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A stochastic individual-based model representing population dynamics in a farrow-to-finish pig farm in order to assess the "sow effect" on an infectious process

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The proposed model is a stochastic individual-based model representing population dynamics in a farrow-to-finish pig farm managed according to a batch-farrowing procedure. Individual representation of the piglets and of their natural or nursing dams (cross-fostering) will permit to assess the sow-effect on piglet's health status during infectious processes. Stochasticity is taken into account for reproduction (abortions, oestrus detection or insemination failure), mortality and culling through age-dependant probabilities previously defined by the user. Decision rules are based on Monte-Carlo simulations. Effects of modifications in management strategies on herd ageing and herd productivity are also assessed. The model was validated by comparing model outputs with actual farm situations and data from the literature

Changes over two years in the *Salmonella* serological status of pig farms with low and high prevalence

Isabelle Corrégé & F. Guyomard

The serological Salmonella status of eight pig farms, four with a high prevalence and four with a low prevalence at the beginning of the study, was recorded for approximately two years. Eleven batches per farm were examined during that period and 20 animals per batch were sampled. Substantial changes in serological status were observed in most farms. However, farms with a very good status at the start appeared more stable. The Salmonella status changed in four farms during the study period. No relationship could be established between the Salmonella status in a given farm and potential risk factors that were examined. In the four farms where a definite change occurred, no changes in practice were identified that could account for the changes in Salmonella status.

Factors associated with *Salmonella enterica* contamination following cleaning and disinfection procedures in pig finishing farms

Christelle Fablet, Corinne Robinault, J-P. Jolly, F. Eono, Virginie Dorenlor, Annie Labbé, P. Fravalo & F. Madec

A study was carried out between April 2003 and September 2005 in 66 French finishing pig farms to identify risk factors for residual contamination by Salmonella following routine cleaning and disinfection and prior to restocking. The *Salmonella* status of the rooms was assessed through the use of sterile gauze swabs rubbed against the wall, the pen partitions and 1 m² of the floor in each pen. The samples were tested bacteriologically for *Salmonella* identification in a conventional four step protocol. After taking samples, a special form was completed by the investigator to record the cleanliness of the pen and the characteristics of the facilities. A questionnaire was filled with the farmer to collect data on the hygiene procedures and on the events which occurred in the farm between disinfection and the sampling day. Logistic regression was used to assess the relationships between the hygiene routine, the characteristics of the facilities and their cleanliness and the Salmonella status of the farm after cleaning and disinfection practices and prior to introduction of new stock. The lack of slurry removal during the cleaning procedure increased the risk of residual contamination by *Salmonella*. The chances of finding *Salmonella* after routine cleaning and disinfection was increased if the wall surface was very rough and if the farm workers entered the stalls during the down period.

Mycobacteriosis in wild boar: Results of 2000-2006 activity in North-Western Italy

A. Dondo, Simona Zoppi, Fransesca Rossi, Laura Chiavacci, A. Barbaro, Annalisa Garonne, A. Benedetto & Maria Gloria

This work reports the results of our investigation on the presence of *Mycobacteria* in wild boar shot down in Piedmont, Liguria and the Aosta Valley between 2000 and 2006. 1254 submandibular lymph nodes were collected to detect *Mycobacterium spp.*; suspected colonies were identified and typed by molecular methods (Multiplex PCR, RD Region analysis, Variable Number Tandem Repeats, Spoligotyping). Most strains of *M. bovis* were isolated in the Liguria region, while in the Piedmont region *M. bovis* was found to be sporadic. Wild boars may also be infected by other Mycobacteria, *e.g. M. microti*, presumably by eating infected dead small rodents. In view of their rooting behaviour, wild boars are exposed to infection by various species of Mycobacteria other than *M. tb* complex.

Correlation between *Yersinia spp.* from faeces and *Brucella suis* infection in wild boar

Carla Grattarola, Maria Silvia Gennero, Stefania Bergagna, Simona Zoppi, Laura Chiavacci & A. Dondo

379 wild boar faeces samples were collected from July 2005 to June 2006 and tested to detect *Yersinia spp.*. The same animals were submitted to bacteriological and serological tests to detect Brucella infection. 62 *Yersinia spp.* strains were isolated. Out of them, 31 were identified as *Y. enterocolitica*. The Chi2 test has showed neither correlation between *Yersinia spp.* and serological tests (X2 = 0.009, p=0.97) nor between *Yersinia spp.* and *Brucella suis* isolation (X2 = 0.03, p=0.87). Contrary to what occurs in cattle, seropositivity in naturally infected wild boars may reflect infection by *Brucella suis* rather than by *Yersinia spp.*.

Epidemiology of scrapie in Italy

Maria Cristina Bona, Maria Caramelli, A. Maroni Ponti, Cristiana Maurella, R. Nonno, Alice Zaira Perazzini, Rosaria Possidente & G. Ru

Scrapie is a rare, fatal neurological disease of sheep and goats, belonging to the group of animal Transmissible Spongiform Encephalopathies (TSEs). A substantial increase in the number of diagnosed conventional scrapie cases was recorded following the implementation of an active surveillance programme for scrapie in sheep and goats in the EU. With the improvement of the PrPSc detection techniques, some cases of scrapie, with unusual features, therefore called atypical scrapie cases, were found in Italy. The first case of atypical scrapie was detected in May 2005. The purpose of our forms of the disease in Italy is based on data from outbreaks reported during the period 2005- 2006.

Use of Bayesian methods to compare the characteristics of two diagnostic tests for detection of infection with Map

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Pascale Mercier, C. Baudry, Jennifer Martin, Claire Bertin, Karine Laroucau, F. Beaudeau, H. Seegers & X. Malher

Two latent class models [maximum likelihood (ML) methods and Bayesian inference (BI)] were used to estimate the sensitivity (Se) and the specificity (Sp) of a serum ELISA test and of faecal culture in the detection of infection with Map in French dairy goats. Samples of blood and faeces were collected from 532 goats in 15 herds. Estimates according to ML and BI methods were compared. The more accurate of the two tests was found to be the BI (WinBUGS) model with informative priors. The Se and Sp of the ELISA were estimated to be 34% and 99% respectively. For faecal culture, the Se was 53% and the Sp was 100%.

Serological survey for *Neospora caninum* in cattle from the Piedmont Region (North West of Italy)

Maria Silvia Gennero, Stefania Bergagna, M. Pasino, A. Barboro, A. Romano & Anna Trisciuoglio

We report the results of three years of serological testing for *Neospora caninum* in dairy, beef and mixed production aptitude bovine herds from the whole Piedmont Region (Northwest of Italy). Serum samples, sent by large animal veterinary practitioners from herds with a history of abortions, were tested for the presence of antibodies to *N. caninum* detected by a commercially available ELISA-kit for bovine serum utilising a whole tachyzoite lysate (HerdCheck1 Anti-Neospora; IDEXX laboratories). A total of 3 749 bovine blood sera were tested. 1 114 (29.7%) tested positive. The overall seroprevalence (at least one animal found positive) on 198 different herds tested was 67.7%. It was higher in beef cattle than in dairy cattle herds.

Sensitivity of *Salmonella spp.* detection in laying-hen houses depending on the number of samples

Aurélie Mahé, Stéphanie Bougeard, Adeline Huneau-Salaün, Sophie Le Bouquin, Isabelle Petetin, Sandra Rouxel, Françoise Lalande, P-A. Beloeil & N. Rose

The prevalence of flocks infected by *Salmonella spp.* was estimated in French laying-hen farms from October, 1st 2004 to September 30th 2005 as part of a European Union-wide baseline study to define targets for Salmonella reduction in member states. The sampling scheme prescribed and financed by the European Commission to detect *Salmonella* in laying-hen flocks was based on 2 dust-samples and 5 faeces-samples per farm. A latent-class Bayesian approach for correlated tests was used to estimate the sensitivity of detection of reduced sampling schemes corresponding to the 16 combinations of 2 dust- and 5 faeces-samples. For each model the full sampling scheme (7 samples) and the reduced protocol were considered as two correlated tests, the biological principle being identical. As the apparent prevalence observed in cage flocks (30.7%) was higher than in other systems (barns, outdoor, or organic) (8.2%) these two sub-populations were considered separately. Bayesian estimation of posterior distributions for prevalence and sensitivity indicated that at least 5 samples, including 2 dust samples were necessary to attain sensitivity levels comparable to the full sampling scheme. In alternative flocks at least 6 samples were required to ensure a good estimation of prevalence. Detection sensitivity was improved by increasing the number of dust samples in cage farms and by increasing the total number of samples of any type in alternative farms.

Ecological study of mosquitoes *(Diptera-Culicidae)* - as potential vectors of arbovirus infections in the Rhône-Alpes region (France)

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

Although no important mosquito borne arbovirus has been reported circulating in the Rhône-Alpes region (South-Eastern France) current and forthcoming environmental changes in the climate may promote the invasion of arboviruses in this region by inducing modifications in mosquito populations. The inventory of indigenous mosquito species identified about forty species whose relevance for public health is unknown but also several species known to be involved in transmission of viruses in other European countries. With the aim to focus studies on few interesting species, we have designed a classification system based on various biological criteria including habitat characteristics for *Culicidae* in this region. We drew thus a list of potentially interesting mosquito species each of which is a leading member of a classification group. The preliminary results reported in this paper fit into a more global framework designed to determine the role of environmental factors on vector populations and to define entomological markers of environmental changes.

A simulation model for the risk of infection of birds from avian influenza virus contaminated ponds

Magalie René & D. J. Bicout

Avian influenza is a worldwide distributed infectious disease caused by type A Influenza viruses that involves waterfowls as natural hosts. These viruses are classified as Low Pathogen (LP) and High Pathogen (HP) avian Influenza viruses according to their experimental pathogenicity in chicken. Recent geographical spread of H5N1 HP avian Influenza virus and the repeated bird-to-human direct transmissions rekindle the spectre of great pandemics. Although faecal-oral transmission of avian Influenza viruses via contaminated water is now a recognized mechanism for transmission within the wild waterfowl population, little is known about the persistence of these viruses in such a medium. The purpose of this study is to develop a simulation model of maintenance and persistence mechanisms of Influenza A viruses in an ecosystem consisting of a wild duck population plus a pond in order to assess the risk of contamination that the water of infected ponds represents for wild and domestic birds. Amplification of viruses in the bird population was modelled using a SEIR compartmental model and the survival of viruses in the water using the kinetics of depletion. Parameters of the model were determined based on an exhaustive review of the literature. Results of various simulations, applied to the environmental conditions of the Dombes area in Eastern France, lead us to conclude that the risk of infection for birds from contaminated water is high for LP avian Influenza viruses, and that the persistence of LP viruses in the ecosystem is highly likely under certain conditions of bird density and renewal rate of susceptible populations. Regarding HP avian Influenza viruses, the risk of infection for birds from contaminated water is rather low and the persistence of viruses is unlikely except under exceptional conditions.

However, these results are still preliminary because of constant and unpredictable changes in HP viruses.

Development of a statistical method for detecting emergent events: Application to the French National Occupational Disease Surveillance and Prevention Network (RNV3P)

Laurie Faisandier, V. Bonneterre, R. De Gaudemaris & D. J. Bicout

Introduction: Monitoring of health risks takes an important place in the field of the environment / health. In France, since 2001, 30 consultation centres for occupational diseases record in a systematic and standardised way all occupational health problems in the National Occupational Disease Surveillance and Prevention Network (RNV3P).

Objective: The aim of this work is to develop and test using RNV3P, a method designed to identify and describe various groups of "pathological cases" (in this instance disease / occupational nuisance combinations) with their time dynamics, for purposes of vigilance and detection of emerging combinations.

Method: This method identifies various disease/occupational nuisance combinations, their incidence and connects combinations sharing at least one exposure in common. We named exposome such a network of disease cases. The projection or comparison of these exposomes at different times allow both to follow the time dynamics of disease cases observed earlier but also to single out new disease cases never observed before.

Results: As an illustration, the method was applied to "systemic sclerosis". The groups of disease cases identified in 2002-2005 data were reported and compared with the 2006 exposome.

Conclusion: This new method of characterizing data appears very promising to optimise the analysis of databases in the field.

Study on *Salmonella* contamination in pork sausages chain by PFGE analysis

Daniela Manila Bianchi, Laura Chiavacci, A. Barbaro, Fransesca Rubinetti, Silvia Gallina, Daniele Nucera, Sara Lomonaco & Lucia Decastelli

The presence of *Salmonella spp*. in food may result from accidental contamination at any step in the food-production chain. This study was carried out in order to evaluate the relationship between Salmonella strains isolated in pig farms, slaughterhouses and sausage making plants. From April 2005 until November 2005, 22 strains of *Salmonella spp.* were isolated and subtyped by PFGE to evaluate their genetic relationship and to determine the phases in the production chain where contamination occurred. Our study with this approach made it possible to detect where in the food production chain *Salmonella* contamination of two sausage samples occurred.

Contribution of infra-community scale mapping (IRIS) to the epidemiological supervision of lung cancer

Alexandra Senkowski, M. Colonna & D. J. Bicout

The mapping of a cancer atlas for the Grenoble urban area in South Eastern France demonstrated spatial heterogeneities in the incidence of lung cancer among males in the area. Our study was designed to make use of a novel finer spatial scale (‘IRIS’) to determine whether variations in spatial distribution were not obscuring intra-community spatial variations that had remained unnoticed. Statistically significant excesses and lack of cases amounting to 30%-40% approximately compared with the rest of the urban area of Grenoble were recorded thanks to a Bayesian smoothing approach. The median income per consumption unit appeared to be the most discriminating variable characterizing the population studied.

Bluetongue serotype 8 in North Europe in 2006

E. Bréard, Corinne Sailleau, Catherine Cetre-Sossah, Kamila Gorna, Colette Grillet, Céline Bahuon, G. Gerbier, E. Albina & S. Zientara

In 2006, in an unexpected way, the bluetongue (serotype 8) appeared in Belgium. Subsequently, the disease was detected in Germany, the Netherlands, in France and in Luxemburg. In France, only 30 animals, located on the border with Belgium, have been infected. This epizootic disease was characterized by the existence of clinical signs on cattle. The serotype 8 (origin of which remains unknown) being the only one of the 24 serotypes to induce clinical signs on cattle. Further to this epizootic disease, surveillance was carried out during winter 2006. In July 2007, in the absence of vaccination, the only way of an effective fight against BTV, a second epizootic disease began in the North of Europe.

EPIDEMIOLOGIC INFORMATION

Bluetongue serotype 8 epidemic in North-Western Europe in 2007

Morgane Dominguez & Anne-Marie Hattenberger

A bluetongue serotype 8 epidemic occurred in north-western Europe in 2006. A resurgence has begun in July 2007. At the beginning of October 2007, a descriptive analysis of the outbreak in the six affected countries shows that the incidence is much higher than it was in 2006. In France, weekly incidence and geographical extent are continuously increasing. All the factors responsible for the extent of this outbreak have not been identified yet but the lack of means control is one of them.