contamination. Regarding wild fish, there are few and fragmented reports in Italy. The main difficulty in data analysis is the huge number of fish from the same ecosystem to be evaluated. Our study was designed as a contribution to the investigation of the distribution of atypical Mycobacteriosis in wild fish.

Is the health status of a herd exposed and exposed with circulation of *Coxiella burnetii* related to the results of a bulk milk sample or a random blood sample of adult dairy animals?
G. Czaplicki, J-Y. Houtain, C. Mullender, C. Manteca, Fabiana Dal Pozzo & C. Saegerman
Q fever is a zoonotic bacterial infection caused by *Coxiella burnetii* and widespread in Wallonia. The diagnosis of this disease is difficult and recommendations were issued by EFSA in terms of sampling to assess an individual diagnosis. These recommendations are based on expert opinion. In dairy herds, the access to bulk tank milk is a collection of common choice, inexpensive and reliable for the diagnosis at herd level. In the absence of bulk tank milk as in suckling herds, an alternative option could be the random sampling of 20 animals in the productive herd (adult animals) to reduce both the costs of sampling and analysis without decreasing the intrinsic properties of the diagnostic procedure. This procedure has been tested in 226 Walloon dairy herds randomly selected, for which the bulk tank milk was available together with a random serological sample of 20 animals over 24 months.

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Antimicrobial resistance of *Streptococcus agalactiae* and *Staphylococcus aureus* strains isolated from bovine milk over the period 2009-2011 in the Aosta Valley region (Italy)

L. Domenis, Maria Sylvia Gennero, Nicoletta Vitale, Laura Chiavacci, Raffaella Barbero, Daniela Dezzutto & Stefania Bergagna

As part of the bovine mastitis control program conducted in the Aosta Valley Region (Italy) in the period 2009-2011, 574 strains of *Streptococcus agalactiae* and 933 strains of *Staphylococcus aureus* were isolated. All strains were analysed for antimicrobial susceptibility by the Kirby-Bauer method, based on the evaluation of the inhibition zones around the following compounds: amoxicillin, amoxicillin and clavulanic acid, ampicillin, cephalexin, cephalothin, cefoperazone, cefuroxime, cloxacillin, enrofloxacin, neomycin, cloxacillin, penicillin, spiramycin, streptomycin, tetracycline and thiamphenicol. For *Streptococcus agalactiae* the most significant resistance (> 10 % of not-sensitive strains) concerned cloxacillin (54.6 %), neomycin (81.4 %) and tetracycline (25.5 %), while for *Staphylococcus aureus* it concerned amoxicillin (41.7 %), amoxicillin and clavulanic acid (40.2 %), ampicillin (41.8 %), penicillin (41.4 %), cloxacillin (42.6 %), tetracycline (13.9 %) and cefoperazone (15.2 %). Given the high levels of resistance against beta-lactam antibiotics and - through these - especially natural and semi-synthetic penicillin's (or rather the molecules most frequently indicated for the pharmacological treatment of mammary infections), regular monitoring of the susceptibility of udder pathogens bacteria to this category of antimicrobials appears essential for success of a mastitis control program in the geographical area considered by our study.

Prevention of bovine leptospirosis: implications of each serogroup among cattle herds

Florence Ayran, Dominique J. Bicout, M. Artois & A. Kodjo

Bovine leptospirosis is a bacterial disease altering the economic performances of cattle herds. To enhance the prevention of leptospirosis a good knowledge of circulating serogroups, as being the serological and antigenic sub-division of pathogenic Leptospira, is required. A retrospective survey based on Micro-agglutination Tests (MAT) performed at the « *Laboratoire des Leptospires* » from 2008 to 2011 has identified 394 herds infected by the following serogroups Autumnalis, Australis, Grippotyphosa, Icterohaemorrhagiae and Sejroe. The five serogroups had 31 potential combinations which stand for potential infection patterns in cattle herds. Each MAT result corresponded to a given combination and defined the potentially circulating serogroups in the infected herds. Most of infected herds (57 %, n = 225/394) had a single infection pattern from which Australis was the predominant serogroup (51 %, n = 115/225) followed by Sejroe (25 %, n = 57/225) and Grippotyphosa (21 %, n = 45/225). The Probability of Presence Indices (PPI) was defined according to the distribution of the average titres associated to the serogroups involved. The analysis of the multi-infection pattern including Sejroe and Australis revealed that the PPI related to Sejroe were higher and suggested its greater involvement in the concerned herds; thus, the PPI would be useful to consider the implications of each serogroup among cattle herds with leptospirosis suspicious signs.

PAPER

The concept of reservoir in transmissible diseases

B. Toma, Barbara Dufour & P. Dorchies

For each transmissible disease, one reservoir exists. It can be defined as "an entity which, under natural conditions, ensures the preservation of the causative agent as a species and its availability to receptive subjects". This article reviews papers on the subject published in the last decade and offers comments on that definition. Based on a number of examples in human

and animal diseases, the diversity of potential situations is illustrated. For certain diseases, primarily those affecting a single species, the reservoir concept is relatively easy to grasp. By contrast, for many others, particularly those affecting numerous hosts, it becomes more complex since one has to consider the distribution in time and space, as well as the presence and density of receptive hosts. The proper understanding of the components in such a complex reservoir is critical to decide on appropriate control measures.