

## 2008 - Issue 53, Abstracts

### AEEMA MEETING, MAY 23<sup>th</sup>, 2008

#### **Proposal of a multiblock factorial analysis for data treating in animal epidemiology**

Stéphanie Bougeard, E. M. Qannari, M. Hanafi, F. Madec & N. Rose

The analysis of animal epidemiological surveys is usually performed using methods related to generalize linear models. But some difficulties arise regarding the use of these models due to the nature of the data collected. The first limitation is that all the explanatory variables cannot be included in the model. The second limitation is the multicollinearity among the explanatory variables, which is likely to lead to a non-relevant and unstable model. The third limitation is that explanatory variables are organized in meaningful blocks. It seems of importance to assess which blocks of explanatory variables are good predictors of the disease. The last limitation for the use of generalized linear models is that the expression of the animal disease is often described by several variables. In order to circumvent these difficulties, we propose a new method in the field of multi-block factorial method. Multi-block redundancy analysis is a method to be used for the purpose of exploring and modelling the relationships of a set of several data tables, where we wish to predict a dataset (the disease) from several other datasets. The interest of the method is illustrated on the basis of a cross-sectional study in the field of veterinary epidemiology, which was carried out in order to assess the risk factors for seroprevalence of porcine circovirus type-2 in a pig population.

#### **Risk factors associated with Salmonella prevalence in breeding and fattening and in only fattening herds**

Isabelle Corrégé, Florence Barbot, Anne Hémonic & J-L. Pinsard

The aim of this study was to identify and evaluate the risk factors linked to the prevalence of Salmonella infections in slaughter pigs. The Salmonella serological status was determined in 123 farms. On the farms, inquiries were made to collect information on potential risk factors. The statistical analysis was based on a logistic regression model. Sow batch mixing at the farrowing stage and failure to apply an in all in - all out system in fattening rooms were associated with higher seroprevalence in. For animals in quarantine lack of acclimatization to the digestive microbiology of the herd and absence of anti-parasite protocol had a negative impact. Two further risk factors associated with the level of hygiene were identified, the occurrence of diarrhoea in the farrowing rooms and the lack of systematic antibiotic treatment in young piglets. Conversely, a high hygienic quality of water and the strict observance of cleaning and disinfecting protocols were associated with lower prevalence levels. The number of fattening pigs per pen was also associated with positive Salmonella status.

#### **Estimation of PCV-2 transmission rate parameter derived from experimental data**

M. Andraud, Béatrice Grasland, B. Durand, R. Cariolet, A. Jestin, F. Madec & N. Rose

The instantaneous transmission rate, defined as the mean number of new infections produced by a single infective animal per time unit, is a key factor in epidemiological model transmission. It can be assessed by experimental studies under a fully controlled environment much better

than in field studies. The experimental transmission trial reported in this study made it possible to estimate the instantaneous transmission rate parameter in PCV-2 inoculated pigs in terms of time elapsed since inoculation.

### **Surveillance of West Nile Virus in France. Seven years of monitoring in wild birds**

J. Hars, Marion Mortamais, Jennifer Pradel, P. Auge, Elsa Jourdain, D. Chavernac, J. Languille & H. Zeller

West Nile fever is a mosquito-borne viral disease including wild birds as amplifying hosts, and humans and horses as sensitive hosts (accidental victims). West Nile virus (WNV) emerged in southern France (Camargue) in 2000 affecting only horses. Shortly after that outbreak, the French game and wildlife agency (ONCFS) conducted a serological study in 5 bird species and found low seroprevalence in mallards (8%) and magpies (22%). A long-term epidemiological surveillance program, based on the detection of abnormal mortality in wild birds (SAGIR network) and on serological monitoring of sentinel birds from 30 sites distributed along the Mediterranean coast, was established in 2001. No abnormal mortality due to WNV was reported in the avifauna but WNV was isolated from a European magpie (*Pica pica*) and a House sparrow (*Passer domesticus*). Seroconversions were detected in sentinel birds in Camargue, particularly in 2004 prior to the emergence of 32 equine cases. These results illustrate the importance of monitoring WNV circulation in birds as an early warning system.

### **Modélisation of *Ixodes ricinus* population dynamics: influence of hosts migration**

T. Hoch, Y. Monnet & A. Agoulon

Ticks play a major role in the spread of vector-borne diseases since they can transmit various pathogens (viruses, bacteria, protozoa) potentially harmful to animals and/or humans. Epidemiological modelling is a powerful tool to evaluate strategies of disease control. For vector-borne diseases, it requires to first develop a model of the vector's population dynamics, in our case that of the tick *Ixodes ricinus*. This work presents a model that makes it possible to simulate the cycle of the tick depending on biotic (host density) or abiotic (temperature) factors. This model was applied to various habitats (woodland and meadows, separated by an ecotone) between which hosts migrate. The results show a realistic simulation of changes in tick density. Furthermore, the results from the multi-habitat model underline the strong influence of host migration between habitats. Woodland appears as a source of ticks for the meadows, which in turn can be considered as a sink. The spread of pathogens is to be included in this model in the future.

### **Detection of *Neospora caninum* DNA by PCR analysis in bovine aborted fetuses**

Maria Silvia Gennero, Stefania Bergagna, M. Pasino, A. Romano, D. Grande, Anna Trisciuglio & E. Ferroglio

Neosporosis is a common infection in cattle and is a major cause of abortions worldwide. *Neospora caninum* abortions have been reported in both dairy and beef cattle. We evaluated the presence of this protozoal parasite in aborted fetuses by mean of PCR analysis in herds of the Piedmont Region (Italy). Subsequently, we compared these results with those obtained by serodiagnosis in order to establish a correlation with seroprevalence. PCR analysis was carried out on tissues from 71 aborted fetuses (liver, muscle, kidney, head)

collected from 34 selected herds with a prior history of abortion problems and seropositivity for *N. caninum*. Seroprevalence in pregnant beef cattle was higher than in dairy cattle, but, in the latter, we found a higher prevalence of positive aborted fetuses at PCR analysis. This study confirms that *N. caninum* is an important cause of abortion and that DNA detection by PCR analysis is a valid tool for diagnosis of *N. caninum* infection in aborted fetuses.

### **Infection of pigs' batches by five bacterial food-borne zoonotic hazards: variability on farm and at slaughter**

J. Fosse, N. Oudot, M. Laroche, A. Rossero, H. Seegers & Catherine Magras

The Hygiene Package requires a flow of sanitary information from the farms to the slaughterhouse. Among information of interest, the status of contamination of pigs by thermo-tolerant *Campylobacter* spp., *Clostridium perfringens*, *Listeria monocytogenes*, *Salmonella enterica* and *Yersinia enterocolitica* may be considered. This status was characterized for 19 batches from 8 herds slaughtered in 3 different slaughterhouses. On the farms, the status of infection was assessed batch by batch, by bacteriological analysis of pooled fresh faeces. At the slaughterhouses, a bacteriological analysis was made on pooled samples of rectal contents, on meat and tonsils. Significant statistical differences were observed for prevalence in faeces from farm to slaughterhouse and for carcasses from slaughterhouse to slaughterhouse. The status of contamination of carcasses could be explained by the status of infection of slaughtered pigs combined with the level of hygiene control at the slaughterhouse.

### **Multiple imputation of missing data for survey data analysis**

Coralie Lupo, Sophie Le Bouquin, Virginie Michel, P. Colin & Claire Chauvin

Typical management of missing data consists in excluding incomplete observations from the statistical analysis -list-wise deletion- which limits its statistical power. A selection bias can also occur if the sample analysed is no longer representative of the initial sample. Another approach to handling missing data is reviewed. Multiple imputation of missing data allows to keep all data information and to conduct the analysis without loss of power or introduction of bias. An example of application of this method is given with the analysis of risk markers for chicken carcass condemnation at the slaughterhouse.

### **Contribution of the Age-Period-Cohort model to the study of Bovine spongiform encephalopathy in France: trend of the prevalence during 2001-2007 period**

Carole Sala, E. Morignat & D. Calavas

The aim of the Age-Period-Cohort (APC) model is to identify the specific effects of age, birth cohort and period on the trend of a measure or phenomenon over a period of time. However, due to the linear relationship linking the three variables, the model does not fit when age, cohort and period are included simultaneously in the model. Without further assumptions on the specific effect of the variables, the model cannot identify the respective effects of each individual factor. In our study, based on data from the exhaustive BSE surveillance program, we can formulate hypotheses to constrain certain parameters and identify the model. Then, the APC model is a relevant method to study the trend in BSE prevalence and to address the evolution of the disease in relation to the successive control measures adopted in France.

Moreover, the model allows to study other variables after adjustment for the main risk factors for BSE that are age at diagnosis, birth cohort of the animals and observation period.

### **Bluetongue surveillance in Switzerland in relation with risk**

Sara Schärer, Valérie Chaignat, H. Schwermer, Daniela Hadorn, F. Schaffner & E. Breidenbach  
Owing to the spread of bluetongue in the Mediterranean region, Switzerland set up an early warning system in 2003. With the appearance of BTV-8 in Central Europe in 2006, the country was threatened from both north and south, so that the surveillance system was extended to the whole country. The surveillance programme comprises serological monitoring of bovine milk in risk areas, increased clinical monitoring of all susceptible farm animals and monitoring of vector activity. Thanks to the information given to animal owners and veterinarians, the first clinical cases were promptly diagnosed. Sentinel surveillance with serological monitoring of milk has also proved a suitable way to detect outbreaks in the absence of clinical symptoms.

### **Are populations of *Culex modestus*, a major West Nile virus vector in the Camargue region, increasing in the Dombes region?**

Jennifer Pradel, T. Martin, Delphine Rey, R. Foussadier & D.J. Bicout

The West Nile (WN) virus emerged in 2000 in the Rhone Delta in the South of France, and has since regularly been found along the Mediterranean coastline. Although there is no evidence of spread of the WN virus spreading in France it seemed interesting to study one of the main vectors of WN in France, in the Dombes region: *Culex modestus* (Ficalbi). Indeed, this area may be considered at risk of WN virus introduction since (1) it is located along one of the major bird migration routes, (2) it is situated about 300 km north of the Camargue region and iii/ it has hundreds of fish farming ponds which attract many migratory birds, putative carriers of arboviruses like the WN virus. This article reports an entomological study carried out in 2007 on 39 ponds that harbour *Cx. modestus* larval habitats. The main objective of this study was to estimate *Cx. modestus* distribution in the Dombes and to compare it with that in the 1970's. Results show that this species is very common (present in more than 80% of ponds) whereas it seemed much less frequent about 30 years earlier when it was found in fewer than 25% of ponds. We discuss this difference and its cause: is it yearly variations or does it reflect a significant change in population? This study is part of a wider framework observing the bio-ecology of other supposed vectors of arboviruses whose larval habitats are also found in ponds and identifying factors determining their presence.

### **Seroprevalence of *Mycobacterium avium paratuberculosis* infection in French goat herds: preliminary results**

Pascale Mercier, C. Baudry, F. Beaudeau, H. Seegers & X. Malher

A survey was conducted to estimate the prevalence of *Mycobacterium avium paratuberculosis* (Map) infection in goat herds in France. All the animals older than 6 months (n= 9420) from 80 goat-herds were tested using an absorbed ELISA. The apparent and true prevalence have been respectively measured and estimated both at herd and individual levels. The within-herd prevalence was also estimated. The true prevalence at herd level was estimated at 57%, while the individual true prevalence was estimated at 5.6% with 95% CI = [5.1 - 6.0] in the study population. The true within-herd prevalence was 11.29 +/-7.66%. Nearly

half of the infected herds had a true within-herd prevalence higher than 10%. Despite the lack of data from one important area (Rhône-Alpes), the results of this survey showed that infection by Map is widespread in French goat herds and provide the first epidemiological descriptive data necessary to the implementation for any control program against this disease.

**Role of wild boar (*Sus scrofa*) in the epidemiology of bovine tuberculosis (*Mycobacterium bovis*) in the Brotonne forest (Normandy, France) - Results of the 2006-2007 epidemiological survey**

Stéphanie Maeder, J. Hars, T. Rambaud, Yvette Game & Marie-Laure Boschioli

In 2001, while France was declared officially free from bovine TB, the first case of *M. bovis* infection in free-living wild ungulates was found in the Brotonne forest (Normandy). Subsequent epidemiological surveys showed a high prevalence of TB infection and the presence in wild boars (*Sus scrofa*) of a *M. bovis* strain of the same genotype as that of strains isolated from infected cattle in neighbouring areas. As infection is often asymptomatic, diagnostic is obtained by bacterial culture of lymph nodes. In 2006-2007,  $28.6\% \pm 5\%$  of wild boar showed tuberculosis lesions, mostly calcified (83.6%), and 78% were located in retropharyngeal lymph nodes. The high prevalence of infection ( $31\% \pm 5.7\%$ ) reveals that the measures that have been taken since 2001 were not efficient enough to control tuberculosis in this species. It is not only necessary to continue the surveillance of tuberculosis in wild ungulates in the Brotonne forest but also in other regions where bovine TB is not eradicated yet.