26e studiedag van de VEEC

Management of Animal Health and Welfare

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Wageningen UR
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Droevendaalsteeg 2, Gebouw 102
6708 PB Wageningen
PREFACE

Welcome to the 26th Annual Meeting of the VEEC, the Dutch Society for Veterinary Epidemiology and Economics. We thank Wageningen University for hosting our meeting this year.

Veterinary epidemiology has become an established discipline over the last 25 years as did animal health economics. We now see sub specialties such as infectious disease epidemiology, risk analysis, clinical epidemiology, often integrated with animal health economics. The unifying factor remains a focus on quantification of processes in the population, either based on data analysis, simulation models or mathematical abstractions of the real world. This variable background is visible in the membership of the VEEC and the presentations today.

For this year’s Annual Meeting we chose a rather operational topic: Management of Animal Health and Welfare.

We believe that management of Animal Health and Welfare is an important challenge for veterinarians, animal scientists and animal owners. Society expects healthy animal products originating from healthy and happy animals, preferably at a low cost. In addition, health and welfare of non-production animals may be impaired by ‘lifestyle’ management (obesity) or genetics. A quantitative approach may support any management process, hence work for veterinary epidemiologists and economists. For example, health and welfare can be monitored to ‘prove’ that everything is under control or to show ‘improvements’ over time. Management may aim at short or long term improvements, where the investments are valued differently.

Our invited speakers will illustrate various quantitative aspects of management of Animal Health and Welfare this morning, in different animals. We hope their presentations will lead to fruitful discussions during this VEEC. In the afternoon, a wide variety of current research subjects will be presented in shorter presentation. Finally we invite all VEEC members to our (short) Annual General Meeting (AGM) at the end of the day.

We hope you will enjoy the meeting today, both the scientific content as well as the possibility to meet up with each other.

Mirjam Nielen,
President VEEC
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PROGRAM

9.10 Opening

9.15 Economics of animal health management
   Henk Hogeveen (Wageningen UR, Social Sciences Group, Business Economics)

10.00 Salmonella and mycoplasma management on dairy farms, a generic approach
    Liza Rozenbaum Nielsen (University Of Copenhagen, Large Animal Sciences)

10.45 Break

11.15 Management of health and welfare in animal shelters
    Ruth Van Der Leij (UU, Companion Animals)

11.45 Breeding "happy chickens"
    Bas Rodenburg (Wageningen UR, Animal Sciences Group, Behavioral Ecology)

12.15 Management and prevention of respiratory disease in pigs
    Tijs Tobias / Victor Geurts (UU, Farm Animal Health / MSD)

13.00 Lunch

14.00 Efficiency of measures for sow husbandry in terms of their effect on farm income, animal welfare and citizen’s attitudes
    Tamara Bergstra (Wageningen UR, Social Sciences Group, Business Economics)

14.20 Alfatoxins in maize feed and the dairy production chain
    Ine Van Der Fels-Klerx (Wageningen UR, RIKILT)

14.40 Estimating clinical mastitis incidence based on routinely available farm data
    Inge Santman-Berends (GD Animal Health Service)

15.00 European organic dairy farmers preference for animal health management within the farm management system
    Felix J.S. Van Soest (Wageningen UR, Social Sciences Group, Business Economics)

15.20 Break

15.50 Effectiveness of risk-based testing of imported animals for bovine tuberculosis in the Netherlands
    Clazien J. De Vos (Wageningen UR, CVI)

16.10 Two years after the schmallenberg virus epidemic: does the virus still circulate?
    Anouk Veldhuis (GD Animal Health Service)

16.30 The influence of farm size on the transmission risks of classical swine fever in the Netherlands
    Thomas Hagenaars (Wageningen UR, CVI)
EFFICIENCY OF MEASURES FOR SOW HUSBANDRY IN TERMS OF THEIR EFFECT ON FARM INCOME, ANIMAL WELFARE AND CITIZENS’ ATTITUDES


*corresponding author: tamarabergstra@hotmail.com

In response to citizens’ concerns about animal welfare in pig husbandry, the pig sector introduced measures to improve animal welfare that focus on single rather than multiple dimensions of animal welfare concerns without accounting for their impact on citizens’ attitudes. These measures failed to improve citizens’ attitudes toward pig husbandry. The present study uses a more comprehensive approach by evaluating animal welfare measures in terms of their effect on animal welfare, farm income and citizens’ attitudes. Four measures were defined for each of the following issues of sow husbandry: piglet mortality, tail biting and indoor housing of gestating sows. A simulation model was developed to estimate the measure effects and Data Envelopment Analysis was used to compare measures in terms of their effects on both animal welfare, net farm income and citizens’ attitudes. The measures for piglet mortality were the only measures with a positive effect on farm income but had a relatively low effect on animal welfare and citizens’ attitudes. The most efficient measure was the measure that included straw provision, daylight and increased group sizes for gestating sows. The level of improvement of a measure on animal welfare did not necessarily lead to the same relative improvement of citizens’ attitudes or the same relative decrease in farm income. This indicates that a single impact cannot predict the other impacts and that it is essential to use a more comprehensive approach for evaluating animal welfare measures.
In the last decennia, aflatoxin contamination of maize grown in Europe is of increasing importance, amongst others, due to climate change effects. Contamination of maize with this mycotoxin may result into high economic impacts on the feed and food production system, and into potential effects on human health. Understanding the formation and fate of aflatoxins in the maize production chain is necessary to adapt sampling, control, and monitoring such to reduce contamination in Europe. To this end, we have conducted an extensive literature search in the formation and fate of aflatoxins throughout the entire maize feed and dairy production chain.

Aflatoxins are genotoxic and carcinogenic mycotoxins, produced by fungi, in particular by the genus Aspergillus. The group of aflatoxins include the aflatoxins B1, B2, G1 and G2. Out of these four, aflatoxin B1 (AFB1) generally occurs in the highest concentration in maize, and the other three are often found in low concentrations in conjunction with high AFB1 concentrations. Several species of the Aspergillus genus can produce aflatoxins, in particular A. flavus and A. parasiticus. There is general consensus that A. flavus produces aflatoxins B1 and B2, whereas A. parasiticus produces all four aflatoxins B1, B2, G1 and G2. A. flavus is most frequently associated with aflatoxin contamination in maize.

AFB1 can be metabolized to aflatoxin M1 (AFM1) by dairy cows, which is also considered to be genotoxic and carcinogenic. Elevated concentrations of AFB1 in maize feed might result in elevated levels of AFM1 in milk and milk products. In Europe, regulations are in place setting limits to the presence of AFB1 and AFM1 in foodstuffs and feed materials (Regulation EC/1881/2006 and Directive 2002/32/EC).

Contamination of maize with AFB1 originates from the field, where Aspergillus flavus may infect the maize plants during crop cultivation, given conducive environmental conditions. Beside effects of local weather, like water temperature and relative humidity, agronomic conditions like crop variety are also relevant. A. flavus infection and AFB1 contamination of maize in the field is very local; distribution of contamination in the field is thus heterogenous. Conditions during harvest, processing and storage also influence AFB1 contamination of maize lots after harvest. Usually, the overall concentration of aflatoxins in maize lots is low. However, aflatoxin concentrations in individual kernels vary a lot, with extreme high concentrations in some kernels. In addition AFB1 contamination varies widely between individual maize lots. In literature, the largest range of contamination between lots was reported to be 6-1600 µg/kg among 100 samples of maize kernels at three different locations in Brazil. The wide range in AFB1 concentrations between kernels, and between maize lots, may cause serious health effects incidentally.

Maize is a commonly used feed material for dairy cows. Feed manufacturers produce feed by mixing and grinding maize and other feed materials. In recent decades, the maize consumption of dairy cows has increased due to the prices of raw materials and the enlargement of amounts of concentrated feeds in the diets. In the period 2010-2013, the use of maize in feed for cows in the Netherlands has increased from approximately 1 to 18%. These developments have possibly increased the exposure of dairy cows to AFB1 via maize consumption in the Netherlands.

During and after administration of AFB1 to cows, the concentration of AFM1 in milk changes. During AFB1 administration in feed, the concentration of AFM1 in milk increases rapidly, and can already be detected in 10
hours after AFB1 ingestion. A steady state of AFM1 excretion in the milk is reached at 24 h from initial AFB1 ingestion. Then, AFM1 declines to a zero concentration within 3-5 days after the diet of the cow was changed to an AFB1-free diet. In dairy cows, the amount of AFM1 excreted into milk can be in the range of about 0 to 6% of the AFB1 intake, depending of the milk yield and stage of lactation of the cow. Several studies found a higher carryover in cows with a higher milk yield and in early/mid-lactating cows. The carryover percentages varied, possibly due to differences between the metabolisms of the cows and/or the milk yield. A higher carry-over value can imply exceedance of the EC limit for AFM1 concentrations in milk and dairy products.

Thus, AFB1 in the maize feed and dairy production chain is become of increasing importance due to incidentally high contaminations in the maize, increased use of maize in the cow’s feed, and increased carryover of the toxin into the milk. Control of aflatoxin contamination should be done throughout the entire chain: by agronomic practices in the field (e.g. selection of crop variety, cropping system, use of insecticides, time of harvesting), monitoring of aflatoxin formation during maize growth and harvest, drying of maize kernels after harvesting (time, temperature), monitoring storage and distribution conditions (water activity, temperature), and monitoring aflatoxin concentrations before feed processing and after milking.

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ESTIMATING CLINICAL MASTITIS INCIDENCE BASED ON ROUTINELY AVAILABLE FARM DATA

I.M.G.A. Santman-Berends*, J. Keurentjes, J.M. Swinkels, G. van Schaik, GD Animal Health Service

*corresponding author: I.santman@gezondedieren.nl

Currently, udder health in the Netherlands is mainly monitored based on somatic cell count (SCC) of individual cows and bulk milk SCC. The number of cows with clinical mastitis is not objectively recorded and not centrally registered and is therefore not available for all dairy farms. However, clinical mastitis is an important indicator for animal health and welfare and of economic importance. Therefore, it can be a valuable indicator for dairy farmers, especially when the clinical mastitis incidence can be compared with a benchmark for all dairy herds.

The aim of this study was 1) to develop a model that was able to predict the clinical mastitis rate for all Dutch dairy farms with a conventional milking system and 2) to develop a model that was able to detect farms with a high clinical mastitis rate at the individual farm level.

In total randomly 240 dairy farms with a conventional milking system, that participated in the 4-6-weekly milk recording program of CRV, were selected and agreed to participate. Of these 240 farmers, 233 provided complete data on clinical mastitis in their herds, on a monthly basis, in 2013. Besides this information, standard available on farm data i.e. identification and registration records, data on antibiotic use, data on test day records, results of diagnostic tests on bulk milk samples and data on bulk milk SCC, were provided.

For each herd the clinical mastitis incidence per 100 cow days at risk (CMI) per quarter of the year was calculated. Where clinical mastitis was defined as a quarter with a visible alteration of the udder or the milk. The CMI was combined with all standard available on farm data at the quarter of the year level and two models were developed in attempt to predict the CMI for all dairy farms and for individual farms. To develop the models, records of 67% of the 233 farms were used. The remaining 33% of the herd records were used to validate the models. The model for all Dutch dairy farms aimed to predict the exact amount of CMI and the model for individual herds attempted to correctly classify whether a herd belonged to the 25% herds with the highest CMI or not.

The model that aimed at estimating the exact amount of CMI in all Dutch dairy farms, contained 11 explanatory variables. The model estimated a CMI of 32.5 cows in 2013 while the farmers registered a CMI of on average 33.4 cows and appeared to give an accurate estimate of the CMI on the 71 validation herds. The most important variables in the model were antibiotic use for treating clinical mastitis and the bulk milk SCC. The model that aimed at detecting individual herds that belonged to the 25% herds with the highest CMI, contained six explanatory variables and could correctly classify 77% of all herds at the quarter of the year level. In addition, after studying the observations that were not correctly classified by the model (model estimated a higher incidence than the farmer) it appeared that the farmer may have not observed and registered all cases of clinical mastitis. Most of these farms did have a higher than average bulk milk SCC and a higher than average subclinical mastitis incidence and thus may have possibly been classified correctly by the model.

In conclusion, models based on available on farm herd data give an accurate prediction of clinical mastitis incidence for all Dutch dairy farms and can detect individual dairy farms with a high CMI. With the models it is possible to periodically monitor CMI both at the herd and at the national level, which can motivate farmers to continuously improve udder health in their herds.
Organic animal production systems are no guarantee for good animal health. Moreover, consumers are becoming more critical towards animal health. The expectations held by consumers and the current animal health status of organic dairy farms are potentially not in line. This could result in organic dairy farmers losing part of the added value of the organic label. It is therefore vital that farmers improve animal health status on their farms. However farmers’ time capacities are limited. Excessive demands in one field of management may provoke conflicts with other fields. Farmers allocate resources to those management areas which are preferred most. Insight in these preferences could aid farm advisors to tailor their advice to the farmers’ specific preferences. The aim of our study was to investigate how animal health management is preferred within the farm management system when labour restrictions are relaxed and to investigate whether farmers could be grouped based on their preference for animal health management measures.

We used adaptive conjoint analysis (ACA) to elicit farmers’ preferences for five management areas: barn management, calf management, claw health management, pasture management and udder health management. Udder health and claw health were both representatives for animal health, the remaining three management areas represented potential conflicting management areas. Each management area constituted of three levels which represented potential measures which could improve the respective area. ACA was performed on 71 French, 60 German, 28 Spanish and 57 Swedish organic dairy farms, representing the variation of organic dairy farm development within the EU. Each farmer was asked, in four stages, how preferable implementation of one measure or package of measures was to him when labour restrictions were relaxed. The advantage of ACA is that farmers are faced with more real-life trade-off comparison questions. Individual preference scores for each management area, summing up to 100, were calculated with Hierarchical Bayes estimation. Consecutively, two cluster analyses were performed on the utility scores of the measures of udder health management and claw health management.

Results indicate that farmers differ greatly in their preference towards claw health and udder health management. In general, calf management was the most preferred area by farmers (preference score: 24.9) and claw health management was found to be least preferred (preference score: 17.3) the remaining areas barn (19.6), pasture (18.1) and, udder health (20.1) management were of intermediate interest. Cluster analysis on claw health measures and udder health measures resulted in respectively seven and nine distinct profiles. Results of the preference scores and cluster analysis suggest that European organic dairy farmers cannot be treated as a homogenous group. Farmers show a large variation in which management area is most preferred. Moreover farmers are not inconclusive in which measure is most preferred within a certain management area. This makes it more difficult for a farm advisor to give a farm specific advice. Currently farm advisors are not able to identify farmers’ goals and needs correctly. It is therefore vital for farm advisors to have a structured and formalized tool to elicit farmers’ preferences. ACA can serve as this tool, in such a way that preferences can be elicited and advice can be tailored to fit farmers’ needs.
EFFECTIVENESS OF RISK-BASED TESTING OF IMPORTED ANIMALS FOR BOVINE TUBERCULOSIS IN THE NETHERLANDS

Clazien J. de Vos, Jeanet A. van der Goot, Fred van Zijderveld, Manon Swanenburg, Armin R.W. Elbers, CVI, Wageningen UR

*corresponding author: clazien.devos@wur.nl

In intra-EU trade, the health status of animals is warranted by issuing a health certificate after clinical inspection in the exporting country. This certificate cannot provide a 100%-guarantee of absence of disease, especially not for diseases with a long incubation period and no obvious clinical signs such as bovine tuberculosis (bTB). The Netherlands is officially free from bTB since 1999. However, frequent reintroductions occurred in the past 15 years by importation of infected cattle originating from both bTB-infected and bTB-free EU member states. Additional testing (AT) of the animals six weeks after importation with the skin test would enhance the probability of detecting an imported bTB infection in an early stage. In intra-EU trade, AT is only allowed when done randomly, i.e. no distinction is to be made between animals based on exporting country. Testing of all imported cattle would entail a high cost and results in many false-positive diagnostic test results. Therefore, it would be advantageous if AT could be risk-based, i.e., only those cattle are tested that are estimated to have a high probability of being infected. The goal of this study was to evaluate the effectiveness of risk-based AT for bTB in cattle imported into the Netherlands.

A generic stochastic import risk model was developed in Excel and @Risk that simulates disease introduction by importation of live animals on an annual basis. Main output parameters of the model are (1) the number of infected animals that is imported, (2) the number of infected animals that is detected by testing, and (3) the economic losses incurred by importing infected animals. Main input into the risk model are cattle importation data for the Netherlands, bTB prevalence data in EU member states, test characteristics of the skin test, and economic parameters to estimate the economic loss of importing bTB-infected cattle. Model calculations were optimized to either maximize the number of bTB-infected cattle detected by AT or to minimize the economic consequences of importing bTB-infected cattle.

Model results indicate that the annual introduction risk of bTB for the Netherlands is 100%. On average, the Netherlands imports 99 bTB-infected cattle from EU member states annually, > 98% of which are calves. Ireland, Germany, Belgium, Italy, Poland, and France account for > 99% of all imported bTB-infected cattle into the Netherlands. Random testing of 8% of all imported cattle results in detection of on average 7 bTB-infected cattle. Optimizing the sampling strategy for AT to maximize the number of infected animals that is detected greatly improves the effectiveness of AT. Without increasing the sample size, on average 75 bTB-infected cattle are detected. In this scenario, only calves are selected for AT and thus possibly detected, resulting in a higher overall economic loss than in the current situation in which no AT is performed. This is explained by the fact that the cost of detection of a calf (culling of infected animal and tuberculination of all animals on the farm) is higher than the expected gain of preventing an outbreak starting on a veal farm. Therefore, to reduce the economic loss incurred by importation of bTB-infected cattle, the focus of AT should be on those cattle that go to dairy herds and potentially cause larger outbreaks with major consequences. When the sampling strategy for AT is optimized to minimize the economic consequences of importing bTB-infected cattle, only breeding and production cattle are selected for AT resulting in detection of on average 1 bTB-infected cattle. Economic loss is, however, reduced with 75% if compared to the current situation.

Based on the model results in this study, we conclude that the risk of bTB introduction into the Netherlands is very high. AT will not reduce the probability of bTB introduction into the Netherlands, because testing is only
performed six weeks after importation. Early detection of bTB-infected cattle by AT can, however, reduce the potential consequences of a bTB outbreak and will as such reduce the risk of bTB introduction. The effectiveness of AT can greatly be improved by risk-based sampling. The optimal sampling strategy for risk-based AT is, however, highly dependent on the objective of AT. If economic loss is to be contained, AT should focus on breeding and production cattle that go to dairy herds.
TWO YEARS AFTER THE SCHMALLENBERG VIRUS EPIDEMIC: DOES THE VIRUS STILL CIRCULATE?

A.M.B. Veldhuis, M.H. Mars, L. Roos, L. van Wuyckhuise, G. van Schaik, GD Animal Health Service

*corresponding author: a.veldhuis@gddiergezondheid.nl

Introduction

Two years after the introduction of the Schmallenberg virus in north-western Europe, it is unknown if the virus is still circulating in countries that were the first to be confronted with it. When the population level immunity declines in Europe, reintroduction of SBV in Europe might eventually result in an outbreak of similar magnitude of that seen in 2011/2012. Cattle is considered the preferred host for most common Culicoides species responsible for transmitting viruses like SBV. Evidence of SBV circulation is therefore most likely to be found in cattle. The Netherlands was one of the first countries that was affected by SBV in 2011. The aim of this study was to determine if SBV circulated amongst naïve dairy young stock in the Netherlands in 2013, two years after introduction of SBV.

Materials & methods

A two-stage sampling design was used in this study. In August 2013, 1,085 randomly selected dairy farms were invited by mail to participate in a cross-sectional study to estimate the seroprevalence of SBV in young stock in winter 2013. Participating farmers were requested to have their private practitioner collect blood samples from five randomly selected young stock born between October 30th, 2012 and April 30th, 2013. Sampling restrictions were set up to obtain material from young stock between 8 and 12 months old at sampling. By doing so, animals with maternal antibodies or natural immunity following infection in 2011 were expected to be excluded. Samples in which SBV-specific antibodies were detected were investigated by a virus neutralization test for confirmation. In the second stage of this study, serum from an additional sample of 20 young stock within the same age category (including the five initially sampled animals) were collected and tested in the SBV ELISA in herds with at least one seropositive test result.

Results

A total of 1,923 animals from 394 dairy farms were sampled between October 4th and December 31st, 2013. Antibodies were detected in 21 samples (1.1% (95% confidence interval (CI): 0.7-1.7)) from 21 herds (5.3% (95% CI: 3.3-8.0)). The 21 animals with antibodies were born between July 26th, 2012 and March 16th, 2013 and age at sampling ranged from 8.4 to 15 months (median: 12.2). Virus neutralization testing confirmed presence of antibodies in 13 out of 21 samples, with VNT titers ranging from 12 to ≥768 (median: 24). Seventeen out of the 21 farmers agreed to participate in the second stage of the study and collected a larger sample of young stock. From those farms, a total of 316 animals were sampled between July 2nd and July 23rd, 2014. Antibodies were detected in 9 out of 316 samples, from 9 herds. Eleven animals were confirmed positive in the first stage of the investigation and were included in the second investigation. In six of them, aged 9-15 months at first sampling, no SBV-specific antibodies were detected in the second investigation. The remaining five animals tested positive in both investigations and were 12-18 months old at first sampling. In one herd, an animal was seronegative in the first stage but tested positive in the second stage of the investigation.

Discussion & conclusion
The repeated testing of susceptible young stock within a time frame of six to nine months in this study resulted in some interesting test result combinations. In both investigations, the positive samples were single reactors within the sample obtained from each farm, which is unlikely given the characteristics of SBV (highly efficient spreading within a short amount of time). In addition, the proportion of positive test results was below the expected false positive rate given the specificity of the ELISA test used (98.8%). Overall, an explanation for our findings is three-fold: (i) a part of the antibodies measured in this study might be the result of (long-lasting) maternally-derived immunity, (ii) some of the antibodies measured in this study might be the result of active fetal immunity after vertical transmission of SBV, and (iii) some of the antibodies measured in this study could be the result of an active immune response after natural infection in 2013. The latter is however the least likely explanation considering the low number of positive animals per herd while SBV circulation is known to result in high within-herd seroprevalences. Conclusive knowledge on circulation of SBV could be obtained by the serological follow up of a sentinel of calves born seronegative and restricted from colostrum intake from seropositive cows. This study indicated that the young stock population in the Netherlands is almost completely susceptible for infection with SBV.
As the size of livestock farms in The Netherlands is on the increase for economic reasons, an important question is how disease introduction risks and risks of onward transmission scale with farm size (i.e. with the number of animals on the farm). Here we use the epidemic data of the 1997–1998 epidemic of Classical Swine Fever (CSF) Virus in The Netherlands to address this question for CSF risks. This dataset is one of the most powerful ones statistically as in this epidemic a total of 428 pig farms were infected, with the majority of farm sizes ranging between 27 and 1750 pigs, including piglets. We have extended the earlier models for the transmission risk as a function of between-farm distance, by adding two factors. These factors describe the effect of farm size on the susceptibility of a ‘receiving’ farm and on the infectivity of a ‘sending’ farm (or ‘source’ farm), respectively. Using the best-fitting model, we show that the size of a farm has a significant influence on both farm-level susceptibility and infectivity for CSF. Although larger farms are both more susceptible to CSF and, when infected, more infectious to other farms than smaller farms, the increase is less than linear. The higher the farm size, the smaller the effect of increments of farm size on the susceptibility and infectivity of a farm. Since 1997 there has been a continuous trend in the Dutch pig farm structure towards a lower number of farms and a higher average farm size (with the total number of pigs in the country remaining similar). Can we calculate the net effect of these changes on the between-farm transmission risks during a CSF epidemic? Because of the large changes in the Dutch pig farming characteristics, a straightforward model extrapolation of the observed farm size dependencies from 1997/1998 to present times would not be justified. However, we can use the distance and farm-size dependencies estimated to derive some insight into the issue.