

IMPACT OF GLOBALISATION ON ANIMAL HEALTH

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IMPACT OF GLOBALISATION ON ANIMAL HEALTH

Editors: Y. Van der Stede and J. Dewulf

8 November 2013

DRONGEN, BELGIUM

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PROGRAMMA

IMPACT OF GLOBALISATION ON ANIMAL HEALTH

8h00-8h45	Onthaal met koffie en koffiekoeken
8h45-9h00	Verwelkoming door Algemeen Directeur DGZ-Vlaanderen Denis Volckaert en Jeroen Dewulf voorzitter VEE

OCHTEND PROGRAMMA

Plenaire sessie: Jeroen Dewulf

9h00-9h45	Upcoming Zoonoses and its risks <i>Dr. S. D'Hollander, EFSA, Parma, Italië</i>
9h45-10h30	Toward a monitoring of the risk factors of emergence of animal diseases Sabine Cardoen, FAVV, Brussel, België
10h30-11h00	Koffiepauze en postersessie
11h00-11h45	Cost-Efficiency of monitoring Alistair Stott, Scottish Agricultural College, Edinburgh, UK
11h45-12h30	Panelgesprek over de impact van globalisatie op diergezondheid Moderator: Koen Mintiens, Boerenbond
12h30-13h00	Posterpresentaties (Guy Hendrickx) Mogelijkheid tot presentatie van poster (1 dia/poster)
13h00-14h00	Lunch en postersessie

NAMIDDAG PROGRAMMA

Open session: sessievoorzitters: Koen Mintiens & Erwin Wauters

14h00-14h20	Do gastrointestinal nematode affect the productive efficiency of dairy farms? By Mariska van der Voort, ILVO.
14h20-14h40	Towards farm specific risk maps for Fasciola hepatica: which factors determine snail abundance? By Karen Soenen, Ugent
14h40-15h00	Accurate livestock number estimates in mixed farming systems through a multi-model approach. By Ward Bryssinckx, AVIA-GIS
15h00-15h30	Koffiepauze en postersessie

Open session: sessievoorzitters: Bart Balis & Yves Van der Stede

- 15h30-15h.50 Antimicrobial reduction in pig production up to 60% possible without jeopardizing production parameters - preliminary Belgian data. by Merel Postma, UGent
- 15h50-16h10 A descriptive study on biosecurity measures in selected Belgian cattle herds. By Steven Sarrazin, Ugent, CODA-CERVA.
- 16h10-16h.30 The use of antimicrobials on dairy farms in Flanders, Belgium. By Marina Stevens Ugent.
- 16h30-16h-45 VEE-prijs en Poster Prijs
- 16h45-18h00 **Receptie aangeboden door DGZ-Vlaanderen**

Oral presentations

Upcoming zoonoses and their risks assessments: time for creative thinking?

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INTRODUCTION

In recent years several unexpected outbreaks of zoonotic diseases have occurred in Europe. Zoonoses such as West Nile fever have moved up the list of public health issues, with outbreaks in humans in Greece, Bulgaria and Croatia (Sambri et al., 2013). The spill over of Q-fever from animals to humans in Netherlands between 2007- 2010, with over 4000 human cases, raised a public concern and questions about factors contributing to the development of sustained outbreaks (Georgiev, 2013). Recently, *L. infantum* infection has been spreading northwards in Europe and has reached the foothills of the Alps in northern Italy, South- and North-western, France and north-western Spain (Solano et al., 2011). Another example of a recent zoonosis that spread rapidly was the pandemic H1N1 2009 (pH1N1) influenza virus, which spread from human to human and caused an influenza pandemic in accordance with the declaration made by the WHO on June 11 2009.

The EU scientific community has been actively involved over the past years in addressing the many questions related to emerging zoonotic diseases. Similarly, the scientific Panel on Animal Health and Welfare (AHAW) of the European Food Safety Authority (EFSA) has performed several risk assessments that tackle some of those issues (EFSA, 2010a; EFSA, 2010b; EFSA 2011; EFSA 2012a). Greger (2007) reviewed the origin of major human infectious diseases at the human animal interface and the factors underlying their emergence. The analysis of factors of emergence shows that more outbreaks of infectious diseases, both new and already known, are to be expected in the future.

Europe has been characterised as a hot spot for emergence (Jones, 2008). Hence one may refer to emergence of a zoonotic disease as an “expectedly unexpected”. Unexpected events are driven by change. Yet, do we understand the drivers for change? Several reviews explore how different drivers for infectious diseases contribute to disease emergence. A variety of drivers is frequently under investigation, such as those derived from environmental change, social and demographic change, health system capacities, technology and globalisation. For instance, Suk et al. (2011) analyse eight infectious threat scenarios in the light of 3 groups of macro-drivers and conclude on their contribution into disease emergence. A number of reviews address the association between environmental drivers and infectious diseases (Samenza, 2013; Suk, 2011; Patz, 2000; Lingren, 2012; Fineberg, 2010), and use of monitoring in prediction of upsurges of infectious disease (Mills, 2010). Most studies examine links within the group of drivers only or look for multiple linear associations between an outcome and a driver. However, those determinants of emergence rarely act singly (Murphy, 2008). Liverani et al. (2013) recognise the need for a holistic approach accounting for relations between drivers, potentially belonging to different groups of drivers.

MATERIAL AND METHODS

On the basis of a case study, the aim of this review was to have a closer look into an example of a risk assessment performed by the AHAW Panel of EFSA on the zoonoses Rift Valley Fever (RVF), (EFSA, 2013). The risk assessment addressed the risk question of the likelihood of introduction of the RVF virus into countries neighbouring Europe along the southern Mediterranean Basin (Region of Concern=RoC). Only the most important pathways for introduction of RVFV were considered, namely of RVFV introduction via infected animals entering through undocumented movement of animals, and introduction via dispersal of vectors. The second risk question concerned the risk of RVF becoming endemic in the RoC. The transmission model developed by Fischer et al. (2012) was used to determine the initial epidemic growth rate of RVFV infections, which is an indicator of the potential occurrence of RVFV spread to following virus introduction.

This paper reflects on the following three important questions: 1) how were potential drivers for change considered during the development of the scientific opinions and which efforts were made to translate societal questions into the scientific assessment; 2) how well was the preparedness for the given risk questions, to ensure timely and accurate risk management in the given time-frame and which strategies were undertaken to cope with scarcity of data and resources; and 3) how useful was the scientific opinion for guiding the risk managers in targeting their efforts to prevent introduction or enhance early warning in case of outbreaks?

RESULTS

1) How were potential drivers for change considered during the development of our scientific opinions and which efforts were made to translate societal questions into the scientific assessment?

Societal drivers that may have induced undocumented movement of animals into the RoC were discussed at length during an expert elicitation workshop. The group of experts consisted mainly of epidemiologists and virologists, who had built up expertise with research activities related to RVF, prevention and control of RVFV or networking activities in the RoC or in the RVF endemic areas.

The experts were well acquainted with the epidemiology of RVF in their area and knew well the current practices related to trade of animals and traditional farming in their region. Drivers that could have triggered changes in animal movements were taken into account, when making judgements on probabilities, such as the increased demand of sheep during Eid al-Adha in the Arabian Peninsula, long borders in dessert areas which are impossible to control, nomadic farming practices, migration flows due to the instable political climate in northern Africa at the time of the assessment. Moreover, the idea of using historical outbreaks data for the purpose of estimating illegal animal movement was an example of proposed context incorporation into the risk assessment process.

Including a more interdisciplinary team of experts for the elicitation, however, involving also sociologists, ecologists, entomologists, economists, local farmers and traders into the discussions, could have lead to an broader, more in-depth understanding of the drivers for undocumented trade flows, concerning also people migration flows, the Syrian crisis, wildlife ecology, etc more profoundly. Further, civil migration toward south and north, e.g. to Turkey (UNHCR, 2013), may create an opportunity of infected vector importation, together with transport of personal belongings.

2) How was the preparedness for the given risk questions, to ensure timely and accurate risk management in the given time-frame; and which strategies were undertaken to cope with scarcity of data and resources?

A great deal of data was needed to carry out a quantitative risk assessment, which were not available or scarce and scattered, un-harmonised, unpublished, or in hard copy, not readable for further analysis. The data gaps considered, amongst others, livestock and wildlife geographical distribution and density data, data on vector competence, distribution and abundance, data on undocumented animal movements from endemic areas, data on the incidence of RVF in the endemic areas, vaccination coverage, etc.

This was overcome, partly by a rather labour intensive, systematic literature review, extracting information on vector distribution and abundance from published papers, and modelling their distribution and abundance. Building further on already developed models by AVIA GIS or Fisher (2012) enabled further to reduce the time of the assessment. The expert knowledge elicitation workshop aimed at making risk estimates based on the current state of knowledge and scattered information found. However, a great amount of uncertainty in likelihood estimation along the risk pathways was encountered in this process. This highlighted the need for a harmonised data collection on population distributions (vectors, livestock, wildlife), animal movements, and an inventory of available models which could be readily available, adapted and used for risk assessments needed to be carried out under high time pressure.

3) how useful was the scientific opinion for guiding the risk managers in targeting their efforts to prevent introduction or enhance early warning in case of outbreaks?

The risk maps provided by the assessment may help risk managers in targeting their surveillance efforts in high risk areas. The assessment certainly also had an indirect benefit in pointing out data gaps and needs for future research and harmonised data collection.

The actual risk of introduction of RVF into the EU however, was omitted from this mandate and may need updating as well. Further, the geographic vicinity between Syria and Turkey should be of concern and one may wonder why Turkey was not part of the RoC, especially in light of Turkey's potential accession into EU.

The importance of interaction between risk manager and risk assessor is recognised as an area for improvement. Clear communication between both actors before the formulation of the risk question can reassure full understanding of it and make decision making more logical and transparent. The dialogue between risk manager and risk assessor becomes crucial to highlight questions important in the broader sense, which are not related to current needs in the policy pipeline. Integration of efforts in formulation of the risk question can also guarantee its apolitical character. Lastly, reflecting upon uptake of previous EFSA opinions by the risk manager, dialogue is necessary to scale the risk question and fit the risk assessment to its purpose.

DISCUSSION

A key scientific challenge is to correctly define and understand newly recognised and known risk drivers along with their complex interactions and to develop methods that combine evidence from different sources in the risk assessment process. Certain drivers such as impact of policy change or existing illegal activities are difficult to estimate. An interdisciplinary approach that examines multidimensional links between a diverse range of ecological, biological and socioeconomic factors and its application in risk analysis should be in place (Liverani et al., 2013). Additionally, challenges related to data scarcity, or data of poor quality, both of qualitative and quantitative nature, generated and collected in an un-harmonised manner leading to computational problems, need to be dealt with.

Further, it needs to be recognised that for risk assessments to be useful in the process of developing effective risk management policies they need to be underpinned by effective communication, and the perceived need for a strict separation between risk assessment and management can be an obstacle in this respect. . Dialogue should avoid lack of clarity and ensure agreement at an early stage on i) the framing of the questions; ii) the methodology and depth of analyses to be performed and iii) the information available and necessary to feed the process. Hence, in times of emerging disease, it is important to have a good acquaintance with the expectations of the risk manager.

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Towards a monitoring of the risk factors of emergence of animal diseases?

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INTRODUCTION

Emerging infectious animal diseases pose significant threats to animal health and welfare and to global food security. Predicting emerging infectious diseases is amongst the most difficult challenges facing medical and veterinary services and authorities. It appears to be impossible to predict, with an acceptable certainty, the next emerging animal disease(s). Specific risk factors driving the emergence of (zoonotic) animal diseases have been described (King, 2004; Morse, 2004).

It is postulated that a generic approach could be followed consisting in the monitoring of measurable risk factors of emergence of animal infectious diseases. This strategy of “forecasting” should focus on the recognition of conditions that favour emergence of infectious animal diseases. An increase in incidence of specific risk factors should alert the risk managers precociously on the increased risk of emergence of specific types of infectious animal diseases and allow them to focus resources on the key situations as well as to develop effective prevention and surveillance strategies.

The aim of this study is to identify and prioritize risk factors of emergence of infectious animal diseases (1) to identify key risk factors of emergence on which risk managers could act in terms of surveillance or mitigation and (2) to identify measurable risk factors to be included in a still to be developed emerging risk forecasting system aimed at early recognize conditions favouring the emergence of certain types of diseases. The aim of this work is not to provide an accurate prediction of disease epizootics. Only infectious animal diseases were considered. In case of zoonosis, only the emergence in the animal (and not in the human) population was considered. In this study, emerging diseases, potentially emerging diseases (exotic) and (potentially) re-emerging diseases were broadly considered.

MATERIAL AND METHODS

Via a Delphi survey conducted by 50 experts, the effect of 33 risk factors (inspired from King, 2004 and Morse, 2004) on the emergence of a sample of 34 (potentially) (re-)emerging infectious animal diseases was evaluated.

The 34 diseases were chosen based on their epidemiological situation (endemic, sporadic, emerging and exotic), their etiological agent (bacteria, viruses, parasites, prions), their hosts (wild fauna, domestic production animals, pets), their transmission routes ((in)direct, vector-borne, food-borne, etc.) and on the zoonotic nature or not. This allowed (1) a certain representativeness of animal health and (2) to perform scenarios by evaluating the effect of the risk factors on groups of diseases (ex. vectorial, exotic, zoonotic, etc.)

The consensus expert opinions obtained through the 2 round Delphi survey were transformed into scores allowing to rank risk factors according to their impact on the risk of emergence of the studied animal diseases, either considered as one general group or subdivided into different subgroups (zoonotic diseases, vectorial diseases and exotic diseases).

RESULTS

When considering emerging animal infectious diseases as one group (n=34) (**Figure 1**) the following 7 risk factors were judged to have an important impact (score ≥ 2): the general problems associated with the detection of emergence (such as lack of declaration, weak performance of diagnostic tests, ...), the existence of an animal reservoir of the animal disease, the difficulties to control the disease by vaccination, the geographical expansion of the pathogenic agent, the asymptomatic carriage, the increase in incidence of the disease in other countries and the epidemiological role of wildlife.

When considering specific subgroups of emerging animal infectious diseases, other risk factors were also judged to be important. For vector-borne diseases (n=13), 17 risk factors scored high (score ≥ 2 and ≥ 3), which has to alert on the importance of the risk of emergence of vector-borne diseases. The higher risk factors were linked to the vector activity and biology (presence of vector, geographical extension of the agent, increase in incidence in other countries and changes in climate and meteorology). Concerning exotic diseases (n=15), an higher impact of globalization (trade and transport), of the epidemiological situation in other countries (geographical extension and increase in incidence in other countries) and of problems to early detect the presence of the disease, was underlined. Zoonotic diseases (n=23) showed almost the same pattern as for the global scenario.

Some factors appeared to have a limited impact on the risk of emergence of infectious animal diseases because they are mainly related to the risk of emergence of the diseases in the human population, which was out of the scope of this work. These are for example the human demographic growth, the urbanization, the increase in terrorism, the possibility of the pathogen to change the host spectrum from animals to humans, etc.

Legislation and sanitary policy were considered as protective factors against emergence. Indeed, surveillance, prevention, bio-security, specific control measures such as blockage of farms in case of an outbreak are likely to decrease the risk of disease emergence and spread. Intensive production systems were also likely to protect against emergence because these are generally more controlled systems with limited contacts of animals with the outside, which reduces the risk of introduction of diseases in the exploitations. However, if highly contagious diseases are more specifically considered, such as classical swine fever or highly pathogenic avian influenza, this factor can become an important risk factor, due to the high density of animals bred in such systems.

In most of the scenarios, the impact of globalization seemed to be lower, but this was due to the fact that this risk factor was divided in 5 subcategories, leading to a “dilution effect” of the scores. However, globalization scored high when exotic diseases were considered, due to the high impact of trade and transport on the risk of introduction of new diseases in the country.

In this study, the experts were of the opinion that the changes in climate and meteorology have few impact on the risk of emergence of infectious animal diseases, except for vector-borne diseases. Indeed, heat and humidity condition the multiplication and geographical distribution of some vectors. Larvae of mosquitoes develop better in organic matters in stagnant waters which are influenced by warm and dry climatic conditions. In consequence, heat and rain have an influence on the geographical distribution of mosquito populations. Warm and dry weather influence tick populations and their geographical distribution.

DISCUSSION

These rankings give information about the most important risk factors of concern in disease emergence whether in general or focused on the emergence of zoonotic, vectorial or exotic diseases. Some of these important risk factors could be more surveyed or mitigated. For example, the high score concerning the role of vectors on the risk of emergence of exotic diseases could lead to an increased surveillance of the vector populations and of the infection of these vectors by pathogenic agents. The high score obtained in all the scenarios concerning problems of detection should motivate to mitigate these problems by stimulating the vigilance of the vets and breeders for early detection, by stimulate the mandatory notification, by developing non specific screening methods to detect new diseases, by developing systems of sentinel vets, etc.

The main interest of this study concerns the future use of measurable risk factors in a (still to be developed) forecasting tool of emerging animal infections. The detection of the appearance or of an increase in incidence of some risk factors can draw the attention to diseases whose emergence are conditioned by these risk factors and alert before the real emergence of a new disease. For example, an important increase in the tick population, detected by a monitoring of vectors, should warn for the possible emergence of tick-borne diseases and may result in a strenghtening of tick-borne disease surveillance. An increase in import statistics of living animal or animal products (cf. increase in trade and transport) from infected countries, detected by a systematic analysis of importation databases, or a geographical extension of a diseases, detected by participation to international networks, should draw the attention on specific diseases.

The message of this study is to introduce, in addition to the traditional passive and active surveillance of animal diseases, an additional concept consisting of a more generic monitoring of measurable risk factors of emergence (Advice 06-2013 of the Scientific Committee). The forecasting of risk factors of emerging diseases should precociously alert the risk manager of the increased risk of emergence of animal diseases and urge him to prepare for surveillance, prevention and control on those diseases whose emergence is conditioned by these increased risk factors.

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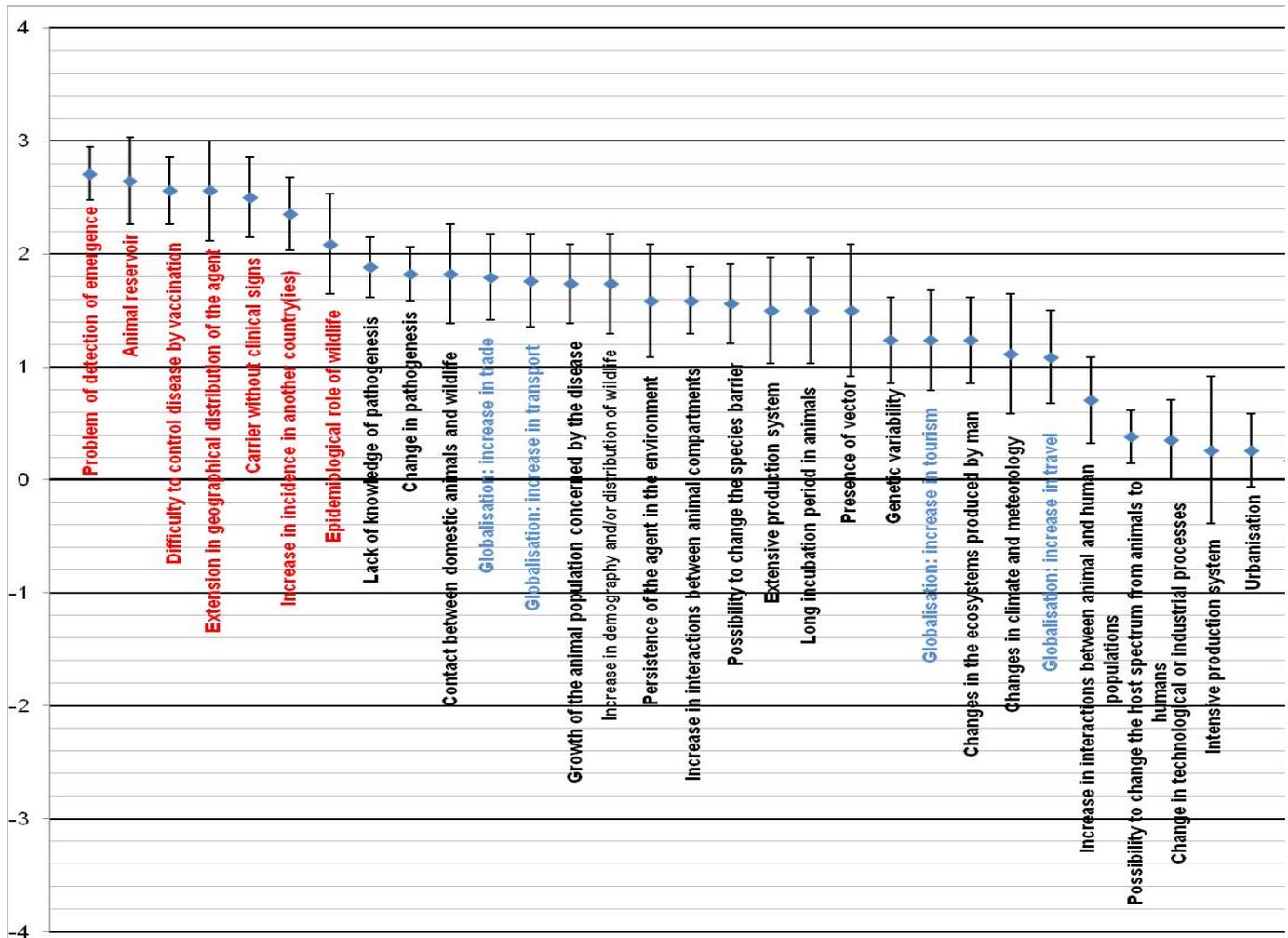


Figure 1. Ranking of the risk factors of the 34 animal diseases representing animal health

In this scenario, the 34 examples of infectious animal diseases were considered as one group, representing animal health. The x-axis represents the strength of the influence of the factor on the risk of emergence of the diseases, according to the scores (from -4 to 4) given by the experts. Factors with positive values are risk factors. The risk factors having a high impact (>2) on the risk of emergence of the animal diseases are indicated in red. The factors concerning globalization are indicated in blue. Factors with negative values represent protective factors and are indicated in green. The factors near zero have a low influence on the risk of emergence of the considered diseases in the animal population.

Cost Efficiency of Monitoring to ensure Sustainable Intensification in Agriculture

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VEE Conference 8th November 2013, Ghent, Belgium
Impact of Globalisation on Animal Health*

INTRODUCTION

The world population recently exceeded 7 billion. By 2050 it is predicted to expand to as much as 9 billion. Food consumption per capita and the proportion of animal products in the diet are also expected to rise as developing countries grow more affluent. Global food production will need to increase greatly and yet the resource stocks required to achieve this, particular those based on fossil fuels, are in short supply. This whole problem will be exacerbated by global warming, which agriculture is both a contributor to and likely to suffer from. John Beddington, England's Chief Scientist in 2009 described this scenario as the 'perfect storm', saying that by 2030 the world will need to produce around 50 percent more food and energy, together with 30 per cent more fresh water, whilst mitigating and adapting to climate change (Sample, 2009). This situation highlights how important it is to improve the productivity and efficiency of global agriculture. An important contributor will be cost efficient monitoring of animal health. This paper outlines how bio-economic concepts of cost efficiency in animal health monitoring can be aggregated up from the farm level to address the global 'grand challenge' of sustainable food security.

SUSTAINABLE INTENSIFICATION

An often cited response to the grand challenge is the aspiration for sustainable intensification in agriculture. This calls for increases in productivity per unit of input (usually land) that can be maintained in perpetuity i.e. that ensures sufficient economic, natural and social capital is generated or preserved to sustain the productivity. Garnett and Godfray (2012) explore the concept and the controversy that surrounds it. They conclude that it is a useful concept, providing an intellectual analytical framework rather than a clearly defined set of principles and practices. In this sense it mirrors development of thinking in animal health economics and therefore provides an umbrella under which this and other contributing processes may be assembled to tackle the grand challenge.

EFFICIENCY OF MONITORING ANIMAL DISEASE

McInerney et al., (1992) present a framework for the economic analysis of animal disease prevention and control. Yalcin et al., (1999) applied it in practice as shown in Figure 1. Each cross indicates a particular farm investing in a particular disease control intervention (e.g. monitoring) and experiencing a corresponding level of disease loss. Generally speaking, greater investment leads to lower losses but there is considerable variation in efficiency between farms. The most efficient farms lie on the efficient frontier (bold line). The dotted (isocost) line joins all combinations of investment and disease loss that give a total cost (investment + loss) of about £65. This particular isocost line represents the lowest total cost recorded in the sample and hence identifies the most economically efficient farms with the optimal monitoring strategy.

Expected diseases losses (£/animal)

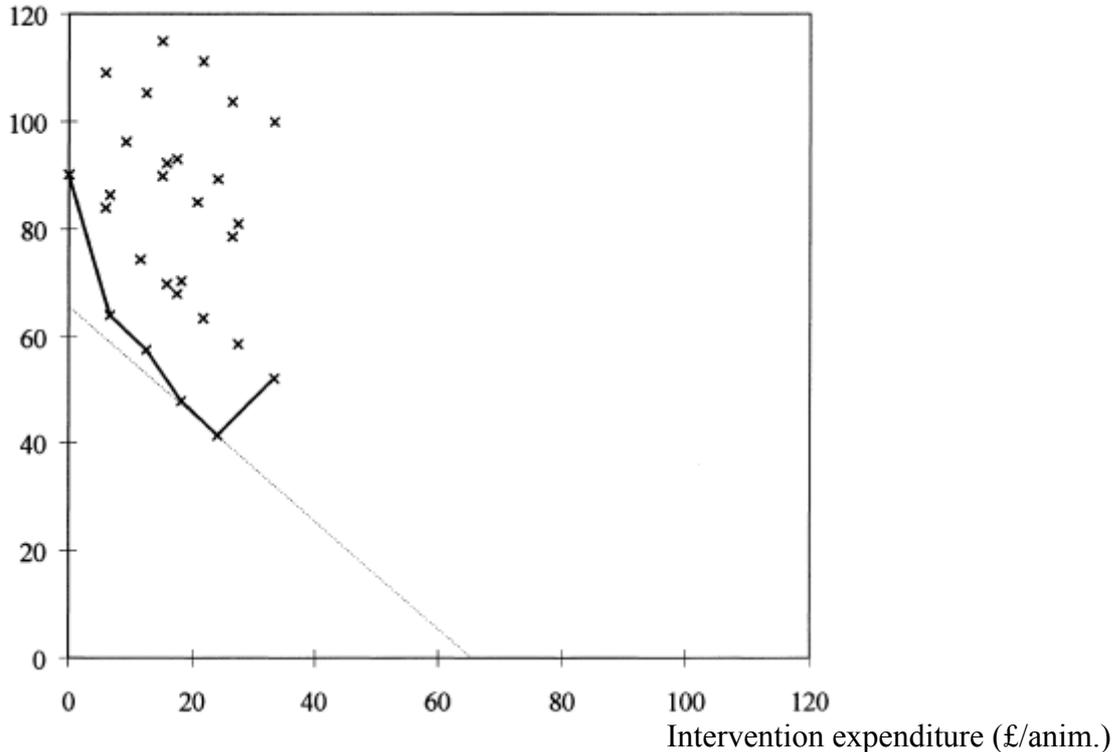


Figure 1: Efficiency frontier for interventions to reduce animal disease (Yalcin et al., 1999)

SCALING UP TO WHOLE FARM LEVEL

Although the loss-expenditure frontier depicted in figure 1 can provide useful insights into the efficiency of disease monitoring in a population sample it may not identify the optimal solution for a particular farm or farmer. For example, individual farm circumstances may favour contra-indicated disease monitoring strategies. Furthermore, the farmer may have limited resources to invest and/or prefer alternative investment opportunities. His or her objective may not be to implement the economically optimal strategy because of some perceived trade-off against other goals. For example, reduced exposure to disease may increase the risk of catastrophic losses should the infectious agent be reintroduced to the naïve herd. Alternatively the farmer may wish to limit his exposure to such large losses simply by running a farm with a mix of crop and livestock species.

Stott et al., (2003) tackled this problem by using a whole farm approach to investment in disease prevention (e.g. monitoring) and by seeking to minimise risk (variation in farm income) rather than minimise total disease costs. This was done using a linear program (LP) to find the combination of farm enterprises (e.g. sheep, cows, barley and including alternative disease prevention options) that minimised the variation in risk. The contribution of each enterprise to risk was measured using time series data for farming activities and the output of a stochastic epidemiological model for the disease prevention options. Farm income target was set as a constraint in the LP. By altering this constraint it was possible to explore the relationship between risk and reward on the farm and the role that disease prevention could play in this trade-off. An important by-product was to be able to express the benefit of disease prevention at constant farm income and minimum risk in terms of farming activities. For example, simply establishing that the beef herd was free of BVD rather than of unknown status at a target farm income of £7,500 pa reduced sheep numbers by 3% and increased biosecurity by 30% (to reduce risk of re-infection).

The lower stocking density could be converted into a reduced environmental footprint and hence help to assess the contribution of disease prevention to sustainable intensification.

SCALING UP TO NATIONAL LEVEL

For a recent example of the scaling up of farm level economic analysis to national level see Stott et al. (2012). When the interventions are applied at national rather than farm level commodity markets are likely to be affected i.e. indirect costs of disease need to be taken into account. For example, Weldegebriel et al., (2009) established that eradication of BVD from the dairy sector in Scotland would increase milk supply and therefore reduce retail prices benefiting consumers by £11m. Producers that were free of the disease suffered a corresponding loss of £2m. However, producers with BVD gained benefits of £39m after eradication as they had more milk to sell albeit at lower prices.

GLOBAL TRADE-OFFS

Figure 2 shows a schematic representation of a partial equilibrium (PE) model to examine the impact of a scientific advance applied in Scotland resulting in pig welfare (and productivity) benefits that has global impact within a specific sector of the economy.

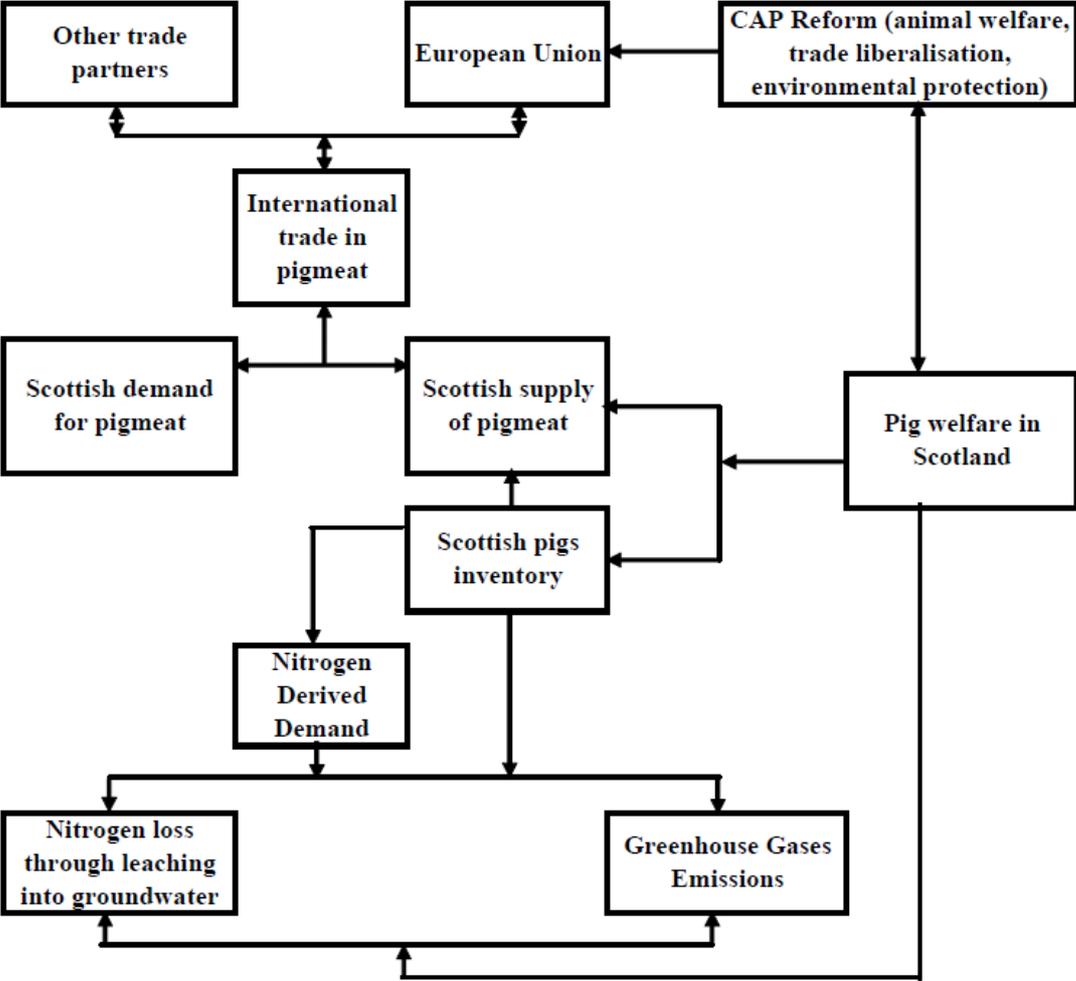


Figure 2: Animal welfare, trade and environment PE Model (Toma et al., 2008)

The innovation creates a supply shock in the domestic market which in turn affects international trade. For example, an improvement in the cost efficiency of disease monitoring might increase domestic supply thus displacing imports. The larger domestic herd may produce more greenhouse gases and nitrogen pollution potentially compromising the sustainability of the intensification. However, the innovation may also reduce pollution from individual animals. The net environmental impact therefore needs to be established by the model using comparisons with a baseline scenario. The interaction with international agricultural policy interventions can also be incorporated. Epidemiological and/or bio-economic models established at the whole farm level can be incorporated into the PE thus allowing alternative innovations to be assessed for their relative contribution to sustainable intensification and hence to the grand challenge.

CONCLUSION

Interdisciplinary research between epidemiologists and economists is essential to ensure that the intensification implied by more efficient monitoring of animal disease properly addresses the increased disease risks from globalisation and constitutes a sustainable response to the global grand challenge.

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Do Gastrointestinal Nematode Infections Affect the Productive Efficiency of Dairy Farms?

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INTRODUCTION

Gastrointestinal (GI) nematode infections are an important cause of production losses in dairy cattle. Although GI nematode infections generally are at subclinical level, they can be responsible for decreased feed intake and reduced milk production and fertility [1, 2, 3]. Research addressing the impact of GI nematode infections and related prevention strategies traditionally studies the effect on particular technical key performance indicators such as daily weight gain and average milk yield per cow. Knowing the effects on key performance indicators is useful [4, 5] because these indicators are often correlated with the aggregate economic performance of dairy farms [6]. Nevertheless, an important drawback of this approach is that the key performance indicators are mostly partial productivity indices, while the effect on the overall productive efficiency of the farm remains unclear [7].

Efficiency analysis can be used to analyze the impact of animal diseases on the whole farm performance [8]. The approach is based on production theory, which studies the transformation of input(s) into output(s). Efficiency analysis in fact bundles partial productivities into an aggregate performance measure. Despite its frequent use in management science, efficiency analysis has not often been applied in animal health sciences nor in parasitology. The growing interest in incorporating non-economic factors in productive efficiency models has resulted in some studies introducing animal health factors into efficiency analysis [9, 10, 11].

In the present study we analyze the relation between GI nematode infection in dairy cattle and the technical efficiency. We investigated to what extent the exposure to and control of GI nematode infection affect the transformation of inputs(s) into output(s) on dairy farms. Also we identify the inputs whose productivity is mostly influenced by the infection.

MATERIALS AND METHODS

In this study farm accountancy data are collected from two networks, the Belgian Farm Accountancy Data Network (FADN) and the Tiber Farm Accounting System (TFAS) of *Boerenbond*, the Flemish farmers' union. Data from both networks were linked to GI nematode infection data gained from a longitudinal parasitic monitoring campaign. The level of exposure to GI nematodes was based on bulk tank milk ELISA and is expressed as an optical density ratio (ODR). The final dataset consisted of two unbalanced panel populations of 50 FADN and 152 TFAS dairy farms over the 5-year period, respectively. In total, the datasets consisted of 198 and 622 observations for FADN and TFAS, respectively.

Two stochastic inefficiency effect model [12, 13] were used to analyze the relationship between technical efficiency and GI nematode infections. In the first model, the inefficiency effects were estimated as a function of the input variables and the explanatory variable (GI nematode exposure) believed to influence the technical inefficiency. This model is also called a neutral stochastic frontier model. The second inefficiency effect model is an extension of the first model. By including the interaction between level of exposure to GI nematodes and the input variables, it is possible to evaluate whether some or all input variables have a constraining or beneficial effect on the inefficiency of farms. This model is also called a non-neutral stochastic frontier model.

To assess efficiency scores, milk production in liters fat protein corrected milk (FPCM) was considered as the main output variable. Our model included the six following input variables: *concentrate* and *roughage*, both defined as the kilograms of feed consumed; *pasture*, defined as the hectare of grazed grassland by dairy cattle; *dairy cows*, defined by number of lactating dairy cattle present on the farm; *dairy health*, defined as the cost for veterinary services and medicines; and *labor*, defined as labor (in hours) performed by family members and hired laborers.

Calculating the stochastic production model for the two inefficiency effect models requires the selection of a functional form for the production function. The functional forms which are most commonly used in research on production efficiency of dairy farming are Cobb-Douglas (CD) and Translog (TL) [14]. We applied both functional forms because the result may have been affected by the chosen model. A likelihood ratio test was performed to compare the CD with the TL model.

In total four models were estimated for FADN and TFAS. First a neutral production model for the CD and TL functional form was calculated followed by the non-neutral production model for again CD and TL functional form. All models were estimated by the maximum likelihood with the FRONTIER 4.1 computer program [15].

RESULTS

The likelihood ratio test for comparing the two functional forms rejects the H_0 hypothesis of CD in favor of the TL model at 5% significance level. Hence, the TL functional form is more appropriate than the CD functional form for both the FADN and TFAS samples.

The technical efficiency (TE) scores obtained using the TL production function indicate the presence of inefficiency among dairy farms. The mean TE is 0.81 for FADN and 0.88 for TFAS farms, respectively. Farms in the data sample can increase their milk production level on average by 1083 (FADN) and 788 (TFAS) liters per cow per year using the current input quantities. Technical efficiency ranged from 0.24 (low) to 0.98 (high). More than 61% of FADN farms and 42% of TFAS farms are below the efficiency score of 90. The average milk loss due to inefficiency by FADN farms in low (0-90), medium (90-95) and high (95-99) efficiency score groups was approximately 1596, 811 and 498 liters per cow per year, respectively. The average milk production loss due to inefficiency for TFAS farms was similar to the FADN farms. The TFAS milk production losses were 1389, 690 and 376 liters per cow per year, in the low, medium and high efficiency score groups, respectively.

The null hypothesis, which assumes that no inefficiencies related to GI nematode exposure was rejected ($P < 0.05$) for all estimated models. The estimated coefficients of the inefficiency effect model have a significant ($P < 0.05$) relation between inefficiency and infection under the FADN and TFAS sample. The results indicates a positive effect of GI nematode exposure upon the inefficiency levels.

The average marginal effect of exposure to GI nematodes indicated that an increase in exposure by 1 ODR is associated with a decrease of the technical efficiency by 0.003 (1%) and 0.006 (2%) for FADN and TFAS, respectively. To investigate the effect of lowering the level of infection on milk production between efficient and inefficient farms, a decrease of 0.271 ODR was calculated. This reduction in ODR is based on the study of Charlier [16], which associates a change in ODR from the 25th to the 75th percentile (0.766-1.037 ODR) with a drop in the annual milk production of 0.9 kg per cow per day. For FADN farms, a decrease of *O. ostertagi* by 0.271 ODR results in a TE increase of 0.003 and corresponds with an average milk production increase of 27 (0.46%), 19 (0.25%) and 9 (0.10%) liter per cow per year in the low (0-90), medium (90-95) and high (95-99) efficiency score groups, respectively. For TFAS farms, decreasing GI nematode exposure by 0.271 ODR resulted in a TE increase of 0.006 and corresponded to an increase in average milk production of 63 (0.95%), 49 (0.61%) and 23 (0.26%) liter per cow per year in the low (0-90), medium (90-95) and high (95-99) efficiency score group, respectively.

The non-neutral model inefficiency effect model illustrates how *O. ostertagi* infection is associated with the input variables. The negative coefficients of the cross products in the TFAS sample, i.e., ODR × Concentrate, ODR × Roughage and ODR × Cows, indicate that the negative effect of GI nematode exposure on technical efficiency decreases with increasing feeding levels and herd size. The positive coefficients of the cross products ODR × pasture, ODR × health and ODR × labor indicates that the technical inefficiency associated with infection is predominantly caused by low productivity of pasture, health and labor. However, the FADN sample had no significant effect of *O. ostertagi* on the technical inefficiency in the non-neutral model, the productivity of pasture and health seemed to be negatively affected by infection.

DISCUSSION

The magnitude of the coefficients in the inefficiency model are similar for both samples. This shows that efficiency analysis can be used to detect the subclinical impact of *O. ostertagi* infection on efficiency, even for the relatively small sample size of the FADN population. In this study we also compared the CD and TL production functions to investigate if the functional form would affect the results. This did not appear to be the case, because the CD and TL model yielded similar coefficients in the production model. The TL functional form gives a better representation of data according to the likelihood ratio test, but our results indicate that the CD production function may also be an appropriate model for estimating the relation between GI nematode and efficiency. This is of interest as the CD model is relative easier to interpreted and allows in further research to calculate the cost-efficiency based on the production function.

The relationship between GI nematode exposure and annual milk production was considerably lower in this study compared with previous studies [16, 17]. Previous studies performed a linear regression between GI nematode exposure (ODR) and annual milk production, while controlling for a number of potential confounding variables. In those studies, an increase over the interquartile range of GI nematode exposure was related to a decrease in annual milk production of approximately 1 kg per cow per day in contrast to an estimate of 0.13 liter per cow per day in the present study. In addition, in recent clinical trials, the average estimated effect of anthelmintic treatment against GI nematodes under European conditions is estimated at approximately 1 kg per cow per day. The differences may be explained by previous studies' inclusion of indirect effects of GI nematode infections on milk production. For example, reduced feed intake is considered to be an important mechanism of lowered performance in GI nematode infected farms [3].

In efficiency analyses, farms with or without reduced feed intake can yield similar efficiency scores when the transformation of feed into milk is unaffected. With efficiency analyses only the direct effect of GI nematode infection on milk production is calculated.

The results show that farms with the lowest technical efficiency (TE between 0-90) can increase their milk production by an average of 1,600 liters per cow per year if they would become fully efficient. For these low-efficiency farms, a decrease in infection over the interquartile range results in an average increase of milk production of 63 liters per cow per year. This represents 3.8% of the potential increase in production through efficiency improvement. For highly efficient farms (TE between 95-99) the contribution to the total possible increase to become fully efficient (i.e., 338 liters per cow per year) is 6.7%. This was significantly ($P < 0.05$) different. This suggests that although the absolute direct effect of GI nematodes on milk production becomes smaller with increasing farming efficiency, GI nematode infection becomes a relatively more important factor to consider to further improve this efficiency.

This study assumes that infection affects the productivity of dairy farms. However, it should be noted that our analysis approach does not assess the direction of the causality. In goats, it has been reported that highly productive animals (potentially associated with higher efficiency) are more susceptible to infection [18]. On the other hand, the non-neutral model indicated that the negative relationship between GI nematode infection and efficiency was mainly due to low productivity of pasture and health, and that this relationship was weakened when concentrate and roughage are more in line with a direct effect of infection on efficiency. It is generally accepted that higher feeding levels result in lower susceptibility to GI nematode infection [19].

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Towards farm-specific risk maps for *Fasciola hepatica*: which factors determine snail abundance?

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INTRODUCTION

Fasciolosis, caused by the trematode parasite *Fasciola hepatica*, causes serious production losses in dairy cattle worldwide. In Flanders, about 30% of the dairy farms are infected with *Fasciola hepatica* and the cost for liver fluke infections was estimated at € 8.2 million a year [1,2]. Control of bovine fasciolosis is hampered by the limitations of the currently available flukicidal drugs: few drugs are available to treat dairy cows, many have low efficacies against juvenile stages of *F. hepatica* and there is evidence for the development of drug resistance. This urges for more research into non-chemotherapeutic control options through pasture management.

Fasciolosis is a vector-borne disease spread by the snail *Galba truncatula* which thrives in aquatic habitats. Subsequently the epidemiology of the disease comprises an important spatial component as the development of *F. hepatica* depends on climatic and environmental conditions. Several spatial distribution models have been developed for different regions across the world [3,4,5,6,7,8,9,10], but they cover large regions and are not suitable for farm level decisions. It has been shown that more insights in the local environmental factors affecting the abundance of the intermediate host snail are key for the development of farm-specific risk maps.

This study covers three research questions: (i) where and when is *G. truncatula* present, (ii) how can this distribution pattern be explained and (iii) are infection dynamics in the herd related to abundance patterns of the snail.

MATERIAL AND METHODS

The study was conducted in four dairy cattle farms in Flanders (Belgium) in 2012, two farms in the region of Bruges and two farms in the region of Zoersel. All farms had a liver fluke history and comprised permanent and transient potential habitats for *G. truncatula*. We defined these potential habitats as small water bodies (SWB). Preselected habitats were monthly examined (April-November) for *G. truncatula* abundance by transect analysis [11]. The sampled snails were measured and morphologically identified. A negative binomial regression model with robust standard errors assessed the probability to retrieve *G. truncatula* in relation to climatological factors (air temperature, rainfall), SWB type, agricultural region and micro-environmental factors (pH and temperature of soil and water of each SWB; occurrence of indicator plants). In addition, *F. hepatica* infection dynamics in the animals were monitored by coprological examination (egg detection) and serum ELISA (*F. hepatica* antibody detection) of different age classes before (April) and after the grazing season (November) and during winter.

RESULTS

In total 54 SWB were monthly searched and 953 *G. truncatula* snails were retrieved. Five types of SWBs were distinguished: pond, ditch, trench, furrow and moist area. Descriptive analysis showed highest number of snails in July in both areas. A new generation of snails peaked in October/November in the Bruges area. The multivariate model indicated that snail abundance is driven by SWB-type, agricultural region and rainfall. Highest snail densities were found in trenches followed by the pond/furrow/ditch/moist area complex. The associations between these three variables are shown in figure 1. Additional univariate modelling of a subset of the data indicated that soil pH and *Ranunculus sp.* were positively associated with snail abundance while mowing, grass-like sp., water and mean air temperature were negatively associated. Exposure to *F. hepatica* was confirmed in all four farms.

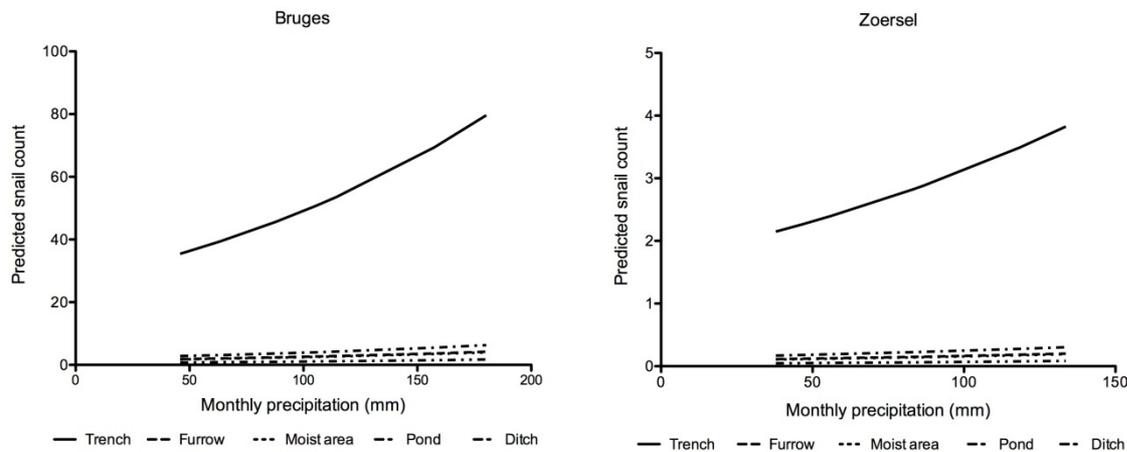


Figure 1: Multivariate associations between significantly different factors and snail counts in the negative binomial regression model: SWB, monthly precipitation and region.

DISCUSSION

The study demonstrated that SWB type, agricultural region and rainfall are significant drivers for *G. truncatula* abundance. Construction of farm-specific risk maps will thus require this information on a detailed level. Furthermore, these maps can be further improved by adding information on soil pH, vegetation and water temperature. While theoretically such information could be obtained by ground visits, it is time-consuming and requires trained staff. Currently, we are investigating if satellite- or UAV (unmanned aerial vehicle) -derived Very High-Resolution (VHR) images can identify and describe SWB associated with *G. truncatula* presence. These would allow to develop a standardized methodology and develop risk maps over a larger area. Previous successful applications of VHR imagery are small-scale risk mapping of malaria [12] and Rift Valley fever [13]. Ultimately, this should result in a methodology for farm-specific risk mapping of *F. hepatica* and an aid for veterinarians and farmers for control measures through pasture management and targeted use of anthelmintics.

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Accurate Livestock Number Estimates in Mixed Farming Systems Through a Multi-Model Approach.

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INTRODUCTION

In countries where livestock keepers are not obligated to report birth, decease, intake and offtake of animals, livestock population data is often sparse, inaccurate and incomplete². Therefore important information is lacking to assess e.g. livelihood, food security and transmission risk of diseases among livestock and humans⁷. In such situations decision makers generally rely on distribution estimates from survey records or projections of outdated enumeration results¹¹. Given the cost of large-scale surveys, sample size is often restricted and the accuracy of estimates is low. Furthermore, temporal resolution is limited due to the large time span between livestock counts.

In the past efforts have been made to fill this gap and to estimate livestock distribution in areas lacking reliable livestock abundance data. One way to do so is by training statistical models using spatial data such as environmental variables as done in the FAO's Gridded Livestock of the World¹². Because remote sensing images with a high spatial resolution are easily accessible (e.g. on a 5x5 km basis), the resulting livestock abundance maps show the same spatial detail. Although this may lead one to assume a high accuracy on a pixel by pixel basis, values cannot be evaluated as is and should be aggregated before being interpreted. The operational scale on which confidence levels become acceptable is difficult to determine as validation data is often unavailable in sufficient quantities.

Another method to assess livestock abundance more accurately in data-sparse environments was proposed by the authors in 2012³. They used an inverse distance weighted (IDW) interpolation based on observed livestock numbers to make estimates for areas where no samples were taken. Subsequently, pixels on the resulting map were aggregated on different administrative unit levels resulting in significantly lower error values as compared to traditional data processing of livestock survey results. The added value is attributed to data from adjacent administrative units which is included when livestock number estimates are made for the administrative unit of interest. However, only nearby areas contribute to the improved livestock number estimates and the influence of samples outside the administrative unit depends on the course of the borders.

To overcome these issues, an alternative approach was developed using a random forest modelling technique so denominator data from more distant but similar areas is included as well. The method was tested using the existing political borders of local government units within Uganda as well as using artificial areas delineated by a regular hexagon grid. The latter was done to assess operational scales as existing administrative units differ in size even when units from the same administrative level are considered. In addition an internal validation procedure was built upon resampling techniques to eliminate the need for a separate set of samples to allow for error estimation.

MATERIALS AND METHODS

To test different data processing approaches, the Uganda 2008 National Livestock Census was used¹⁰. Its size of 964,047 sampled households grouped in 8870 enumeration areas allows for simulating livestock surveys of smaller sample sizes, process these subsets of data and compare the resulting livestock abundance estimates with the reported NLC 2008 figures. During the planning stage of the livestock enumeration in 2008, Uganda consisted of 80 districts which are further subdivided into counties, subcounties and parishes. The most detailed geographical reference of enumeration areas is the parish in which it is located, for which shapefiles are available. Environmental variables which are used to train spatial models were extracted for these parishes and also on subcounty level to assess the importance of spatially aggregating predictor variables which corresponds to not only considering the homestead of herds but also the home range used during daily grazing activities. Predictor variables included estimated human population numbers for rural and all areas, travel time to closest city⁵, distance to nearest water body⁹ and a set of remote sensing imagery such as night-time light¹, summary statistics of normalized difference vegetation and Bioclim variables representing precipitation and temperature⁴. Another predictor variable was the landcover type as defined by the International Food Policy Research Institute (IFPRI)⁶. All predictor variables used are freely available for countries worldwide.

Random forests were selected as statistical modelling technique because (i) few statistical distribution assumptions are made, (ii) categorical variables are easy to include and (iii) there is no risk for overfitting even when the number of predictor variables is large compared to the number of observations as subsets of training data and predictor variables are taken randomly when training the individual regression trees. This makes this partitioning method very suitable to be used in an automated fashion such as in software packages, also when a wide range of predictor variables is used.

To simulate different sampling strategies sample locations were selected using a (i) regular grid, (ii) systematic sampling, (iii) random sampling, (iv) sampling with differential probability of inclusion, (v) stratified sampling according to landcover classes and (vi) clustered sampling. Because it is not guaranteed that in 2008 households were sampled at the selected locations, for each sample the nearest enumeration area was taken. In case more than one enumeration area share the same location (when more enumeration areas are located in one parish, they all get the centroid of the parish as georeference), one is selected randomly.

In a first stage, political borders of local government units as of 2007 (the year in which the Uganda 2008 NLC was planned) were used to aggregate model results per administrative unit. Later livestock number estimates were aggregated using artificial administrative units sharing the same area size in order to assess the operational scale. Areas of 1000 to 5000km² with an interval of 1000km² were tested covering average sizes of subcounties, counties and districts in Uganda, and sample sizes included 100, 200, 400, 800 and 1600 enumeration areas per administrative unit.

The model predicted cattle numbers for the same areas as for which training data was available which generalizes livestock abundance data within similar areas and reduces the risk of under- or overestimating livestock numbers. Apart from the modelling results, livestock numbers were also estimated by averaging model results and direct estimates in an ensemble approach⁸. For both approaches and a null-model (estimating cattle numbers by averaging direct estimates with the median of sampled cattle numbers), the null-hypothesis that error values were similar was tested using an ANOVA test together with Tukey Honest Significant Difference post-hoc tests in order to rank the different approaches.

While in this study error values can be obtained by comparing modeled livestock number estimates with aggregated Uganda 2008 NLC entries, this wealth of data is generally not available in a mixed farming environment. Therefore a resampling procedure was set-up to estimate error values based on cattle number estimate variance for a set of 50 subsamples. The resampling procedure was repeated 400 times on different sets of samples and tested for each combination of administrative unit size, sample size and subsample size. The approach was

tested for subsets of 30% and 60% of all samples, as well as for one sample being left out of the total set. Linear regression models were used to assess the correlation between variance and error. Because the error-variance ratios are larger for small variance values as compared to large variance values, both variables were transformed (Equation 1 and Equation 2).

$$var_t = \frac{var}{1 + var}$$

Equation 1: The variance is transformed so its value is bounded by 0 and 1.

$$err_t = err^x$$

Equation 2: The absolute error is exponentially transformed. The value of x is chosen from a sequence starting at 1/8 and ranging up to 3 using increments of 1/8 and the exponent resulting in the lowest residuals is selected.

RESULTS

A statistically significant accuracy increase was obtained for all sample sizes except for sample sizes exceeding five enumeration areas per district when only administrative units with high average herd sizes were considered (Figure 1). This was found to be a result of the unbalanced training data as only few administrative units were found with large average herd sizes (>9 animals per household; Figure 2). The accuracy increase was also found for each landcover class. When considering an ensemble of direct estimates and random forest results, accuracy increases were found in each of the livestock abundance classes (Figure 3).

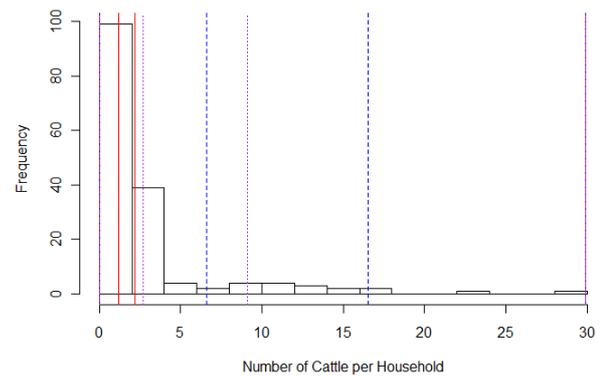
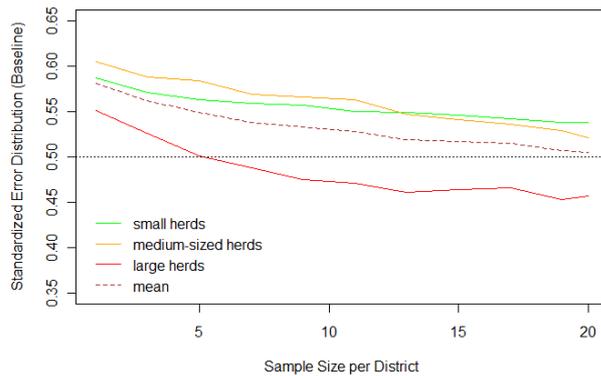


Figure 1: The standardized error distribution shows the ratio of error values of the direct estimate to those of the model results. Values below .5 denote an accuracy increase when livestock figures were estimated by the random forest instead of by direct estimation.

Figure 2: Distribution of mean number of livestock per household and categorization into three classes using a k-nearest neighbor technique.

The post-hoc test indicated that model results outperformed the direct estimates. The null-model performed worst.

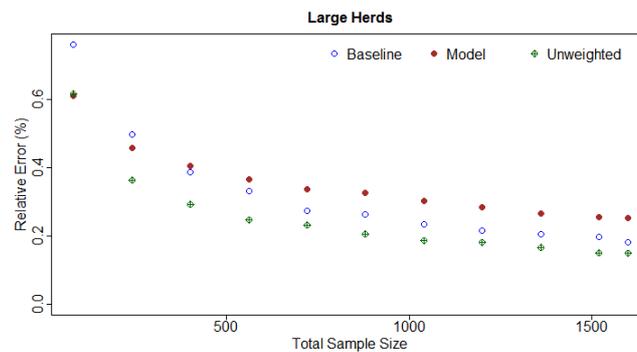


Figure 3: Ensemble model results (unweighted; green) have lower errors compared to direct estimates (baseline; blue) even when model errors (model; red) are higher.

When the same test was repeated for the artificial administrative units, similar results were obtained though accuracy levels differed among (i) area sizes for which estimates were made and (ii) administrative unit levels for which predictor variables were extracted. The added value of the ensemble model over direct estimates was most pronounced when predictor variables were extracted on parish level.

When assessing resampling variances, the absolute error clearly shows increasing values for higher variances. The relative error also shows low values for high variances (Figure 4 - Left). However, when evaluating data from all repetitions, a clear increasing tendency can be observed for the highest of 60, 70, 80 and 90% of the lowest error values. Exponents to transform variance values and which resulted in the lowest linear regression residuals were selected and used to model .6, .7, .8 and .9 error percentiles (Figure 4 - Right). The exponents increase towards larger sample sizes and smaller administrative units (Figure 4 - Middle).

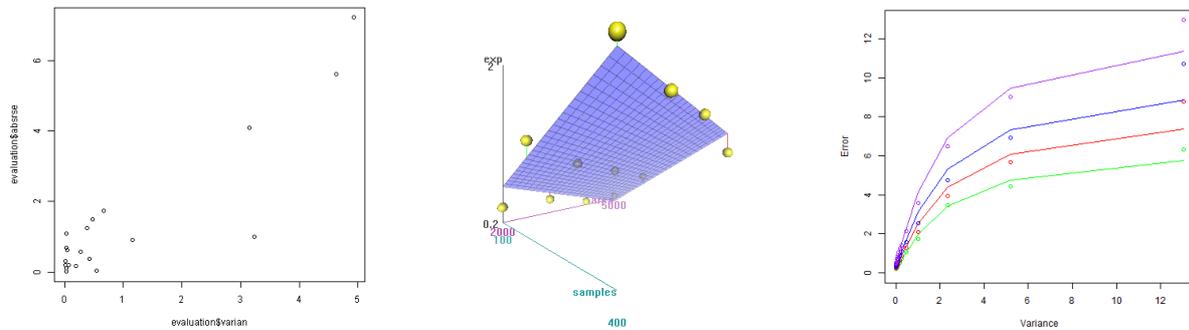


Figure 4: Left - Scatterplot of variance and error for one repetition (20 administrative units). Middle – Exponents used to transform variance in an error prediction model. Right – Modeled (lines) and observed (points) error values.

DISCUSSION

Random forests estimate cattle numbers more accurate than direct estimates when considering administrative units with low or medium livestock numbers per household. High livestock numbers are often underestimated. While this could be improved by balancing the training dataset (i.e. an equal number of enumeration areas for each of the livestock density classes), it was preferred to keep the training dataset unbalanced to avoid the overall accuracy increase to diminish because sample size would decrease tremendously and the majority of livestock numbers in areas with low livestock densities would be overestimated. The ensemble of modelled cattle numbers and direct estimates lowers error values in all livestock abundance classes offering a robust methodology to improve the accuracy of livestock number estimates while only additional data is required which is freely available for countries worldwide. Therefore the presented approach also lowers sample size requirements.

Using the test results which were obtained during this study, operational scales to report livestock abundance on can be determined for a range of targeted confidence levels. Linear models also permit to assess worst case error values for 60, 70, 80 and 90% confidence levels.

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Antimicrobial reduction in pig production up to 70% possible without jeopardizing production parameters - preliminary Belgian data

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INTRODUCTION

Reduced and prudent use of antimicrobials is high on the international agenda (1). Attention is drawn towards it because of increasing awareness of antimicrobial resistance selection. Furthermore the European Surveillance of Veterinary Antimicrobial Consumption (ESVAC) recently published a paper on sales of veterinary antimicrobial agents in 25 EU/EEA countries in 2011 (2). This ESVAC paper shows that in many EU countries veterinary antimicrobial consumption is high and that differences between countries are large. This suggests the possibility to reduce the consumption in the high-consuming countries.

The paper of Callens et al. highlights that an average fattening pig in Belgium is being treated for 20% of their lifespan and that the majority of treatments are prophylactic (3). Failure to treat animals adequately, posing a risk to animal-originated food production, and antimicrobial resistance genes transmitting from animals to humans emphasize the need for action. On the Flemish level, Boerenbond and Belpork VZW initiated the project “reduction antimicrobial usage”, executed by the Epidemiology Unit of the Faculty of Veterinary Medicine of Ghent University. In this project pig farmers are guided in the optimization of their herd management and biosecurity level. On the other hand they are advised in the reduced and prudent use of antimicrobial in their herds. This abstract provides preliminary results on changes in production parameters, biosecurity status and antimicrobial usage.

MATERIALS AND METHODS

In total 64 herds have voluntarily applied for participation. Until this moment 33 herd results have been analyzed and their results will be described here.

The initial herd situation on production parameters, disease problems, diagnostic results, biosecurity status and antimicrobial usage was established during a first herd visit. To analyze the biosecurity status the freely online web tool Biocheck.UGent was used (www.biocheck.ugent.be). This system provides a scientifically based score, with a maximum of 100 points, for six subcategories of external and six subcategories internal biosecurity. Antimicrobial usage was quantified using the ABcheck.UGent system (www.abcheck.ugent.be). This, also freely online available, web tool calculates treatment incidences (TI) based on the formula of Timmerman (4). The TI expresses the number of animals out of 1000 animals that have been treated with a daily doses of antimicrobials or the number of days an average animal has been treated within a (fictive) period of 1000 days. For prophylactic usage the TI based on “used daily doses animal” (UDDA) was calculated and for curative treatments the TI based on “defined daily doses animal” (DDDA). Two animal categories were differentiated, the breeding animals (mainly sows) and the production animals. The latter being the piglets and finishers from birth till slaughter over a standardized period of 205 days.

Based on the gathered information, herd specific interventions were advised on biosecurity, herd management and antimicrobial usage. Herd veterinarians and if relevant other herd advisors were involved in the herd advisement.

Six till nine months later the herds were re-evaluated. During this third herd visit once more data on production parameters, biosecurity and antimicrobial usage were gathered and calculated.

Changes in production parameters, biosecurity status and antimicrobial usage between the initial situation and after herd visit three of 33 herds are given here. An ANOVA test in SPSS (IBM, version 21) was used to find statistical differences ($p < 0.05$) between the scores at the initial visit and after the third visit.

RESULTS

The average number of sows at the 33 herds was 276 with a minimum of 85 and a maximum of 600. On average the herds had 1362 finisher places. The majority of the herds ($n= 11$) work with a 3-week farrowing rhythm, followed by a 4-week system ($n= 9$).

On average the herds produced 25.8 weaned piglets per sow per year at the initial evaluation. The mortality till weaning was 13.1% and within the finisher period 3.4% on average. Growth was on average 665.2 gram/day with a feed conversion ratio of 2.7.

For external biosecurity the on average highest score was for the subcategory “purchasing policy” with a score of 83.9%. The subcategory with the on average lowest score was the “supply of fodder, water and equipment” with 40.0%. The average scores for the internal biosecurity were lower than for the external biosecurity, with 49.5% versus 64.1% respectively. The highest scoring subcategory in internal biosecurity is the “fattening period” with 60.4%. 38.1% for “compartmentalizing, working lines and equipment” is the lowest score in the internal biosecurity.

Antimicrobial usage in both sows and piglets/finishers showed large variation between herds in both prophylactic and curative usage at the initial evaluation. The average $TI_{\text{prophylactic}}$ for sows was 31.7 with a minimal of 0 and a maximum of 182. From birth till slaughter this was 93.9, with a minimum of 0 and a maximum of 354.

Herd specific advices were provided on additional vaccination based on for example diagnostic evaluation, optimization of working lines, manipulation of piglets and the implementation of the hygiene lock. In general advices on antimicrobial usage focused on breaking-through the historical routine, the insurance that treatment with antimicrobials provides according to the farmers. A switch from prophylactic group treatment to treatment of individual animals was also advised. Having a detailed and structured overview of the (disease) situation on the herd and acting according to that, checking the correctness of the vaccination scheme, optimizing the biosecurity level are the general area's where the emphasis was on in the suggested interventions.

Re-evaluation after implementation of interventions shows that the number of weaned piglets per sows per year increased with 0.8 piglet to 26.6. The mortality till weaning decreased with 3.4% to 12.6%. In the finishers the mortality decreased with 6.7% to 3.1%. The growth was slightly less on average at herd visit 3 with 662.7 gram/day (-0.4%). However the feed conversion ratio decreased with 2.8% to 2.6. None of the production parameters showed statically significant differences between visit 1 and visit 3.

The external biosecurity increased with 6.6% to 68.3% on average. The largest increase could be found in the subcategory “vermin and bird control” with 9.4%. The internal biosecurity increased with 18.8% to 58.6%. The largest increase of 28.8%, was seen in the initially lowest scoring subcategory “compartmentalizing, working lines and equipment”, rising to a score of 49.1%. Statistically significant differences were seen in the internal biosecurity subcategories “management of diseases” ($p= 0.03$) and “farrowing and suckling period” ($p= 0.04$).

Prophylactic antimicrobial usage significantly ($p= 0.02$) decreased by 73.6% in the breeding animals to a TI of 8.4. From birth till slaughter it was not statistically significant, however we saw a reduction of 27.6% to a TI of 67.9. Eleven herds with sows completely stopped with prophylactic antimicrobial treatment to this animal category. One herd increased the TI with 145% in the sow prophylactic treatment. From birth till slaughter seven herds completely stopped with prophylactic treatments, while one herd increased antimicrobial treatment with 218% and another two herds with 343%. For the curative treatments the decreases were 0.8% and 80.6% respectively for breeding animals and production animals. Table 1 shows all changes between herd visit 1 and 3.

Table 1 Changes in number and percentages between herd visit 1 and herd visit 3 for production parameters, biosecurity status and antimicrobial usage. Statistical significant level provided for the ANOVA test (bold = $p < 0.05$).

	Herd visit 1	Herd visit 3	Difference	Percentage	Sig.
W/S/Y	25.84	26.62	0.78	3.01%	.173
Mortality till weaning (%)	13.08	12.63	-0.45	-3.43%	.637
Mortality finishers (%)	3.35	3.13	-0.22	-6.69%	.142
Growth (g/day)	665.22	662.70	-2.52	-0.38%	.913
Feed conversion ratio	2.67	2.60	-0.08	-2.84%	.142
TI Prophylactic sows	31.65	8.36	-23.29	-73.58%	.017
TI Prophylactic birth-slaughter (205 days)	93.87	67.93	-25.94	-27.64%	.282
TI curative sows	21.79	21.62	-0.17	-0.78%	.991
TI Curative birth-slaughter (205 days)	125.74	24.44	-101.30	-80.56%	.045
External biosecurity	64.08	68.30	4.22	6.59%	.068
Purchasing policy	83.87	88.55	4.68	5.58%	.161
Removing animals, manure, carcasses	65.58	71.09	5.51	8.41%	.116
Supply fodder, water, equipment	40.05	41.33	1.28	3.20%	.783
Access check	62.74	67.55	4.81	7.66%	.219
Vermin and bird control	63.42	69.39	5.97	9.42%	.216
Location and environment	49.79	50.30	0.51	1.03%	.936
Internal biosecurity	49.53	58.85	9.32	18.82%	.017
Management of diseases	49.47	61.82	12.34	24.95%	.033
Farrowing and suckling period	50.03	59.23	9.20	18.40%	.043
Nursery unit	60.44	62.27	1.83	3.02%	.726
Fattening period	59.92	70.16	10.24	17.09%	.125
Compartmentalizing, working lines, equipment	38.11	49.06	10.96	28.75%	.052
Cleaning and disinfection	48.68	59.45	10.77	22.12%	.053

DISCUSSION

The large variation between herds on biosecurity status and antimicrobial usage seen during the first herd visit suggests room for improvement. External biosecurity scores are on average higher than internal biosecurity. This might be due to the fact that imposing rules upon external visitors might be easier for a farmer than changing his own routines.

Interesting to notice is that the average TI found in this study from birth till slaughter is lower than in the study of Callens et al. (3). This might on the one hand be because this study was carried out slightly later and farmers might have been more aware and already reduced their usage. However the impact of the fact that all farmers in project “reduction antimicrobial usage” applied on fully voluntary basis, most likely selecting herds/farmers that have more interest in the topic and/or are the forerunners, will probably be the most important reason for the difference.

These preliminary results show that on average Flemish herds it is possible to improve the biosecurity level. Even the own routines of the farmer can be improved. A reduction in antimicrobial usage is most certainly possible in Flemish herds, as has been shown with an average reduction in TI of 73% in breeding animals and 27% from birth till slaughter. However it has also been shown that not all herds were able to reduce antimicrobial usage. In some of the cases the motive for the increased usage was not fully transparent.

In general the preliminary conclusion of project “reduction antimicrobial usage” is:
Clear guided interventions in improving the biosecurity level, overall management practices and the focus on prudent use of antimicrobials allows for an important reduction in antimicrobial usage without jeopardizing the productivity.

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A descriptive study on biosecurity measures in selected Belgian cattle herds

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INTRODUCTION

In modern veterinary medicine, disease prevention becomes increasingly important in replacement of curative medicine. This shift from cure towards prevention involves the implement of biosecurity, which includes all measures preventing pathogens from entering a herd and reducing the spread of pathogens within a herd (Laanen et al., 2010).

In Belgium, a very densely populated livestock area, biosecurity measures in pig and poultry herds have already been studied (Ribbens et al., 2008; Van Steenwinkel et al., 2011). However, for cattle herds no studies have been conducted yet. Therefore the aim of the present study was to map the current application of biosecurity measures in cattle herds.

MATERIAL AND METHODS

Data were collected as part of a cross-sectional study about management practices in cattle herds free from bovine viral diarrhoea virus (BVDV). The study was conducted in 74 herds, of which 70 Flemish, 2 Walloon and 2 Dutch herds. By means of a face-to-face interview semi-closed and closed questions about the presence of biosecurity measures, herd and BVDV management were asked. The dataset was composed of 33 milk herds, 16 beef herds and 25 mixed herds.

Data processing was performed according to Van Steenwinkel et al. (2010). Briefly, all information was coded numerically to enable descriptive analysis of biosecurity measures and recoded into categorical data for further analysis. Therefore, all variables were divided into groups, each expressing a different aspect of farm biosecurity. The following biosecurity variable groups were considered: (1) Presence of and contact with other animals [Other animals], (2) On farm movements of persons [Visitor frequency], (3) On farm movements of animals [Animal purchase], (4) Off farm movements of animals [Off movements Anim], (5) Hygiene of infrastructure [Infrastructure] and (6) Hygiene of persons [Hygiene visitors]. All variables were coded using values of 1 (biosecurity measure present) or 0 (absent). Then, for each biosecurity variable group (made up of several measures) the values for each individual variable were added up to generate a biosecurity score. Finally, each group score was scaled from 0 to 10. A higher score implies a better biosecurity level for the variable group concerned. Two supplementary variables were included and attributed a multiple nominal measurement scale: type of herd (dairy, beef, mixed) and capacity of herd (small, medium, large). These categorical data were analysed with the categorical principal component analysis (CATPCA) procedure in SPSS. The object scores were included in a two-step cluster analysis to identify possible clusters of cattle herds with a similar biosecurity level.

RESULTS

An overview of the most relevant and striking results of biosecurity measure applicaiton can be found in Table A. Visitors frequently entering the herd are the veterinarian , the artificial insemination person and the cattle dealer with on average 60, 83 and 45 visits per year, respectively.

All six biosecurity variable groups substantially contributed to the analysis, accounting for 59,8% of the variance. The two-dimensional CATPCA reduction was able to distinguish between different herd types, while no difference in biosecurity between different herd sizes was noticed (Fig. 1). Beef herds tend to have higher scores for biosecurity measures concerning visitors and the purchase of animals compared to dairy and mixed herds. Biosecurity measures are less applied in mixed herds compared to dairy and beef herds. A two-step cluster analysis was not able to distinguish different risk-groups for biosecurity.

DISCUSSION

Although the concept of biosecurity is easy to embrace (Villaroel et al., 2007), the level of implementation of biosecurity measures in cattle production was poor as observed during this study. It is recommended that cattle farmers, in close collaboration with their veterinarian, develop a comprehensive written biosecurity plan as such a plan is easier to execute, evaluate and revise than are unwritten measures (Villaroel et al., 2007; Negron et al., 2011).

A two-step cluster analysis was not able to distinguish different risk-groups for biosecurity indicating that no typical groups with low or high biosecurity profiles could be identified. Consequentially all cattle herds can be approached in a comparable manner as consulting regarding biosecurity is concerned.

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Table 1. Most relevant results of categorical variables concerning biosecurity status

Off farm movements animals	
Use of material in common with other farmers	33%
Truck of cattle dealer is empty when loading animals	16%
Hygiene infrastructure	
Presence of a calving box	72%
Calving box is used to house sick cattle	58%
Hygiene visitors	
Use of disinfecting footbath	9%
Use of farm-specific boots	20%
Use of farm-specific coverall	14%
Visitors have direct access to the stables	77%
Animal purchase	
Presence of quarantine stable (no contact with own animals)	23%
Application of quarantine period > 3 weeks	12%
Testing of all purchased animals	64%
Other animals	
Presence of a rodent control programme	86%
Contact with neighboring cattle on pastures	70%

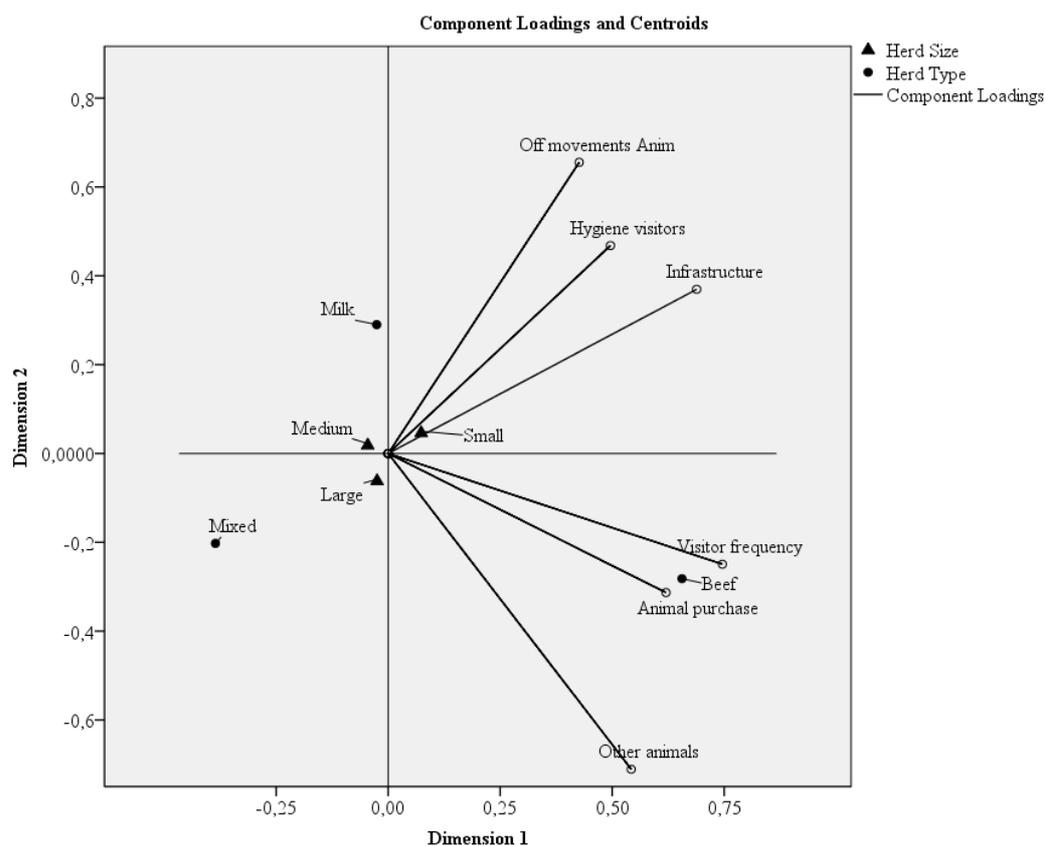


Fig. 1.

Biplot of component loadings for the active variables and multiple nominal category points, CATPCA analysis.

THE USE OF ANTIMICROBIALS ON DAIRY FARMS IN FLANDERS, BELGIUM

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INTRODUCTION

Antimicrobials are an indispensable tool for decreasing the prevalence and incidence of infectious diseases. Obviously, their use in veterinary medicine has a positive effect on animal health, well-being and productivity. Still, the society demands accountability when using and/or selling veterinary antimicrobials especially in food producing animals. Excessive and/or injudicious use of antimicrobials is seen as a health threat as it potentially promotes the development of antimicrobial resistance of veterinary and human-associated bacteria. The dairy industry has a well-respected image when it comes down to safeguarding the quality of its products, based on substantial testing of multiple milk quality parameters, residue testing, Still, data quantifying and qualifying the use of antimicrobials are lacking.

That in mind, a project was designed to (1) quantify the antimicrobial use (AMU) on Flemish dairy farms, (2) to determine the association between AMU and the prevalence of antimicrobial resistance of mastitis pathogens and commensals cultured from milk samples, (3) to study how AMU is related to udder health status of the herd, and (4) to evaluate to what extent AMU and the prevalence of antimicrobial resistance can be reduced via proactive udder health and milk quality counseling. This paper describes some preliminary results on the usage of antimicrobials on Flemish dairy farms.

MATERIALS AND METHODS

Herds

Data are collected on sixty-one dairy farms distributed over the 5 different Flemish provinces. Half of the included herds ($n = 30$) are visited on a regular basis to actively monitor udder health and milk quality, whereas the other half serve as controls ($n = 31$). To quantify the AMU on Flemish dairy herds, only farms belonging to the control group were eligible for inclusion. Initially, this control group consisted of 31 dairy farms of which 1 organic one and 30 conventional ones. Yet, four farms have been excluded from the study for reasons of incomplete AMU data collection.

Six farms only housed dairy cows. The other 21 farms also kept beef cows, farmed other animals such as poultry, pigs and veal or combined livestock farming with agriculture.

The majority (51%) of the farms is equipped with a fish bone milking parlor. On the other farms, the cows are milked in a tie stall ($n = 1$), tandem milking parlor ($n = 4$), side-by-side milking system ($n = 1$) or rotary ($n = 2$). Five farms are equipped with an automatic milking system. Except for three farms, cows are housed in a free stall barn with slatted floor. Sawdust is the most frequently used bedding material.

On 24 farms, blanket dry cow therapy with long-acting antimicrobials was applied. On 15 of those farms, long-acting antimicrobials were combined with an internal teat sealer. Selective dry cow therapy was applied on three farms. On those farms, cows that were not infected at the end of lactation were dried-off with an internal teat sealer only.

Data collection

On all participating herds, the usage of antimicrobials was recorded between January 2012 and March 2013 through so-called garbage can audits. Farmers were instructed to deposit all empty drug containers used for the treatment of adult lactating and dry dairy cows in the receptacles.

In March 2013, the empty drug containers were collected and counted. The gathered data were entered in an Excel-file for further calculation.

Statistical analysis

The antimicrobial drug use rate (ADUR) or treatment incidence, defined as the number of animal defined daily-doses (ADD) used on a farm per 1000 cows per day, was calculated.

$$\text{ADUR} = \frac{\text{Active substance used in the study period (g)} \times 1000}{\text{ADD} \times \text{number animals} \times \text{number of days in the study period}}$$

The animal defined daily dose was defined as the average daily on-label dosage multiplied by the approximate weight of an adult dairy cow (i.e. body weight = 600 kg) and was based on the Belgian compendium of veterinary products (www.bcfi-vet.be). Dry cow therapy consists of four intramammary tubes, and was counted for four animal daily doses. The number of animals consisted of the total number of adult lactating and dry cows at the dairy farm during the study period as determined by the Dairy Herd Improvement test-day data (CRV, Oosterzele, Belgium). Because the total number of adult cattle varied only very little from month to month, an average of the total number of adult cattle per farm was calculated. The number of antimicrobial drug use on a dairy farm was calculated from the time that the receptacle was foreseen on the farm until the date that the empty drug containers were collected. The study period lasted on average 281 days with a minimum of 252 days and a maximum of 332 days.

RESULTS AND DISCUSSION

The average herd size varies between 42 and 156 lactating dairy cows. The average bulk milk somatic cell count was 184,765 cells/ml and varies between 88,394 cells/ml and 305,135 cells/ml. The average milk production was estimated at 9,004 kilograms milk per cow per year.

Preliminary results indicate an average herd ADUR of 18.0 with a median value of 17.3. A large variation among the different herds is evident from the range in ADUR from 8.5 up to 44.4. The highest proportion of AMU was used for intramammary treatments (i.e. ADUR = 9.6) of which 44% for antimicrobial dry cow therapy. The ADUR of 3th and 4th generation cephalosporins is 4.1. With an ADUR of 0.60, fluoroquinolones are apparently less frequently used.

In Canada, a similar study was conducted. Compared to those data, the average ADUR on the Flemish dairy herds seems to be slightly higher compared to the Canadian one (ADUR = 14.2). Strikingly is the large difference in the use of antimicrobial drugs of high importance in human medicine, i.e. the 3th and 4th generation cephalosporins and fluoroquinolones, between Canada (ADUR = 2.2) and Belgium (ADUR = 4.7).

CONCLUSIONS

The large variation in ADUR among the farms indicates that there is still room for improvement on some farms at least. Beta-lactam antibiotics have the highest ADUR (15.9). Antimicrobial drugs of high importance in human medicine still account for more than 25% of the total AMU, which is worrying.

In the upcoming months, collection of AMU data will continue, and the gathered AMU data will be further explored. In addition, the association between the herds' udder health status and the AMU on the one hand and the association between AMU and the prevalence of antimicrobial resistance of mastitis pathogens on the other hand will be determined.

Poster presentations

VIRULENCE COMPARISON AND QUANTIFICATION OF HORIZONTAL BOVINE VIRAL DIARRHOEA VIRUS TRANSMISSION FOLLOWING EXPERIMENTAL INFECTION IN CALVES.

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Bovine Viral Diarrhoea Virus (BVDV) is a worldwide spread virus that most commonly infects cattle and can cause considerable economic losses. When infecting susceptible animals in early gestation, BVDV is able to cause persistent infections by infecting the foetus. These persistently infected (PI) animals are important sources of infection. On the contrary, transiently infected (TI) animals are believed to be less important in the epidemiology of BVDV. However, transient infections with a severe BVDV-2 strain can spread explosively. Only few studies were performed to determine the transmission potential of TI animals. Nevertheless, understanding the transmission capacity of TI cattle is very useful when establishing BVDV control programmes, especially in cattle-dense regions like Belgium. Therefore the aim of this study was to compare BVDV strain virulence and to estimate basic reproduction ratios for horizontal BVDV transmission by TI cattle following experimental infections using two Belgian virulent BVDV field isolates.

Transmission capacity by TI animals was determined during two trials. In trial 1 and 2 a BVDV-1b and a BVDV-2a strain were used, respectively. In each trial three calves were inoculated with BVDV through intranasal instillation and housed together with seven contact animals. In case there remained BVDV seronegative animals following the first inoculation of each trial, all seroconverted animals were removed and the experimental design was repeated. To compare virus transmission capacity of TI animals with PI animals, a third trial was initiated. For this a calf persistently infected with a Belgian BVDV-1b strain was commingled with all ten calves of trial 2. During the experiments nasal swabs, whole blood and serum samples were collected and clinical characteristics were monitored. Virus isolation, determination of degree of viraemia, PCR, virus neutralization and analysis of blood composition were performed on the collected samples. The basic reproduction ratio (R_0), a measure of transmission of infection, was calculated using the maximum likelihood estimator.

It was possible to isolate virus and to detect BVDV in nasal swabs from each inoculated animal. The severe clinical symptoms observed in the field with these isolates could not be reproduced during these experiments. Following the first inoculation with BVDV-1b no virus transmission was detected. The experimental infection was repeated by inoculating three animals and following this second inoculation 1 of 4 contact animals was infected. For trial 1 this resulted in a R_0 of 0.25 (95% CI 0.01-1.95). Following the first inoculation with BVDV-2a 1 of 7 contact animals was infected. The experimental infection was repeated by inoculating three animals and none of the three remaining contact animals was infected. For trial 2 this resulted in a R_0 of 0.24 (95% CI 0.01-2.11). In trial 3 all three remaining seronegative calves were infected by the PI animal, which resulted in a R_0 of $+\infty$ (95% CI 0.68- $+\infty$). No blood samples of the seven animals which seroconverted for BVDV-2a in trial 2 were PCR-positive during trial 3.

A very limited horizontal BVDV transmission was observed when TI animals were introduced into a group of susceptible calves, whereas very rapid and efficient transmission was found when a PI animal was introduced. These results suggest that TI animals poorly contribute to BVDV spread compared to PI animals. This stresses that the removal of PI animals is essential for BVDV control and eradication, whereas focussing on TI animals should not be necessary.

VIRUS TRANSMISSION AND CLINICAL SYMPTOMS IN CALVES EXPERIMENTALLY INFECTED WITH A RECENTLY DISCOVERED HYPERVIRULENT BVDV-2C STRAIN.

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Bovine Viral Diarrhoea Virus (BVDV) is a worldwide spread virus that most commonly infects cattle and can cause considerable economic losses. The virus is characterized by a strong genetic diversity and can be divided into two species: BVDV-1 and BVDV-2. When infecting susceptible animals between the second and fourth month of gestation, BVDV is able to cause persistent infections by infecting the foetus. These immunotolerant persistently infected (PI) animals are important sources of infection as they continuously shed BVDV in large quantities. On the contrary, transiently infected (TI) animals are believed to be less important in the epidemiology of BVDV.

In spring 2013 a BVDV-2c strain causing severe clinical symptoms and high mortality in calves was described in Germany and the Netherlands. No PI animals were detected on these herds, suggesting virus was spreading horizontally. The aim of this study was to try to reproduce the severe clinical symptoms observed in the field and to determine the transmission potential of animals transiently infected with this hypervirulent BVDV-2c strain following experimental infections in calves.

Ten BVDV-free and BVDV seronegative calves were selected, of which three calves were experimentally infected through intranasal instillation of 5.0×10^6 TCID₅₀ of the BVDV-2c field isolate and housed together with seven contact animals in a single box. Direct contact between all animals was possible during the experiment. In case there remained BVDV seronegative animals following the first inoculation, all seroconverted animals were removed and the experimental design was repeated. Nasal swabs, whole blood and serum samples were collected and clinical characteristics were monitored. Virus isolation, determination of degree of viraemia, PCR, virus neutralization test and analysis of blood composition were performed on the collected samples. The basic reproduction ratio, a measure of transmission of infection, was calculated using the maximum likelihood estimator. Following the first inoculation all three inoculated animals became infected, as whole blood samples became PCR-positive from 2 dpi onwards. A significant raise in body temperature was noticed from 7 dpi to 10 dpi. One animal remained subclinically infected and was PCR-positive until 13 dpi. A second experimentally infected animal suffered from severe diarrhoea and loss of appetite, which started at 8 dpi. This animal recovered 13 dpi, but whole blood samples remained PCR-positive until 16 dpi. The third inoculated animal developed severe diarrhoea 10 dpi, had complete loss of appetite with subsequent significant loss of body weight and died 17 dpi. One of seven contact animals became PCR-positive 11 dpi, indicating the inoculated animals were able to (limitedly) spread the virus. This contact infected animal developed severe diarrhoea with some loss of appetite between 19 and 24 dpi, but recovered afterwards. A second contact animal was infected and became PCR-positive between 24 and 38 dpi. The experimental design was repeated by inoculating 2 out of 5 remaining BVDV seronegative calves 63 days after the first inoculation. These animals were PCR-positive between 3 and 14 dpi. During this second inoculation, none of three contact animal were infected by the inoculated animals, which remained subclinically infected. For both inoculations this resulted in an overall basic reproduction ratio of 0.56 (95% CI 0.08-3.47). With a point estimation lower than one, this means virus transmission will theoretically fade out. This result suggests, as generally assumed, TI animals poorly contribute to BVDV spread, also when infected with the BVDV-2c strain.

During the experiment a broad range of clinical symptoms, ranging from subclinical infections over severe diarrhoea to death, were observed. This confirms the BVDV-strain itself is able to cause the severe clinical symptoms observed in the field. The inoculated animals during the second inoculation remained subclinically infected. This may indicate that age influences the clinical manifestation after infection. This was also noticed in the field as most severe clinical symptoms were noticed in young animals, while older animals were subclinically infected.

SPATIAL DISTRIBUTION OF RIFT VALLEY FEVER VECTORS IN THE EU AND THE NEIGHBOURING COUNTRIES OF THE MEDITERRANEAN BASIN.

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Although Rift Valley Fever (RVF) is mainly affecting large parts of sub-Saharan Africa, there is an increased concern that this vector-borne disease could be introduced into the European Union. Transmission of this viral zoonosis can occur through various pathways of which infected mosquitoes are one of the most important. In Southern Europe several species have been suspected as putative vector. These include for the genus *Aedes*: *A. vexans*, *Ochlerotatus caspius*, *O. detritus* and for the genus *Culex*: *C. pipiens*, *C. perexiguus*, *C. antennatus*, *C. theileri*, *C. tritaenorrhynchus*. The possible occurrence and/or distribution of these eight species in the Mediterranean basin are not fully clarified though crucial for the development of a risk assessment for the European Union. To acquire this information a stepwise approach was adopted. Firstly, a systematic literature review was initiated to compile all existing presence/absence data of these eight species in the area under study. A database of relevant explanatory environmental and eco-climatic data needed to model the spatial distribution and potential areas of spread was established. Predicted presence maps were computed using Random Classification Forest. Outputs were validated using accuracy assessment and compared to existing maps. For six of the eight species sufficient data was obtained covering a representative range. For *Culex tritaenorrhynchus* and *Culex antennatus* only few publications and/or scattered data were available. Despite some gaps in data coverage, for all species predicted presence maps showed an adequately high accuracy with AUC values ranging from 0.905 to 0.995. The produced distribution maps highlight specific regions in the European Union and countries around the Mediterranean Basin that are highly suitable for the occurrence of the putative vectors of RVF. Strengths and weaknesses of the adopted methodology and obtained results are discussed and further steps are shown to develop abundance models. This research was funded by EFSA who will use the computed model outputs as part of data driven spatial risk assessments for the introduction of RVF in the EU.

SATHELI: SPATIO-TEMPORAL CHARACTERIZATION OF SMALL WATER BODIES.

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Liver fluke epizootic outbreaks in livestock may cause spontaneous mortality and production losses. The liver fluke parasite (*Fasciola hepatica*) is transmitted by an intermediary snail-host, mainly *Galba truncatula* in Europe. This species thrives in Small Water Bodies (SWBs) such as ponds, ditches, trenches and their transition zones. The vector abundance shows seasonal peaks and is strongly influenced by SWB dynamics. Current modelling tools for the spatial distribution of disease vectors are limited to area-wide distribution models or static landscape models. SATHELI focuses on the development of earth-observation based tools to detect these SWBs and their dynamics. The goal is to develop spatio-temporal forecasting models for areas under potential liver fluke threat.

Recently, Unmanned Aerial Vehicles (UAVs) became available for remote sensing. The advantages are an increased very high temporal and spatial resolution, flexible deployment, and the potential for very rapid data acquisition and processing in comparison to traditional remote sensing methods. As part of the SATHELI project (Belspo), a multi-copter (FALCON 8 by Ascending Technologies) was chosen as opposed to a fixed wing model because it is able to hover and hence to hop within its action radius from one landscape element to another. This allowed us to focus on the relevant parts (SWBs) of the landscape, and monthly imagery was obtained from four farms in Belgium. Direct geo-referencing techniques were used to create image mosaic time series.

In order to detect and delineate the SWBs, a segmentation and classification algorithm was created in eCognition. The algorithm was applied to the monthly UAV images enabling to study the dynamic behavior of the SWBs. Obtained results are presented and discussed. At a later stage the obtained information on SWBs dynamics will be used as model input to create a probability map of snail occurrence for the study sites.

VETERINARIAN'S PERCEPTION ON ANTIMICROBIAL CONSUMPTION IN THE NETHERLANDS AND BELGIUM.

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Introduction

Antimicrobial use in animals poses a risk for development and selection of resistant bacteria. Since veterinarians are responsible to oversee antimicrobial use in animals, they might potentially play a crucial role in the reduction of antimicrobial consumption.

This study investigated the attitude, knowledge and behavior of large animal veterinarians towards antimicrobial usage and reduction of antimicrobial usage in animals. It also compared Belgian (Flemish) and Dutch veterinarians on this matter.

Materials and methods

A questionnaire was developed by Utrecht University, the Netherlands, containing questions about knowledge, attitude, self-reported behavior regarding antimicrobial consumption in farm animals, prescribing practices and perceived role in antimicrobial reduction. Large animal veterinarians were invited by email to fill in an online survey using SurveyMonkey. For Belgium the questionnaire was slightly adjusted to fit the Belgian situation. Email addresses of the practitioners were obtained from databases of the Royal Dutch Veterinary Association (KNMvD) for The Netherlands and from the mailing list from post veterinary education (IPV diergeneeskunde) in Belgium.

Results

118 Belgian and 390 Dutch veterinarians, with on average 16 years of experience, responded. The total number of farm animal practitioners in both Flanders and The Netherlands is estimated to be around 1000 and 1200 respectively. The estimated response rate is therefore 19% for Belgium and 32% for The Netherlands.

The respondents see the overall management of farmers (average scores 3.90 and 3.70 on a 5-point Likert scale respectively for Belgium and The Netherlands), suboptimal immunity of purchased animals (average score 3.74 Belgium and 3.91 The Netherlands) and the farmers economically driven mentality to treat with relatively cheaper antimicrobials (average score 3.71 Belgium and 3.70 The Netherlands) compared to taking preventing measures as an important cause for use of antimicrobials. The fact that prescribing antimicrobials is associated with the financial profit of selling antimicrobials is not seen as an important factor (average scores of 2.66 and 2.00 respectively for Belgium and The Netherlands).

Dutch respondents were more optimistic about the achievable reduction of antimicrobial use in 2015 compared to the situation in 2009. The highest reduction is expected to be achievable in the pig sector in The Netherlands (53.1%) and the poultry sector in Belgium (31.7%). In general the Belgian veterinarians are less confident in their estimated percentage reduction achievable (cattle 19.3% Belgium versus 35.0% The Netherlands, poultry 19.3% versus 32.7%, pigs 29.3% versus 53.1% and veal calves 26.0% versus 39.3%).

Improvements in housing and climate conditions are seen as most effective in the reduction of antimicrobial usage. Belgian veterinarians also expect an effect of improving hygienic measures on farms and the eradication of infectious animal diseases on the reduction of antimicrobial usage. In The Netherlands there is a higher expectation from individual treatment of animals. Implementation of educational interventions of farmers or veterinarians, complementary therapies, an antimicrobial tax or uncoupling of prescription and sales of veterinary antimicrobial are on the contrary seen as non-contributing in the reduction of antimicrobial usage.

High costs or too time consuming are two important perceived reasons for farmers not to implement veterinary advices in both countries. However, in Belgium conflicting advises given by other advisors is also seen as a major reason and scores significantly higher than in The Netherlands. Furthermore veterinarians in Belgium, more often than in The Netherlands, feel forced at least once every two months to prescribe antimicrobials (31.9% versus 14.8%).

Conclusion

In both Belgium and The Netherlands veterinarians are facing the challenging task to actively participate in reduction of antimicrobial usage in the herds under their veterinary care. Suboptimal management practices and economic reasons are believed to be important factors of high antimicrobial usage. However, introduction of an antibiotic-tax or the decoupling of prescribing and dispensing antimicrobials is not seen as the ultimate solution. A focus on improvement of housing, climate and hygiene would be more beneficial according to the veterinarians. In Belgium the influence of other advisors in the herd advice and feeling forced to prescribe antimicrobials is also more worrisome than in The Netherlands. In general the Belgian veterinarians estimate that a reduction of antimicrobial use of around 24% in the farm animal sector should be possible for the period between 2009 and 2015.

ANTIMICROBIAL RESISTANCE PREVALENCE AMONG PATHOGENIC AND COMMENSAL ESCHERICHIA COLI FROM FOOD-PRODUCING ANIMALS IN BELGIUM.

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Introduction

The necessity of monitoring programs on antimicrobial resistance has been acknowledged by the World Health Organization. Belgium has responded positively to the call of European Food Safety Authority and presented detailed studies for antimicrobial resistance in commensal *E. coli* (poultry, pigs, bovines, veal calves) and pathogenic *E. coli* (pigs and bovines).

Material and Methods

Commensal bacteria: Faecal samples were taken from randomly selected apparently healthy animals. Susceptibility testing was performed using a broth micro-dilution method. The EUCAST epidemiological cut-off values were used to indicate resistance on fourteen antimicrobial agents.

Pathogenic *E. coli*: Strains from pigs or bovines showing symptoms compatible with *E. coli* infection were isolated and identified at the species-level. Multiplex PCR tests were performed for virulence genes and the resistance profile was determined according to the CLSI protocol, using the Kirby-Bauer disk diffusion method and the CLSI clinical breakpoints to interpret the outcomes. For pigs, fifteen antimicrobial tablets were used, while for bovines twenty-four.

Results & Conclusions

Poultry and veal calves isolates of commensal *E. coli* demonstrated higher antimicrobial resistance prevalence than isolates from pigs and bovines. Fifty percent of poultry *E. coli* isolates were resistant to at least five antimicrobials, whereas sixty-one percent of bovine *E. coli* isolates were susceptible to all antimicrobials tested. On the contrary, antimicrobial resistance in bovine pathogenic *E. coli* showed a high resistance profile with more than half of the isolates being resistant to ten or more antimicrobials. As far as pigs are regarded, fifty percent of pathogenic *E. coli* isolates in pigs were resistant to five antimicrobials.

The obtained results were not significantly different from available study results in Belgian pigs (Callens et al., 2013) and broilers (Persoons et al., 2012). When comparing commensal and pathogenic studies, interesting outcomes were presented. Overall, methods and interpretation of resistance differed in many occasions among the reviewed studies, thus, revealing the need for a further data harmonization between such studies. Nevertheless, this was the first large scale Belgian report concerning antimicrobial resistance in commensal and pathogenic *E. coli*.

SALMONELLA SURVEILLANCE IN BREEDING PIG HOLDINGS.

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Following its evaluation of the pig *Salmonella* surveillance program in 2012, the Federal Agency for the Safety of the Food Chain (FASFC) decided to focus the program in the future on the breeding pig population instead of the fattening pig population and to use bacteriology instead of serology as it has been done so far.

The main objective of this study is to prepare an appropriate sampling design and to define a good criterion to assign a *Salmonella* positive (or negative) status to a farm based on the bacteriological testing results. For this, a sample of 52 breeding holdings was selected randomly. Each holding was visited once a month from April to September 2013 (6 sampling rounds). On each visit, 6 pairs of overshoes and 6 pairs of hand swabs were collected in the different units (insemination, gestation and farrowing) in order to be representative of the environment of the farms. In holdings with a fattening unit, two additional pairs of hand swabs were taken. The samples were taken in each unit and then pooled two by two for *Salmonella* isolation. The two sampling methods (overshoes versus hand swabs) will be compared in order to select the most appropriate method for the future surveillance program. Both the spatial and temporal distribution patterns of *Salmonella* in the breeding holdings will be evaluated to set up the new sampling design.

INVESTIGATION INTO THE PREVALENCE OF KETOSIS IN PERIPARTURIENT DAIRY COWS IN EU DAIRY HERDS IN 2011-2012.

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The prevalence of ketosis in EU dairy cows around the period of calving is largely unexplored and the aim of this study was to determine the prevalence of ketosis in West European dairy cows and its association with fresh cow diseases. A total of 4709 transition cows from 130 dairy farms were enrolled in Germany, France, Italy, the Netherlands and the UK during 2011-2012. Farms were a convenience sample selected from 39 participating veterinary clinics, and considered representative of the farms in the country and no ketosis prevention was regularly used on these farms. Herds were included where complete information was obtained on at least 12 cows including calving date, parity and Keto-test results. A milk-based test for ketones (Keto-Test, Elanco) was used for screening fresh cows and ketosis was defined as Keto-Test 100 μ mol/l or higher between 7-21 days after calving. Study cows were observed for clinical disease to 35 days post calving. Clinical diseases recorded included milk fever, retained placenta, metritis, mastitis, displaced abomasums, clinical ketosis, lameness and gastro-intestinal disease. Cow conditions included dystochia and twins. Multivariate analysis (general estimating equations logistic regression) was performed to determine country, farm, management, feed and cow factors associated with ketosis. The models ketosis controlled for clustering of cows within farms and within countries.

The associations between ketosis and fresh cow diseases or conditions within 35 days of calving were assessed through a series of multivariate GEE logistic regression models for each individual diagnosis. Thirty-nine percent of the 4709 cows were classified as having ketosis. The herd average of ketosis was 43% in Germany, 53% in France, 31% in Italy, 46% in the Netherlands and 31% in the UK. While clinical ketosis was not reported in most farms, 111 out of 130 (85%) had 25% or more of their fresh cows screened positive for ketosis. The risks of ketosis were significantly lower in Italy and the UK compared to France, the Netherlands and Germany. Larger herd size was associated with a decreased risk of ketosis. Cows that calved in April – June had the highest odds of ketosis, with about twice as high odds compared to cows that calved July-Sept. The cows that calved January-March tended to have 1.5 times higher risk for ketosis compared to cows that calved in July-September. The odds of ketosis in parity 2 and parity 3-7 was significantly higher (1.5 and 2.8 times higher) than the odds of ketosis in parity 1. The odds of ketosis was significantly smaller in parity 2 compared to parity 3-7. Ketosis was associated with significantly higher odds (OR= odds ratio) of all common fresh cow diseases; milk fever (OR:2.1), retained placenta (OR:1.6), metritis (OR:1.5), mastitis (OR:1.9), displaced abomasums (OR:3.4), clinical ketosis (OR:14.7), lameness (OR:1.8) and gastro-intestinal disorders (OR:3.8). There was no significant association between dystochia or twins and ketosis. This study shows that ketosis is very common in European dairy cows and that ketosis may be a gateway disease for periparturient disorders.

EVALUATING ANTIMICROBIAL USE RISK FACTORS ASSOCIATED WITH CEFTIOFUR RESISTANCE AND MULTIPLE RESISTANCE IN FECAL *E. COLI* IN PREWEANED CALVES.

Berge, A.C., Dewulf, J.
Ghent University

Reducing the use of antimicrobial drugs is one way of controlling antimicrobial resistance. However, it is not known to what extent a reduction of antimicrobial use will also result in a reversion to susceptibility WHO has indicated that the use of certain classes of antimicrobials should be avoided in animal husbandry in order to minimize the evolution of resistance for human health use. However, good scientific evidence for the best approaches for prudent use are lacking and these need to be addressed in high quality field research.

Various epidemiological and statistical approaches to describe antimicrobial use and single or multiple antimicrobial resistance result may all provide valuable information that need to be assessed together to find the optimal approach to minimize antimicrobial resistance while enabling treatment of bacterial disease in animals.

The objective of this study was to identify and compare antimicrobial use factors influencing ceftiofur and multiple drug resistance in fecal *Escherichia coli* isolated from pre-weaned dairy-source calves. Cohorts of 10 to 15 newborn calves on 26 dairies and 7 calf ranches in California were enrolled and sampled every 2 weeks until weaning (approximately 8 weeks of age). On smaller farms, cross-sectional cohorts of 15 pre-weaned calves were sampled 4 times. One fecal *E. coli* per sample was isolated and susceptibility tested to 12 antimicrobials using the disk diffusion method. Isolates were categorized as resistant or susceptible based on epidemiological cut-points of the data set.

Antimicrobial use factors associated with multiple antimicrobial resistance patterns containing resistance to 5 antibiotic classes (PENTAR); ampicillin, chloramphenicol, streptomycin, sulfisoxazole and tetracycline and single resistance to ceftiofur (XNLR) were described using separate GEE logistic regression models. The models controlled for geographical location, farm type and age of calves by including these factors as covariates and a repeated measure of calf nested within a farm. Prophylactic in feed antimicrobials was not significantly associated with ceftiofur resistance but significantly increased the likelihood of PENTAR. For both measures; MDR, PENTAR and XNLR, antimicrobial treatment strategies in the calves were the most important management factors associated with increasing odds of resistance. Isolates obtained from calves having received antibiotic treatment within 5 days prior to sampling were more likely to be MDR, PENTAR and XNLR. Increasing treatment intensity in the calf cohort was further associated with increasing MDR, PENTAR and XNLR. Although individual ceftiofur use and cohort use of ceftiofur increased XNLR, the use of other therapeutic antibiotics, such as florfenicol similarly increased ceftiofur resistance. This study indicates that changes in third generation cephalosporin resistance cannot simply be accomplished by minimizing the use of third generation cephalosporins. The factors selecting for multiple drug resistance, may be similar, and it may not be possible to study single drug resistance without evaluating several other antibiotic use and resistance patterns. The overall most important factors selecting for increasing multiple antimicrobial resistance were the overall use of prophylactic and therapeutic treatments, and this emphasizes the need to focus our efforts on management and other therapeutic approaches for calf health to effectively decrease the overall use.

DESCRIPTIVE AND SPATIAL ANALYSIS OF MORTALITY IN BELGIAN HONEYBEES DURING WINTER 2012.

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Over the last 6 years, an increase in honeybee mortality has been reported in several countries within and outside the EU. In 2011, the EC set up and co-financed a standardized and Europe-wide voluntary surveillance program in order to obtain reliable and accurate estimates of honeybee colony losses and health as well as information about the risk factors for these losses (EPILOBEE project).

The Belgian surveillance program was based on the study by Nguyen et al. (2011), which documented recent Belgian bee-pathogen prevalence. These pathogens are potential causes of winter colony mortality. The EU guidelines were adapted for a small-scale Belgian beekeeping scenario. The sampling strategy was multi-stage (apiary/colony levels) and stratified by province: 150 apiaries were selected from a sampling frame of 3000 registered beekeepers.

These apiaries were visited twice - in autumn 2012 and spring 2013 - and questionnaires were completed, collecting info on potential risk factors and mortality. Honeybee samples, systematically taken at the first visit, were screened for *Varroa destructor* by mite counts. Subsequently, the samples were then stored (frozen at -80°C) until spring 2013. During early Spring, winter mortality was recorded at the second visit (number of dead and live selected colonies observed at the apiary) and a number of the stored samples were selected for a case-control study, based on apiary level colony mortality rate. The assigned case and control apiaries were screened for bee-specific RNA-viruses by PCR.

With ArcGIS® software, several data layers from the apiary visit questionnaires (such as mortality, management practices, and surrounding landscapes) as well as the obtained laboratory test results, will be visualized on maps.. The spatial scan statistic will be used to highlight potential clusters (SatScan®) of apiary winter high mortality rates and of potential risk factors. The available data, procedures and maps will be presented.

This descriptive spatial analysis of honeybee winter colony mortality will generate hypotheses for future risk factor and spatial analyses. The putative risk factors (e.g. *Varroa* infestation rates, presence/absence of viruses, management, landcover data) will be evaluated as covariates in a logistic regression analysis with apiary mortality rates as dependent variable.

Reference:

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EVALUATION OF A DOUBLE-ATTENUATED *SALMONELLA* TYPHIMURIUM VACCINE (SALMOPORC[®]) IN THREE *SALMONELLA*-POSITIVE HERDS.

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Salmonellosis in humans was the second most commonly reported zoonotic disease in the EU in 2011. Moreover, 56.8% of the confirmed human salmonellosis cases could be attributable to pigs. In contrast to humans, *Salmonella*-infected pigs rarely present clinical symptoms, but several studies have demonstrated a reduced weight gain in pigs that are subclinically infected with *Salmonella*. Therefore, control measures in primary production that contribute to reducing *Salmonella* infections in pigs are of utmost importance, as they decrease both the risk towards human health and pig performance. Vaccination is one possible on-farm intervention strategy which has been explored previously in mainly piglet experiments. However, scarce information is available about *Salmonella* vaccination in finisher pigs under field conditions. In addition, only one *Salmonella* vaccine in pigs is currently commercially available in the EU, and it is nationally authorized only in Germany and Poland.

This study evaluated the effect and applicability of an early oral vaccination in suckling piglets with a double-attenuated *Salmonella* Typhimurium vaccine (Salmoporc[®], IDT Biologika). For this, three *Salmonella*-positive herds with a high level of *Salmonella*-specific antibodies and a confirmed bacteriological presence of *Salmonella* Typhimurium were selected. In each of these herds, 20 pregnant sows were selected three days after farrowing and their piglets were randomly allocated at litter-level to either a vaccinated (V) or unvaccinated control (C) group ($n = 2 \times 120$ piglets from 10 sows). At 3 and 24 days of age, 120 piglets were vaccinated, while another 120 piglets were left unvaccinated and served as control animals. After weaning and during fattening, the V and C groups were housed in separated pens. Both groups in each herd were monitored till slaughter age. All pigs were weighted individually at 3 days and 29 weeks of age. At 3 days and 10, 16 and 29 weeks of age ($n=25-30$ per group), blood and individual faecal samples were collected to assess possible *Salmonella*-specific serum antibodies (HerdChek Swine *Salmonella*, IDEXX Laboratories) and *Salmonella* spp. (ISO 6579 annex D). At slaughter (31 weeks of age), ileocaecal lymph nodes ($n=70$), caecal content ($n=35$) and carcass swabs ($n=10$) were collected from each group in every herd. An additional bacteriological *in vitro* test was performed on the isolation-positive samples from the V pigs to detect the vaccine strain.

Between 3 days and 29 weeks of age, the daily weight gain was significantly higher in the V ($546.8\text{g} \pm 78.4$) compared to the C animals ($509.3\text{g} \pm 87.6$) ($P < 0.05$). Furthermore, over all herds, the V animals showed a significantly higher (10 weeks of age) and lower (29 weeks of age) mean S/P ratio in serum, when compared to the C animals ($P < 0.01$): 0.49 ± 0.51 (V) vs. 0.31 ± 0.46 (C) at 10 weeks of age, and 1.07 ± 0.55 (V) vs. 1.52 ± 0.68 (C) at 29 weeks of age. In addition, significantly less *Salmonella*-excreting pigs were present in the V group at 29 weeks of age: 7/79 (9%) (V) vs. 22/79 (28%) (C) ($P < 0.01$). No significant differences over all herds were found between both groups in the mean S/P ratio at 3 days of age, nor in the proportion of *Salmonella*-excreting pigs at 10 and 16 weeks of age, or in the proportion of *Salmonella*-positive slaughter samples ($P > 0.05$). The vaccine strain was detected in all three herds, in faeces during the trial, as well as in lymph nodes and caecal content at slaughter. The serological and bacteriological effects differed substantially between farms, however.

This study showed that vaccination with this attenuated *Salmonella* Typhimurium vaccine can improve the daily weight gain and reduce the overall *Salmonella* infection pressure in pig herds, although the effect level was farm-dependent. Hence, vaccination is a promising tool in a *Salmonella*-contaminated environment, but in national control programmes, supplementary bacteriological testing for the presence of the vaccine strain may be required.

MYCOPLASMA HYOPNEUMONIAE PREVALENCE AND SEASONAL EFFECT IN BELGIAN AND DUTCH PIG HERDS USING A TRACHEO-BRONCHIAL SWAB TECHNIQUE.

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Introduction – *Mycoplasma hyopneumoniae* (*M.hyo*) – one of the main pathogens of the Porcine Respiratory Disease Complex (PRDC) – is still important in modern intensive swine farming in Europe. Recently, a new sampling technique has been developed and validated for use in pigs, namely the tracheo-bronchial swab (TBS) technique [1]. The aim of the present study was to obtain data on distribution of *M.hyo* infection throughout closed pig herds in Belgium and The Netherlands using the TBS technique during an entire year. Sampling was mainly focused on early diagnosis, since piglets can already be infected during suckling through the sow [2,3,4] and further spread of infection occurs after weaning [5,6].

Materials and Methods – Closed pig farms (n = 176) were randomly selected and in every pig herd, at least 30 piglets were sampled in three age groups. The standard sampling protocol included 20 piglets at 3-5 weeks of age and 10-20 piglets in the 2nd half of the nursery stage (6-11 weeks of age). TBS were collected as described previously [1]. The collected mucus was suspended into 1 mL of buffered saline solution and stored fresh until analysis. Real-time PCR (RT-PCR) analysis was performed according to the standard operating procedure of the laboratory (IVD GmbH, Hannover, Germany) [7] and PCR results were reported as negative or positive for the presence of *M.hyo*. The detection limit of the RT-PCR test was set at 300 DNA copies of *M. hyo* per mL of TBS suspension. Several weather data related to the specific sampling period were collected from a central weather station point in the Benelux. Statistical analysis was performed towards seasonal differences and effect of weather characteristics on *M. hyo* prevalence.

Results – The prevalence of *M.hyo* in piglets around weaning was highest in Q2 (spring; 9.7%) and lowest during Q3 (summer; 3.8%). In older post-weaning piglets, an increase in *M. hyo* prevalence could be observed during all seasons, with the highest prevalence in Q4 (autumn; 17.2%) and the lowest prevalence in Q3 (summer; 2.3%). The presence of *M.hyo* at herd level at 3-5 weeks of age was significantly affected by the precipitation rate ($\beta = -0.026$; $P = 0.03$) during the week preceding sampling. In older post-weaning piglets, the risk for a herd to be *M.hyo*-positive was significantly affected by season [with the highest risk (OR = 1.91) for *M.hyo* positivity during autumn and the lowest risk (OR = 9.8) during summer ($\beta = 0.65$; $P = 0.003$)] and the average outdoor temperature ($\beta = 0.02$; $P = 0.007$) during the week preceding sampling.

Discussion – In our study, the individual animal prevalences at 3-5 weeks of age were higher (7.1%) as compared to the study of Villarreal and coworkers [3] using nasal swabs (3.3%). This difference could be explained by the use of the more sensitive TBS technique. Furthermore, in the study of Villarreal et al., 2010 [3], only pig farms with typical clinical signs related to *M.hyo* were selected, whereas in our study, inclusion criteria did not require specific clinical respiratory problems. These results are in accordance with Segalés et al. (2011) [9], who also observed a seasonal variation in *M.hyo* prevalence and circulation. In conclusion, although early *M.hyo* infection may show a seasonal effect, piglets may be infected with *M.hyo* throughout the entire year.

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PREVALENCE OF DIFFERENT RESPIRATORY PATHOGENS DURING POST-WEANING AND FATTENING PERIOD IN BELGIAN AND DUTCH PIG HERDS USING A TRACHEO-BRONCHIAL SWAB TECHNIQUE.

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Introduction

Besides *Mycoplasma hyopneumoniae* (*M.hyo*), many other viruses and bacteria can be concurrently present during respiratory problems in pigs, provoking the disease complex known as Porcine Respiratory Disease Complex (PRDC). Diagnosis of infections with these pathogens can be performed using different approaches, including the detection of the pathogen through Polymerase Chain Reaction (PCR) assays. Recently, a new sampling technique [1] has been developed and validated for the detection of *M.hyo* in pigs using PCR, namely the tracheo-bronchial swab (TBS) technique. With this technique, pathogens present at the level of the trachea-bronchial junction can be recovered and analysed through PCR-analysis. The aim of the present study was to obtain data on the distribution of different pathogens involved in PRDC in closed pig herds in Belgium and the Netherlands using the TBS technique.

Materials and methods

Three hundred and four pig farms were sampled using the TBS technique. In every herd, at least 30 coughing piglets were sampled in at least two age groups (3-5, 6-11 and 12-20 weeks of age). TBS were collected as described previously and analyzed using mPCR and/or dPCR (IVD GmbH, Hannover, Germany). A multiplex (m) [porcine respiratory coronavirus (PRCV), porcine reproductive and respiratory syndrome virus (PRRSV), swine influenza virus (SIV), porcine cytomegalovirus (PCMV), porcine circovirus 2 (PCV2)] and duplex (d) [*Actinobacillus pleuropneumoniae* (App), *Haemophilus parasuis* (Hps)] PCR assay were used to detect the different pathogens in the TBS. PCR results were reported as negative or positive for the presence of PRCV, SIV, PCMV, PCV2, App and Hps. For PRRSV, strain type EU/US or both was also reported.

Results

Overall, Hps with virulence factor was present in 78.0, 86.7 and 82.0% of the pigs samples at 3-5, 6-11 and 12-25 weeks of age. In piglets of 3-5 weeks of age, the most prevalent pathogens were SIV (25.3%), PCMV (19.5%), PRRSV-EU (12.7%) and *Mhyo* (6.4%), whereas in piglets of 6-11 weeks of age, PCMV (25.0%), PRRSV-EU (24.9%), SIV (16.3%) and *Mhyo* (9.6%) were the most prevalent pathogens. In older pigs (12-25 weeks of age), coughing was mostly provoked by *Mhyo* (61.3%), PCV-2 (40.3%) and PRRSV-EU (27.3%). Combined infections between PRRSV and SIV, *Mhyo* or PCV-2 did also occur at a prevalence level of 4.2%, 6.5% and 6.9%, respectively. The prevalence of triple infections were as following: PRRSV-*Mhyo*-SIV 0.6%, PRRSV-PCV-2-SIV 1.0% and PRRSV-*Mhyo*-PCV-2 2.3%.

Discussion

The present study clearly shows that different viral pathogens responsible for PRDC may already be present during the post-weaning period. Concerning PRRSV, the most prevalent type was PRRSV-EU, whereas PRRSV-US was far less frequent. It is clear that in several herds, *Mhyo* is already present in piglets at weaning, further increasing in the second part of the nursery period. These observations are in accordance with Villarreal et al. and Meyns et al. [2,3,4]. Hps was more prevalent than previously assumed. The prevalence of co-infection and triple infections of PRRSV with SIV, *Mhyo* or PCV-2 also may occur, but their prevalence is rather low as compared to double infections. In conclusion, the present study showed that many other respiratory pathogens are present during the post-weaning and fattening period, which may complicate the clinical picture of respiratory disease.

References

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BAYESIAN ESTIMATION OF TRUE PREVALENCE FROM APPARENT PREVALENCE IN R: INTRODUCING THE 'PREVALENCE' PACKAGE.

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Diagnostic tests are crucial tools in many epidemiological studies. However, due to imperfect sensitivity and/or specificity, these tests provide biased estimates of the true prevalence. Based on prior knowledge about the test characteristics, however, it becomes possible to estimate the true prevalence from the apparent prevalence. To this end, a Bayesian approach is considered most appropriate, as it is able to flexibly incorporate such prior knowledge in the estimation process. Different Bayesian models have been proposed in the literature to estimate true prevalence from apparent prevalence. However, the application of these models has remained cumbersome, as there are no tools available that implement them. Researchers have therefore been compelled to derive and develop their own models, most often in spread sheet documents or in Bayesian software such as WinBUGS and OpenBUGS. This approach is error-prone, and hampers transparent and reproducible research.

To address this gap, we developed the 'prevalence' package in R, a free and open-source language and environment for statistical programming. As R, the 'prevalence' package is freely available and open-source. The package currently provides functions for the Bayesian estimation of true prevalence from individual samples tested with a single test; pooled samples tested with a single test; and individual samples tested with multiple tests. A variety of numerical and graphical diagnostics are available to assess model fit and convergence. The package further provides functionalities to establish prior Beta and Beta-PERT distributions for test sensitivity and specificity based on expert opinion. Work is in progress to develop functions for dealing with clustered samples and for including covariates in the different models.

By combining a variety of established methodologies for model fitting and evaluation, the 'prevalence' package provides a harmonized and comprehensive environment for true prevalence estimation. We therefore hope that the 'prevalence' package may become a useful tools for veterinary epidemiologists.

VEE studiedagen

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