MANAGEMENT AND EFFICIENCY OF SHEEP BREEDING IN FORMER TRANSKEI, SOUTH AFRICA

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ABSTRACT

Until recently smallholder farmers in the former Transkei region had minimal access to a profitable market for their wool. In response, the South African wool industry and government took the initiative to help farmers by building shearing sheds, under which the local association can bulk the wool and trade directly with brokers who sell the wool on the auction. Yet major constraints in the production environment limit the farmers to produce large amounts wool of good quality. This article aims to analyse the wool production in the Transkei region and to investigate the influence of the local woolgrowers' association on wool production and price of the farmers. The higher production by farmers member of the association seems to be the result of the farming system applied, which is characterised by the higher use of inputs.

SAMENVATTING

Tot voor kort hadden kleinschalige boeren in de voormalige Transkei slechts beperkte toegang tot de rendabele wolmarkt. Als antwoord hierop namen de Zuid-Afrikaanse wolindustrie en de overheid het initiatief om schapenhouders te helpen door de bouw van scheerschuren. In deze scheerschuren kunnen lokale wolassociaties de geschoren wol sorteren, verpakken en verhandelen naar de veiling. Toch zijn er grote beperkingen in de productieomgeving die de boeren verhinderen om grote hoeveelheden van kwaliteitsvolle wol te leveren. Dit artikel wil de wolproductie in Transkei analyseren en onderzoeken wat de invloed is van de wolassociatie op de wolproductie en de prijs die boeren voor de wol krijgen. De hogere wolproductie door leden van de associatie lijkt het resultaat van het toegepaste productiesysteem, gekenmerkt door een hoger gebruik van inputs.

1. INTRODUCTION

The former homelands of South Africa are still lagging behind in economic development compared with the rest of South Africa. Eradication of poverty and economic development of the deprived areas are therefore high on the South African political agenda. One of the strategies followed is the development of the agricultural sector. Modern development strategy reports [1,3] emphasise the importance of increased market participation to trigger agricultural development.

In the Transkei region one of the initiatives of South African government focuses on wool production, because sheep farming is a traditional activity in this area. Sheep are an asset for social ceremonies and occasions. The wool is regarded as a by-product. Comparison with commercial sheep farming indicated a high potential for improvement. Therefore the National Wool Growers' Association (NWGA) took the initiative to establish shearing sheds in selected villages to increase the market capacity and provides training. The local wool growers' associations are responsible for the management of the shearing sheds.

2. MATERIAL AND METHODS

This article reports on a survey conducted in three villages in the Transkei region: Lucy, Xume and Mhlahlane during August and September 2000. In Xume and Lucy a shearing shed was established and equipped. The shearing committee in Lucy was active and well organised at the time of the survey. The shearing committee in Xume was existing, but dormant. Finally, Mhlahlane is a village neighbouring Xume, which does not have its own shearing shed. The respondents were selected through a non-probability sampling. All interviews were executed personally and translation was done by local extension officers. A total of 105 farmers were

interviewed (18 in Mhlahlane, 47 in Xume and 40 in Lucy), of whom 38 were member of a shearing shed. Twelve outliers were rejected from the analysis based on the number of animals on the farm. The questionnaire investigated on the farm business. An elaborate list of questions on the structure, inputs and revenues from sheep farming were included. Furthermore, to compare production, productivity and total sales of the farming systems, the budgets of members and non-members in Xume and Lucy were compared with a budget for farmers in Mhlahlane, and that of a commercial farm.

3. RESULTS AND DISCUSSION

The rural areas of the Transkei region are among the worst developed in South Africa. It is only since recently that farmers have started to produce wool as a cash product. The risks taken by the farmer to introduce new production techniques in sheep farming are relatively low compared to those of milk, meat and fruits. Nevertheless, during the field studies many constraints for wool production were recorded.

Low income from wool is the result of a low production volume and the low price farmers receive. Both the quality of the wool and the trader to whom the wool is sold are important in the price formation process. When sold to local traders, farmers receive a lower price but are paid immediately. In villages with a shearing shed, the farmers member of the association can bring their sheep to be properly shorn in the shed. The wool is graded and packaged. Brokers on the auction of Port Elisabeth or Durban trade the wool. Scab infection, weeds and a dirty kraal decrease the quality of the wool, and consequently also the price of the wool.

Farmers do not own enough sheep to produce wool at a 'commercial' level. Because of lack of breeding control, inbreeding is frequent and causes a deterioration of the productivity of the sheep. Poor feeding, no protection against the cold and inbreeding are mostly linked to the fact that sheep are grazed on communal land and not brought back into a fold at night. Because the communal grazing areas are not managed as pastures and are overgrazed, the overall quality of the grass is low. Communal grazing systems provide no incentive for individual owners to invest in pasture management. The lack of property rights therefore makes it impossible for the farmer to isolate infected flocks. Losses caused by infection of sheep scab are high. Scab affects both the amount of wool a sheep produces and the quality of the wool itself. Due to a lack of finance, treatment is insufficient to eradicate the endemic disease [2]. The sheep are not regularly dipped in adapted tanks, as many farmers regard it as a responsibility of government.

To investigate the influence of a membership of the shearing shed on the wool production table 1 shows the calculation of the value and expenditure on inputs of a flock of hundred sheep. The farm budgets enable us to compare the averages of some production characteristics between both members and non-members in Xume and Lucy, farmers in Mhlahlane and a commercial farm. The groups were not compared with a statistic test as the sizes of the groups differed considerably.

Table 1 Comparison of farm characteristics of members and non-members in Xume and Lucy, farmers in Mhlahlane and a commercial farm (for a standardized flock of 100 sheep)

	Non-member in Xume (n=36)	Member in Xume (n=7)	Non-member in Lucy (n=10)	Member in Lucy (n=25)	Mhlahlane (n=15)	Commercial farm (n=1)
Flock composition						
Total value (R)	32 025.60	32 041.93	32 905.51	34 615.46	31 827.09	
Farmers applying						
Feeding (%)	5.55	0	60.00	60.00	13.33	n/a
Deworming (%)	61.11	85.71	80.00	92.00	26.66	n/a
Dipping (%)	11.11	14.28	90.00	84.00	0.00	n/a
Inoculation (%)	58.33	57.14	70.00	88.00	46.67	n/a
Expenditure						
Shearing (R)	50.11	62.52	24.17	82.92	11.33	4 120.00
Feeding (R)	90.50	n/a	370.80	296.40	55.33	7 103.00
Veterinary care (R)	948.47	1202.00	2058.00	2510.00	680.27	1 834.00
Total (R)	1089.08	1264.52	2452.97	2889.32	746.93	13 057.00
Wool sales						
Revenue (R)	116.59	270.04	497.37	981.12	198.32	13 366.00

The average value of the flock of farmers in Lucy seems to be higher compared with the farmers in Xume. The average expenditure for feeding are higher in the budget of farmers in Lucy. In the budget for farmers who are member of the local association, more is spent on veterinary care. This is mostly due to a high proportion of

farmers who apply measures of veterinary care and a higher average expenditure per application. Also, average expenditure on shearing are the highest for the members of the local association in Lucy. The budget of members in Lucy considers a higher average production of wool per sheep and a higher average price compared to the non-members and the farmers in Xume and Mhlahlane. But the budgets of members and non-members in Xume do not differ a great deal. The comparison of the budgets shows that the members in Lucy spend on average more than the commercial farm. But in the latter, higher expenditure on feed were still to be taken into account. The budget suggests that a commercial farm earns enough from wool to cover all operational costs, whereas the farmers who are member of the association in Lucy, despite producing wool at a comparable level per sheep, suffered high expenditure on veterinary care which has a negative impact on the profit levels. The high expenditure on veterinary care can be explained by the communal grazing system. The disease load is higher. One sheep with scab can easily infect the rest of the flock and other flocks.

Also the importance of the extension services on the differences in performance between Lucy and Mhlahlane and Xume should not be underestimated. The extension officers are responsible for the motivation of farmers to form an association, as well as the transfer of knowledge. It seems that extension officers in Lucy have more success than officers in Xume and Mhlahlane in motivating farmers to apply a higher input/high output system.

4. CONCLUSIONS

The analyses suggest that the bulking of wool by the local wool association results in higher revenue from the sale of wool. However, the effect of the association on the production system is unclear. Nevertheless, the observation that farmers in Lucy are characterised by larger farms, sheep of an improved breed and relative high expenditure on inputs, suggests they have moved to a higher input/higher output farming system, whereas the farmers in Xume and Mhlahlane are locked in a low input/low output farming system.

Farmers in Lucy invested in sheep production. This could explain the establishment and persistence of the local woolgrowers' association. It would furthermore suggest that the availability of an active shearing shed stimulates the production of wool on farms of the members of the association, mainly because it provides a price incentive. It indicates that a minimal number of conditions are to be fulfilled for the farmer in order to profit from a local association, i.e. higher wool productions, wool of a better quality that can be sold on a better market. This requires more inputs to keep the flock in a good condition in a communal grazing system. The positive experience could then stimulate the farmers to increase production and make investments. Our analysis indicates that the existing communal land tenure system results in some constraints for the farmers to specialize in livestock. Whether or not changing the land tenure system to a system with more private property rights could be effective for the commercialisation of the smallholder farms was not studied and remains a question of debate. Traditional land tenure systems and rules are furthermore very slow to change.

The case study illustrated the importance of collective action among the farmers. A strong social capital is important for the success of development programmes. It therefore calls for the government to support local initiatives in which new governance structures and forms of social organisation are developed, whereby the community accepts changes of individual rights of farmers who are willing to intensify production. Yet further analysis is needed to analyse how the institutional environment, especially at the level of the traditional informal institutions, can be modified so that it yields the right incentives for development.

5. ACKNOWLEDGMENTS

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6. REFERENCES

[1] International Fund for Agricultural Development. *Rural Poverty Report 2001. The challenge of ending rural poverty*. Oxford University Press, New York, 2001.

[2] National Woolgrowers' Association. Sheep scap campaign. *Wool Farmers* 2001; 7: 1.

[3] World Bank. World Development Report 2003: Sustainable Development in a Dynamic World. Transforming Institutions, Growth, and Quality of Life. Oxford University Press for World Bank, New York, 2003.

THE EVOLUTION OF CANINE HIP DYSPLASIA IN BELGIUM BETWEEN 1995 AND AUGUST 2004.

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ABSTRACT

Canine hip dysplasia (CHD) is a highly prevalent disease. In many breeds in Europe prevalence in 1976 was as high as 35%. From 1976 until 1995, a steady decrease of the disorder was seen, but between 1995 and 1997 a slight increase of the prevalence was observed again. In the United Stated, the prevalence seems to keep on decreasing. The prevalence of CHD in Belgium during the ten last years shows no decline of CHD all over breeds and even an increase of dysplastic individuals in some breeds such as the German shepherd is seen. The prevalence of CHD in the medical imaging department is almost twice as high when compared to figures obtained by the official screening program. The results of this survey indicate CHD remains an important problem in the canine population and success of the eradication program is very low to non – existing.

SAMENVATTING

Heupdyslasie (HD) komt frekwent voor bij honden. In bepaalde Europese populaties was de prevalentie in 1976 35%. In de periode tussen 1976 en 1995 daalde de prevalentie van de aandoening zichtbaar. Tussen 1995 en 1997 stagneerde de daling en was er zelfs terug een kleine stijging te zien. Nochtans lijkt het er op dat in de USA de daling zich doorzet. In België is de laatste tien jaar geen daling te zien. Er is bij sommige rassen (o.a. Duitse herder) zelfs opnieuw een stijging merkbaar. In de kliniek van de medische beeldvorming worden er bijna twee maal zo veel dysplastische honden gevonden als in het officiële screening programma van de nationale commissie voor erfelijke skeletaandoeningen. Uit de resultaten van dit onderzoek blijkt duidelijk dat HD een fundamenteel probleem blijft in de Belgische hondenpopulatie en dat het eradicatieplan totaal geen effect heeft.

1. INTRODUCTION

Canine hip dysplasia (CHD) is an abnormal development of the hip joint (1). Laxity is increased, hips are partially or totally luxated, femoral head is abnormal and deformed and finally osteo-arthrotic changes become visible. It is a multi-factorial disorder, meaning both genetic and environmental factors influencing the outcome of the disease (4).

According to Kapatkin et al. (2), CHD is a highly prevalent disease and is nowadays present in 19.3 % of the total canine population (5). Many authors agree that the prevalence of CHD is underestimated because many radiographs of dogs are not officially scored (5, 6, 7).

In many breeds in Europe, such as the German shepherd and the Rottweiller, prevalence in 1976 was as high as 35%. From 1976 until 1995, a steady decrease of the disorder was seen, but between 1995 and 1997 a slight increase of the prevalence was observed in the Rottweiller, Bernese mountain dog and Golden retriever (personnel communication, Iams Eukanuba). The records of the Orthopaedic Foundation for Animals (USA; 3) indicate that between 1980 and 2000, the prevalence of CHD decreased, the amount of excellent hips rose and the ratio of mild versus moderate dysplasia changed positively.
The aim of this study was to estimate the evolution of CHD in Belgium during the last decade.

2. MATERIALS AND METHODS

Records (13006 dogs) of the National Institute of Inherited Skeletal Disorders (NCISD) and of the Medical Imaging Department; Ghent University (MI; 184 dogs) were used. The prevalence (%) all over and within breeds was estimated for every year of the last decade (1995 – August 2004; NCISD) and for the last three years (2002 – August 2004; MI), using an excel worksheet. The main difference between both data sets is that data of NCISD are more biased because radiographs are send by private practitioners, that do not send radiographs of obvious dysplastic dogs for official evaluation, while the radiographs made in our Department are all send in for official scoring, making them less biased. Finally, the amount of moderate hip dysplasia in affected dogs was estimated for different breeds

3. RESULTS

Considering all breeds, no clear rise or fall in prevalence of CHD between 1995 and 2001 was seen, but between 2001 and August 2004, a slight increase of about 2 % CHD was visible as is clear from fig. 1.

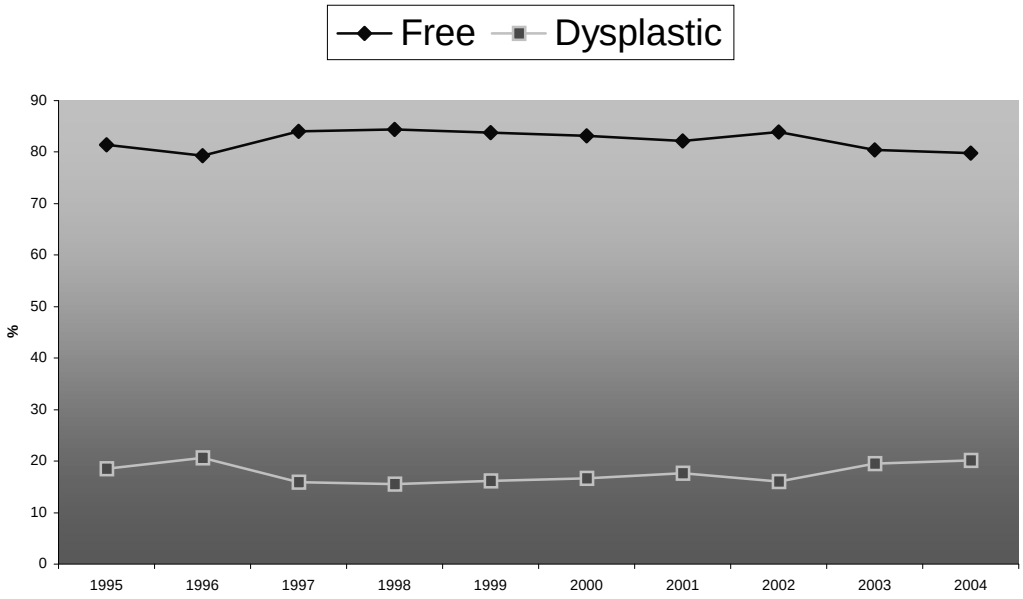

Fig. 1: The amount of sound hips all over breeds slightly decreases during the last three years. Rise of affected hips is almost 2 %

In the German shepherd, this increase is almost 6 % from 2000 on (fig. 2).

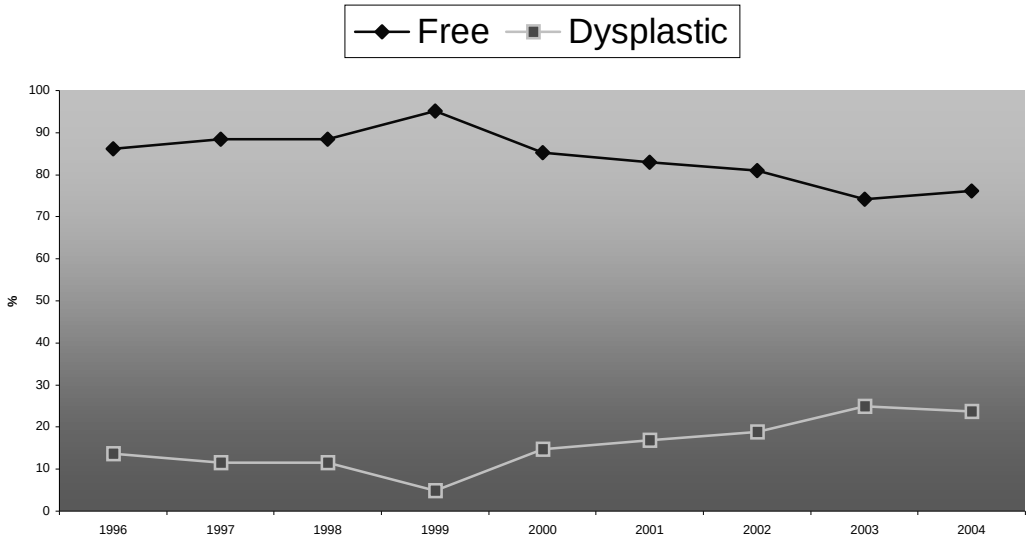

Fig. 2: The evolution of the amount of sound hips in the German shepherd clearly decreases, especially during the last three years. Rise of affected hips is more than 6 %.

In 2001, the amount of excellent hips decreased consistently in favour of nearly normal hips, as shown in fig. 3. For the German shepherd, this evolution already started in 1997.

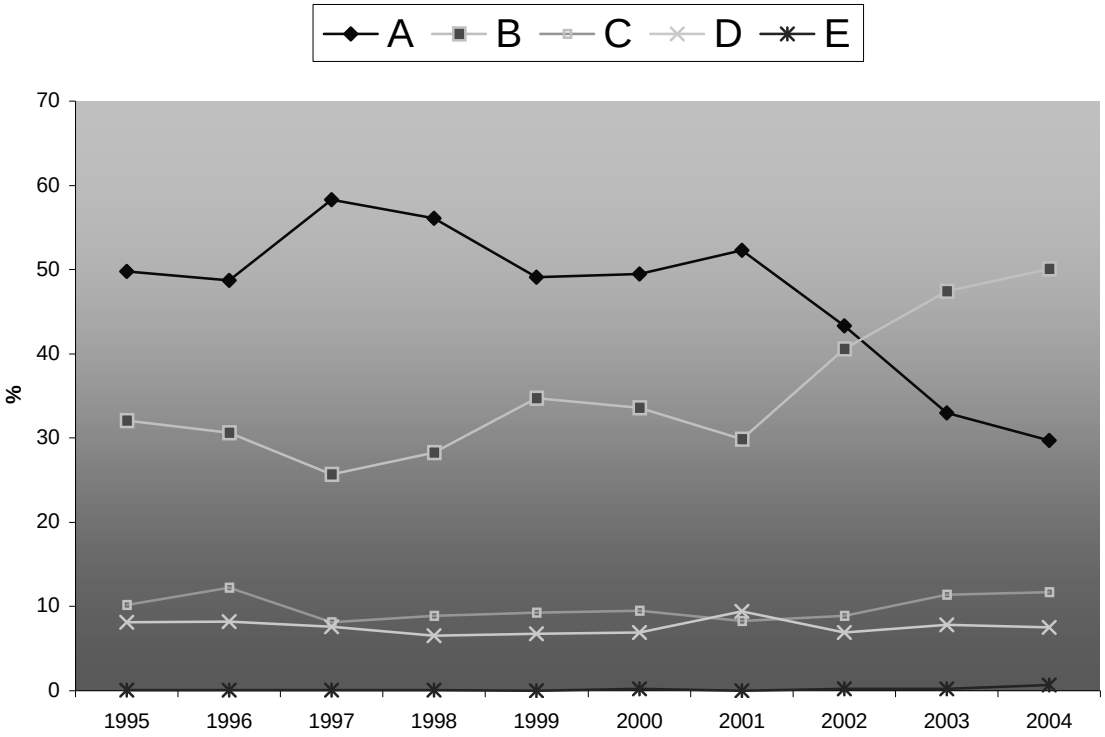

Fig. 3: The evolution of the different scores for hip quality during the ten final years all over breeds. The amount of perfect hips (A) declines and rates of transitional hips (B) increases consistently. The ratio of different types (C; D; E) of dysplastic dogs remains the same.

The ratio of moderate CHD (D) in German shepherd decreased during the last three years, but increased spectacular in de Golden retriever breed.
The prevalence calculated using the data of the MI department shows a comparable evolution but at a 12 to 20 % higher level.

4. DISCUSSION AND CONCLUSIONS

No comparable evolution as seen by the OFA (3) was found in Belgium. The slight increase seen in Europe (personnel communication, Iams Eukanuba) is confirmed and goes on beyond 1997. Although the prevalence of CHD is already high, it even seems to be underestimated and to be twice as high compared to the official screening results. Also the amount of excellent hips decreases consistently. It can therefore be concluded that CHD remains an important problem in Belgian breeding dogs and that the eradication program fails to lower the prevalence of this disorder. The eradication program should therefore be refined.

5. REFERENCES

1. Fox S.M., Burns J., and Burt J. Symposium on hip dysplasia. The dysplastic hip: A crippling problem in dogs. *Vet Med* 1987; 82: 683-693.
2. Kapatkin A.S., Fordyce H.H., Mayhew Ph. D., and Smith G.K. Canine Hip Dyplasia: The Disease and Its Diagnosis. *Comp* 2002; 24: 7: 526-535.
3. Keller. Hip dysplasia. "*In: The use of health databases and selective breeding*". Information brochure of the OFA, 2003: 13-34.
4. Lust G. An overview of the pathogenesis of canine hipdysplasia. *JAVMA* 1997; 210: 1443-1445.

5. Rettenmaier J.L., Keller G.G., Lattimer J.C., Corley E.A., and Ellersieck M.R.. Prevalence of canine hip dysplasia in a veterinary teaching hospital population. *Vet Rad and US* 2002*;* 43: 313-318.
6. Smith G.K. Advances in diagnosing canine hip dysplsia . *JAVMA* 1997; 210: 1451-1457.
7. Tomlinson J., and McLaughlin R. Jr.. Symposium on CHD: Diagnosis and medical treatment. Canine hip dysplasia: Developmental factors, clinical signs, and initial examination steps. *Vet Med* 1996; 91: 25-33.

DEVELOPMENT OF A SANITARY RISK INDEX FOR SALMONELLA IN PIG HUSBANDRY

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ABSTRACT

Risk factors for salmonellosis in slaughter pigs were investigated in a cross-sectional survey on 60 Belgian farrow-to-finish herds belonging to one slaughterhouse co-operation. Herd data were collected using a questionnaire. The blood samples were serologically analysed. Variables significantly related to the Salmonella prevalence in the univariate analysis were subsequently analysed in a multivariate model. The herd seroprevalence was 68% in summer and 78% in winter when using OD40%. The average within-herd prevalence was respectively 27% and 16% for summer and winter. In the multivariate analysis (SRI) the structure of feed seems to be a very important factor of the model with 12 factors. Other risk factors in the multivariate model are: season, programmed temperature, programmed ventilation, adjusting climate in nursery, regulation of air inlet, number of days emptiness after cleaning, width of slats, type of water supply, all-in all-out, acidification of feed and drinking water, incidence of coughing and rodent control.

SAMENVATTING

In een cross-sectionele studie van gesloten varkensbedrijven werd onderzoek verricht naar risicofactoren voor Salmonella bij slachtvarkens. Alle 60 bedrijven behoren tot eenzelfde integratie werkend op basis van een kwaliteitscontrolesysteem. Via een enquête werden bedrijfsgegevens verzameld en het bloed werd serologisch geanalyseerd. Variabelen die in de enkelvoudige analyse significant gerelateerd waren aan Salmonellaprevalentie werden in de meervoudige analyse opgenomen. De bedrijfsprevalentie bedraagt 68% in de zomer en 78% in de winter bij een OD40%. De gemiddelde binnen-bedrijfsprevalenties zijn 27% en 16% voor respectievelijk de zomer en de winter. In de meervoudige analyse (SRI) blijkt de voederstructuur een belangrijke factor in het model met 12 variabelen. De andere risicofactoren in het model zijn: seizoen, ingestelde temperatuur, ingestelde ventilatie, klimaataanpassingen in de biggenbatterij, regeling van luchtinlaat, aantal dagen leegstand na reinigen, breedte van de rooster, type van watervoorziening, all-in all-out, toevoegen van zuren, periode van hoest en knaagdierenbestrijding.

1. INTRODUCTION

For reasons of food safety and economic pressure, risk factor studies are required to have a scientific basis to initiate a control programme for Salmonella in pig herds. The aim of the present study was to determine risk factors for the prevalence of Salmonella in Belgian slaughter pigs. These factors will be combined in a scientifically based sanitary risk index (SRI). This SRI can be defined as an objective measure of the Salmonella prevalence of a farm and/or the risk for introduction and/or the risk of spread of Salmonella from a farm. The SRI is a statistical model of a group of parameters and their weight factors.

2. MATERIAL AND METHODS

60 Belgian farrow-to-finish herds belonging to one slaughterhouse co-operation were randomly selected. Herd data were collected using a questionnaire, consisting of 2 major parts, in order to identify potential risk factors. The general part of the questionnaire concerned all pigs in the herd, the specific part concerned the slaughter pigs to be sampled. Following topics were included: housing and ventilation, management, hygiene and biosecurity and production parameters. The specific part additionally pertained to feeding, disease control and transport to slaughterhouse.

From each of the herds, 33 randomly selected pigs from an average delivery of 77 pigs were blood sampled at slaughter. To take into account seasonal variation in seroprevalence, each herd was sampled two times: in summer (July-Oktober) and in winter (December-March). In total, 3975 fattening pigs originating from 60 farrow-to-finish herds were sampled in the slaughterhouse. Serological examination for specific antibodies to Salmonella was performed by means of an indirect mix-ELISA (IDEXX® HerdChek).

For the determination of risk factors a Linear Mixed Model was used (SAS®). This method was used with the continuous S/P-value on the pig level as dependent variable for the following reasons: there are different cut-off values that could be used and analysis on pig level with a continuous dependent variable has more power then analysis on herd level with a dichotomised variable.

In a first step, the S/P-value has been transformed with a logarithmic function to get a normal distribution. Next, each of the factors obtained from the questionnaire were separately introduced in the model to assess whether any of these factors were univariate associated with the S/P-value. Variables significantly related to the S/P-value ($P<0.05$ and 85% of the observations included) were analysed jointly in a multivariate model with herd and herd*season as random effects.

3. RESULTS

In 60 herds (100%) at least 1 sample was positive when using OD10% as cut-off, for both seasons. 68% of the herds in summer and 78% in winter, were positive when using OD40%. The average within-herd seroprevalence was in the summer: 70% (range: 15%-100%) and in the winter 64% (range: 15%-100%) when using OD10%. When using OD40% as cut-off, the within-herd prevalence in summer and winter were respectively 27% (range: 0%-97%) and 16% (range: 0%-79%). Differences between winter and summer were significant for OD40% ($P<0.05$).

Categorical and continuous variables were studied by univariate analysis, of which 182 were significantly associated with Salmonella prevalence. The significant variables could be sorted into 5 classes: farm characteristics, hygiene, management, climate and feed. The most important variables have been selected for the multiple analysis based on the P-value, the estimate and the biological sense. The variables were introduced in the multivariate model. Factors still significantly ($P<0.05$) associated with the S/P-value in the multivariate analysis are enumerated in table 1 together with their estimates. Incorporating these 13 factors in the multivariate model could considerable reduce the variance between herds, 58% of the variance could be explained by these factors. The sanitary risk index for Salmonella can be defined as the multivariate model with intercept, risk factors (see table 1) and their weight factors (estimates).

4. DISCUSSION

From the SRI the most important factor seems the structure of the feed. Feeding pigs meal instead of granulated or crumb is a protecting factor for Salmonella. Jorgenson *et al.* (1) found that pigs that received meal have the largest population of lactic acid bacteria in the stomach. Also adding organic acids in feed and drinking water gives a reduction effect on Salmonella prevalence. Beside the feed, hygienic measures such as number of days emptiness after cleaning, applying the strict all-in all-out system and controlling the rodent population seems to be important. These factors have been supported by previous research (2, 3, 4). Furthermore it could be deduced from the index that providing the right climate for the pigs (programmed temperature and ventilation, regulation of air inlet) is a factor to consider for reducing the S/P-values.

With the identification of the risk factors, adequate intervention strategies could be designed to reduce Salmonella prevalence and contamination in finishing pigs. The SRI could be used at different levels of the pig production column, e.g. on national level, on individual farm level and also for integral quality control (IQC).

5. ACKNOWLEDGEMENTS

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Table 1 Risk factors for Salmonella in pig husbandry.

	Variable	Class		Estimate
β0	intercept			-2.31
β1	seizoen	1	summer	0.19
		2	winter	0.00
β2	vta1n	0	granulated feed	0.39
		2	crumbed feed	0.81
		3	meal	0.00
β3	aanpvbb	-1	no computer	-0.71
		0	no adjustment of climate	0.14
		1	adjustment of climate	0.00
β4	tempiamk	-1	no temperature programmed	0.27
		1	temperature less then 22 °C	0.03
		3	temperature more then 22°C	0.00
β5	venminak	-1	no ventilation programmed	0.14
		1	minimum ventilation less then 15%	0.12
		2	minimum ventilation more then 15%	0.00
β6	rli2amn	1	natural ventilation, manual or automatical adjustment	-0.22
		2	no adjustment of air inlet possible	0.00
β7	dstandam	continuous	number of days emptiness after cleaning	-0.05
β8	spijlam	continuous	width of slats	0.09
β9	twatern	0	drink trough or drink nipple	0.53
		2	drink nipple in feed trough	0.03
		3	no extra water supply (pulp feed)	0.00
β10	aiaoam	0	continuous system	0.14
		1	all-in all-out	-0.22
		2	no clear system or both systems	0.00
β11	zuur	0	no acidification	0.21
		1	acidification of drinking water	0.19
		2	acidification of feed	0.00
β12	hoestwan	-1	no coughing	0.24
		2	coughing when pigs weight less then 40 kg	0.19
		4	coughing when pigs weight between 40 and 80 kg	-0.18
		6	coughing when pigs weight more then 80 kg	0.00
β13	resknaan	-1	no rodent control	-0.15
		0	no results of rodent control	-0.40
		1	results of rodent control	0.00

Season (seizoen), food structure (vta1n), adjusting climate in nursery (aanpvbb), programmed temperature (tempiamk), programmed ventilation (venminak), regulation of air inlet (rli2amn), number of days emptiness after cleaning (dstandam), width of slats (spijlam), type of water supply (twatern), all-in all-out (aiaoam), acidification (zuur), incidence of coughing (hoestwan) and rodent control (resknaan).

6. REFERENCES

(1) Jorgensen, J., Dahl, J., Wingstrand, A. The effect of feeding pellets, meal and heat treatment on the Salmonella prevalence of finishing pigs. "In: Proceedings of the 3rd International Symposium on Epidemiology and Control of Salmonella in Pork". Washington, 5-7 August 1999. 308-312.

(2) Letellier, A., Messier, S., Paré, J., Ménard, J., Quessy, S. Distribution of Salmonella in swine herds in Quebec. *Vet. Microbiol*. 1999; 67: 299–306.

(3) Lo Fo Wong, D.M.A., Dahl, J., Stege, H., Van der Wolf, P.J., Leontides, L., von Altrock, A., Thorberg, B.M. Herd level risk factors for subclinical Salmonella infection in European finishing herds. Epidemiology and control options of Salmonella in European pig herds. Ph.D. Thesis. Royal Veterinary and Agricultural University, Denmark. 2001.

(4) Van der Wolf, P.J., Wolbers, W.B., Elbers, A.R.W., van der Heijden, H.M.J.F., Koppen, J.M.C.C., Hunneman, W.A., van Schie, F.W., Tielen, M.J.M. Herd level husbandry factors associated with a serological Salmonella prevalence in finishing pig herds in the Netherlands. *Vet. Micorbiol.* 1999; 78: 205-219.

HANDLING MISSING DATA WHEN MODELLING THE FORCE OF INFECTION.

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ABSTRACT

Modelling infectious diseases data is a relatively young research area in which clustering and stratification are key features. There exist many ways to deal with clustering [1]. However an additional complication is the not unlikely occurrence of missing values in the data. If the missingness is ignorable as defined by Little and Rubin [2], the analysis can be based on the complete cases only. If however the missingness is non-ignorable, analyses can be affected by merely using the complete cases. We will show the effect of ignoring missing data to model the force of infection of the bovine herpesvirus-1 in Belgian Cattle and we will propose the use of weighted generalized estimating equations to deal with both clustering and missingness in the data.

SAMENVATTING

Het modelleren van infectieziekten is een relatief jong onderzoeksgebied waarbinnen clustering en stratificatie een cruciale rol spelen. Er bestaan reeds vele technieken om rekening te houden met clustering [1]. Het is echter niet ondenkbaar dat sommige subjecten ontbrekende gegevens hebben. Als het ontbreken van gegevens negeerbaar is zoals gedefinieerd door Little en Rubin [2], kunnen de analyzes gebaseerd worden op de volledig geobserveerde gegevens alleen. Als het ontbreken van gegevens niet genegeerd kan worden, dan kunnen analyzes beinvloed worden door enkele de volledig geobserveerde gegevens te gebruiken. We zullen deze invloed aantonen aan de hand van het modelleren van de infectiedruk van de boviene herpesvirus-1 in Belgisch vee. Hierbij stellen we het gebruik voor van gewogen veralgemeende schattingsvergelijkingen die rekening houden met de clustering en ontbrekende gegevens in de data.

1. INTRODUCTION

The sero-prevalence survey of the bovine herpesvirus-1 (BoHV-1) in Belgian cattle is a study of a transmissible disease in cattle, which is of economic importance and significance to international trade. A central characteristic of infectious disease dynamics is the transmission of the infection from infectious to susceptible subjects. The force of infection (FOI) is the rate of acquisition of the infection for a susceptible host. Empirical data show that, in general, the FOI is age-dependent. Like many other infectious diseases data, the BoHV-1 data suffers from several complications and thus statistical modelling has to deal with these.

A first complication is clustering. Indeed, animals within clusters (herds) have a higher chance of becoming infected once the infection is introduced onto the herd. Thus, individual responses are more homogeneously distributed within herds than in the whole population. There are several ways of dealing with such clustering [1].

A second complication is that some subjects have one or more missing values. If the missingness is ignorable as defined by [2], the analysis can be based on the so called complete cases, i.e. all observations for which all values are observed. If, however the missingness is non-ignorable, analyses can be affected by merely using the complete cases. Several methods to handle missing data are known [2]. None of them are without limitations.

2. MATERIAL AND METHODS

In the present dataset, from a Belgian 1998 sero-survey, the response variable is the gB-test result for the presence of antibodies to BoHV-1. Additionally, the age and origin (purchased yes/no) of the cows were recorded. Unfortunately, there were a lot of missing values for origin. The FOI as a function of age was derived from the sero-prevalence function that, in case animals act independently, can be modelled using logistic regression.

Since in this dataset clustering occurs, the sero-prevalence function was fitted using a generalized estimating equation (GEE) which accounts for the clustering. A GEE is a marginal model which evaluates the population-averaged trend as a function of covariates while accounting for the correlations in the data. Additionally, it can be shown that animals from a larger herd have a higher prevalence than animals from smaller herds for the BoHV-1. This phenomenon is known as informative cluster size and should be taken into account by the use of cluster weighted generalized estimating equations [3] where the GEE is weighted with the inverse cluster size.

One of the techniques to deal with missing data, which gained a lot of attention recently, is the use of weighted estimating equations [4], where each contribution of a case is weighted with the inverse of the probability that this case is observed. In this way cases with a low probability to be observed gain more influence in the analysis and thus represent the missing values. One can look at this approach as an implicit imputation of missing values. To illustrate the effect of ignoring missing data, Section 3 describes the results of modelling the force of infection as a function of age, based on all cows, termed as ‘all cases’ on the one hand, and on the other hand based on those cows for which origin is observed, termed as ‘complete cases’. Next to showing the effect of merely using the complete cases, the use of weighted estimating equations is illustrated to correct the analysis as described above.

Combining both techniques to deal with informative clustering and missing data, the method to model the sero-prevalence can be termed as weighted generalized estimating equations, where the weights are the product of the inverse cluster size and the inverse probability for an observation to be observed. Taking the product implies assuming independence between the informative cluster size and the occurrence of missingness in the data. When this assumption is not valid, the weights should be estimated jointly. The latter however is topic of further research. Since a parametric model relies on assumptions, preference goes out to a non-parametric technique to estimate the probability for an observation to be observed. From the resulting sero-prevalence model, the force of infection can be derived.

In practice however, the interest often goes to company-specific research questions and not to overall animal-specific research questions. An alternative modelling approach to model the force of infection from a company-specific point of view is to incorporate the herdsize as a covariate and to use weighted generalized estimating equations where the weights are the inverse probabilities for the observations to be observed.

Both modelling approaches rely on an additional complication, namely the constraint that the force of infection cannot be negative which should be taken into account when modelling the seroprevalence function. This constraint was not considered as a part of the modelling process (constraint GEE is another topic of current research). Therefore the modelling was done without constraints and the constraint was verified for the resulting model.

3. RESULTS

As an illustration of the effect of ignoring missing data, in Figure 1, FOI-curves for three different methods are shown. The long-dashed line shows the FOI based on all cases (CA), while the full line shows the FOI based on the complete cases (CC). One can see an adverse effect on the FOI when using complete cases only. When we use a weighted generalized estimating equation, where the weights are the inverse of the non-parametrically

estimated probability for an observation to be observed, we obtain the small-dashed line (NPWCC). This latter analysis gives a substantial correction not only on the magnitude of the force of infection but also on the location of the maximum force of infection.

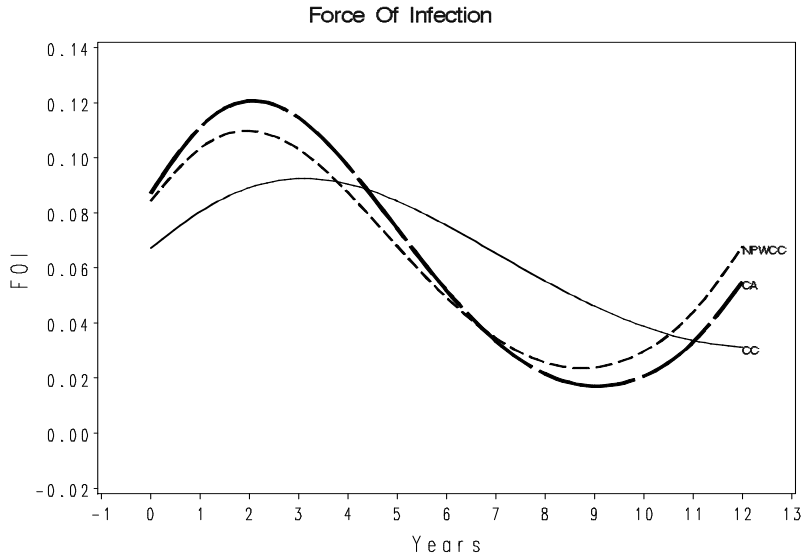

Figure 1: The force of infection from an animal-specific point of view as a function of age based on 'all cases' (CA), on the 'complete cases' (CC) and using a non-parametric weighted generalized estimating equation (NPWCC).

4. DISCUSSION

Since modelling infectious diseases has to deal with key features as clustering, stratification and missing values, specific modelling techniques have to be used. Modelling the FOI for the BoHV-1 data is done by using weighted generalized estimating equations with the cluster size as a covariate and where the weights correct for the missing data, whereas the GEE takes the clustering into account. It has been shown that merely using those observations for which none of the variables were missing, leads to wrong models and as such, wrong conclusions. Applying these techniques when constraints are put upon the parameters is a topic of current research.

5. ACKNOWLEDGEMENTS

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REFERENCES

[1] Aerts, M. , Geys, H. , Molenberghs, G. and Ryan, L.M. *Topics in Modelling of Clustered Data*, Chapman and Hall, London, 2002.
[2] Little, R.J.A. and Rubin, D.B. *Statistical Analysis with Missing Data.* New York: Wiley, 1987.
[3] Williamson, J.M. , Datta, S. , and Satten, G.A. Marginal Analyses of Clustered Data when Cluster Size is Informative, *Biometrics*, 2003, 59, 36-42.
[4] Zhao, L.P., Lipsitz, S., Lew, D. Regression Analysis with Missing Covariate Data Using Estimating Equations. *Biometrics,* 1996, 52, 1165-1182.

CONTROL STRATEGY, AND CLINICAL PICTURE AND EPIDEMIOLOGICAL CHARACTERISTICS OF THE BELGIAN HIGHLY PATHOGENIC AVIAN INFLUENZA EPIDEMIC IN 2003

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ABSTRACT

This paper describes the control strategy, and the clinical and epidemiological characteristics of the Belgian 2003 highly pathogenic avian influenza outbreak (HPAI) that occurred in the Provinces of Antwerp and Limburg, where a policy of intensive surveillance, and eradication was applied. Between April 18 and April 30, eight herds, located in 2 different areas, were officially confirmed HPAI-positive. Although the modes of between-herd virus transmission remained unknown, the peracute course of the disease, resulting in an immediate and steep increase of mortality, made it possible to detect infected herds in an early stage. The early detection together with a rapid depopulation of the HPAI infected herds and an extensive preventive stamping out procedure resulted in a rapid elimination of the HPAI virus.

1. INTRODUCTION

Highly pathogenic avian influenza (HPAI) is a highly contagious viral disease, affecting the majority of birds and especially poultry. Highly pathogenic AI is included in the List A diseases of the World Organisation for Animal Health (OIE) and in the European Union any outbreak with HPAI is eradicated by stamping out infected flocks. This paper describes the control strategy, and the clinical and epidemiological characteristics of the Belgian HPAI outbreak that affected the poultry industry from March to July 2003.

2. PERIOD FROM MARCH 1 TO APRIL 18, 2003

Due to the notification by the Dutch authorities of the first HPAI outbreaks on the 1st of March 2003, the crisis prevention and management unit (crisis unit) of the Federal Agency for the Safety of the Food Chain (FASFC), the competent Belgian authority on animal disease issues, was put into a state of alert and was reinforced. As a consequence, control measures were implemented and actions were undertaken to prevent HPAI introduction from the Netherlands and to detect a HPAI virus infection, if present in the Belgian poultry population, in an early stage.

3. PERIOD FROM APRIL 18, 2003 ONWARDS

Between 18 and 30 April 2003, eight flocks in two different areas were officially confirmed infected with HPAI virus. Five flocks were located in the northeastern part of Limburg province and 3 flocks were located in the northern part of Antwerp province. In accordance with the Council Directive 92/40/EC (CEC, 1992) protection zones around each HPAI infected flock, surveillance zones and a buffer zone subdivided into 3 smaller parts were established.

3.1. Control measures, post-mortem and laboratory examinations

During the initial visit of a suspected flock, a veterinary officer of the FASFC placed the farm under official surveillance, performed a clinical investigation and collected samples to confirm the presence of HPAI. In all cases, birds were sent to the regional laboratory of the Animal Health Care Flanders for post-mortem

examination. During autopsy, samples (lung, trachea and caecal tissue) were collected and sent to the national reference laboratory (Veterinary and Agrochemical Research Centre, Brussels) for virological diagnosis.

In case of a positive RT-PCR result, which was available within 24 hours, an inquiry team of the FASFC visited the infected flock. An inventory was taken of all animals on the farm and the layout of the farm was mapped. Investigations were carried out with respect to disease history, clinical symptoms, within-flock virus transmission, and biosecurity measures. All movements on the farm that occurred up to three weeks earlier were registered. All high-risk contact flocks, i.e. contact through transfer of poultry, and contact through persons, which had entered the poultry houses of an infected flock during the infectious period, were preventively emptied. The other contact flocks were placed under official surveillance for a 21-day period.

All flocks confirmed to be HPAI-positive were emptied and disinfected. In addition all professional flocks located in the protection zone were preventively emptied and disinfected. Later on, preventive slaughter was extended to all professional flocks located in the surveillance zone of the province of Limburg. Additionally, all backyard poultry within a one-kilometre radius of an HPAI-infected flock was killed.

3.2. Clinical symptoms, and morbidity and mortality

In all cases, the owner was alerted and consulted the herd veterinarian due to increased mortality. It was then the herd veterinarian who reported the suspicion of an HPAI infection to the FASFC. On average, mortality increased a 100-fold within a 36 h time period. The number of diseased animals varied from 1 to 5 times the number of dead animals at a given point in time. The majority of the diseased birds were found dead after a peracute course of disease with few clinical signs (depression, recumbence, and decreased water and feed intake). In the other birds the clinical symptoms were depression, congestion and/or cyanosis of the comb and wattles, swollen heads, oedema of the eyelids, diarrhoea, and torticollis. Respiratory signs were nasal discharge, and respiratory distress.

3.3. Between-flock virus transmission

To identify the modes of virus transmission, the registered contacts which visited an infected flock on the estimated date of first infection (= 2.5 days (range: 1 – 4 days) before initial clinical symptoms) were listed and checked whether they had visited the up stream-infected flocks during their infectious period (= period from first clinical symptoms, as reported by the farmer, to stamping out). Tracing back could however not link any of the registered contacts to an up-stream infected flock. In 2 HPAI-infected flocks, airborne or dust borne virus introduction was considered. Based on the location of the first infected birds within the initially infected houses of the flocks 2003/02, and 2003/03, it was concluded that HPAI virus was most probably introduced through the air inlets of the ventilation system (Figure 1). This was motivated by the fact that the first infected birds were found closer to the air inlets rather than adjacent to the entrance of the houses, and that the first infected birds were found in the top-floor cages.

4. DISCUSSION

Because of the large economic impact of a HPAI epidemic and the considerable costs associated with HPAI eradication, the main objectives of the animal health strategies applied to HPAI control are prevention of HPAI introduction and, in case of HPAI introduction, an early detection and a rapid eradication. Eradication of the disease was obtained by a combination of various control measures. These included (i) bio-security measures to prevent the introduction of the HPAI virus to naive flocks (bio-exclusion), (ii) control measures minimizing the number of between-flock contacts, (iii) bio-security measures that confines the HPAI virus on infected flocks (bio-containment), (iv) early notification by the herd veterinarian and immediate stamping out of infected flocks, and (v) preventive depopulation of high-risk contact flocks, professional flocks in the surveillance and/or protection zones, and backyard flocks in the one-kilometre area around a HPAI infected flock. The decision to kill all poultry on the professional flocks in the surveillance zone of the province of Limburg, in addition to the standard preventive depopulation of all professional flocks in the protection zones, was motivated by the spacious spread of the HPAI flocks, and the hypothesis that airborne or dust born virus transmission over long distance may have contributed to the between-flock virus spread (see also below).

4.1. Between-flock virus transmission

In order to further improve the control strategy of HPAI outbreaks, investigations on the modes of between-flock virus transmission are essential. It is generally accepted that the most important modes of between-flock virus

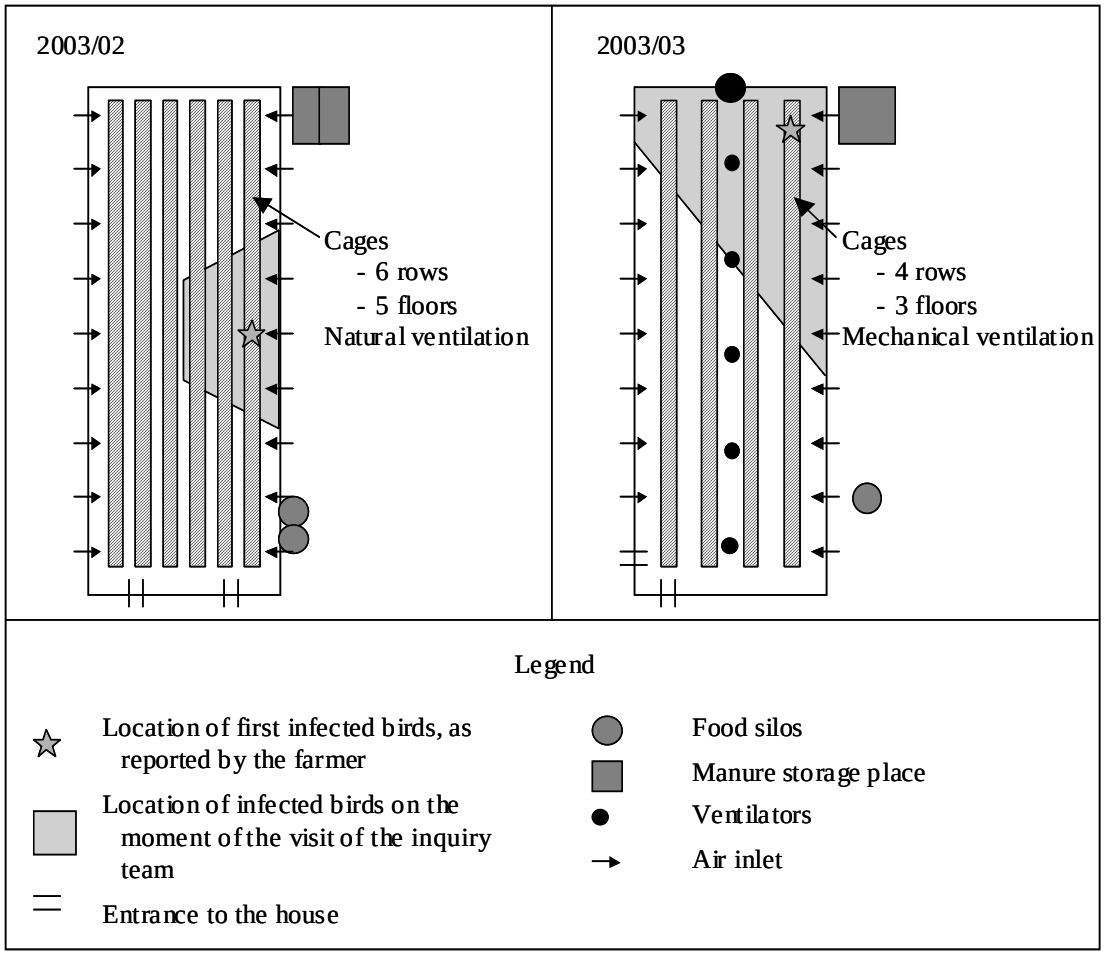

Figure 1: Location of clinical symptoms within the initially infected house of the flocks suspected to be infected by HPAI virus through introduction via air inlets of the ventilation system.

transmission are transfer of infected poultry and indirect contact via contaminated mechanical vectors (King, 1984; Alexander, 1995; Koch and van der Goot, 2000). None of these 'traditional' modes could however be identified as modes responsible for between-flock virus spread. Therefore airborne spread of the HPAI virus was considered in at least the HPAI infected flocks 2003/02, 2003/03, 2003/04, and 2003/06. This was motivated by (i) the 'straight line' spatio-temporal distribution of these four HPAI infected flocks, (ii) the indications of virus introduction through the ventilation system in two HPAI infected flocks (2003/02, and 2003/03) (Figure 1), (iii) the dominant wind direction that was ENE during the period of the estimated days of first infection of these HPAI infected flocks, and (iv) the presence of a HPAI infected flock in Hunsel, the Netherlands, with 108,500 layer hens. The flock was assumed to be infectious from April 12 (date of suspicion) to April 18 (date of depopulation) and fits within the spatio-temporal geographical distribution of HPAI infected flocks of the province of Limburg.

During the investigation of the modes of between-flock virus transmission, only contacts registered during the estimated period of first infection were considered. It is also possible that indirect contacts registered prior to the estimated date of first infection, introduced the HPAI virus into the flock and that the birds only became infected after a period of time. For the index case in the province of Antwerp (2003/05), a container transport that delivered wood curls on April 7, i.e. 12 days prior to the estimated date of first infection, also visited, on April 1, a turkey farm in Kelpen, the Netherlands. Later on, two flocks in the municipality of Kelpen were confirmed to be positive on April 14 and April 18, respectively.

5. ACKNOWLEDGEMENTS

Controlling list A disease outbreaks, like HPAI, is a huge challenge involving many people. We, herewith, want to acknowledge all people from the Federal Agency for the Safety of the Food Chain, Animal Health Care Flanders, the Regional Association of Animal Health and Identification, and the Veterinary and Agrochemical Research Centre, who contributed to the collection and provision of the data for this publication.

References and the full report can be obtained from the first author.

ESTIMATING THE PROBABILITY OF FREEDOM OF CLASSICAL SWINE FEVER VIRUS OF THE EAST-BELGIUM WILD-BOAR POPULATION

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ABSTRACT

A report of the Scientific Committee on Animal Health and Animal Welfare of the European Commission (3) includes recommendations for setting up monitoring programmes for classical swine fever (CSF)-infection in a wild-boar population, based on the assumption that one would detect at least 5% prevalence in an infected population. This assumption, however, is not science based. In this study, we propose an alternative method to provide evidence for the East-Belgian wild-boar population being free of CSF, using Bayes theorem. When choosing the least informative prior information, the posterior median probability for freedom of disease was estimated at 0.970 with a 95% credibility interval of 0.149 to 1.000. This represents a big gain of knowledge since we did not use any prior information for the probability of freedom of CSF-virus and took the uncertainty about the accuracy of the diagnostic methods into account.

1. INTRODUCTION

Complete and long-term eradication of Classical swine fever (CSF) in the European Union (EU) is hampered by the incidence of the infection in wild-boar populations in different Member States. From different studies conducted from 1993 to 1997, Fritzemeier et al. (4) estimated that 59% of the primary outbreaks of CSF in domestic pigs in Germany were related to direct or indirect contact with infected wild boars.In 1998, several CSF-outbreaks in domestic pigs and wild boars were identified in the Rheinland-Palatinate region of Germany at a 1- to 50-km distance from the Belgian eastern border. These new cases alerted the Belgian Veterinary Services, which implemented a surveillance programme in the same year.

We describe the results of the surveillance programme over a period from October 1999 to December 2001. Additionally, we propose an alternative method to provide evidence for the East-Belgian wild-boar population being free of CSF.

2. MATERIALS AND METHODS

2.1 The Surveillance Programme

The surveillance programme started in 1998 and involved the monitoring of wild boars for CSF-infections within the three provinces (Namur, Liège and Luxembourg, total 13,798 km^2), which mutually include 95% of the Belgian wild-boar population. The programme consisted of the examination on a voluntary basis of a convenience sample of wild boars that were killed or found dead by hunters. Per province, a minimal annual number of 100 animals to be examined was prescribed. From January 2000 onwards, the programme was extended by dividing the target area into two zones and by implementing additional control measures.

- A surveillance zone (~ 125 km2) bordering the CSF-affected area in Germany was defined. This zone was assumed to have higher risk for introduction of CSF-virus. Therefore, all wild boars that were killed or found dead were required to be examined for the presence of CSF-infection and movement restrictions for domestic pigs were implemented.

- In the screening zone (the remaining parts of the three provinces and with lower risk for CSF-virus introduction) the monitoring of wild boars killed or found dead continued on a voluntary basis. For only Liège and Luxembourg provinces, an additional 50 animals were to be examined every year in the communities bordering Germany and the Grand Duchy of Luxembourg.

Blood samples and lymph nodes were collected from each wild boar that was examined within the surveillance programme. For each animal that was sampled, additional information was recorded (e.g. sampling date, postal code of the municipality in which the animal was shot or found dead, sex, age group (young, sub-adult, adult), estimated weight).

2.2 Diagnostic Methods

The collected samples received three types of diagnosis:

Antibody detection: A serial testing procedure was performed to detect antibodies against CSF-virus in serum samples.

Virus detection: Organ-tissue suspensions were inoculated on a monolayer of sub-confluent PK15 cells, cultivated on multi-cup plates to isolate CSF-virus. The virus was identified by an anti-CSF immunoglobulin conjugated at fluorescein isothiocianate (6).

Virus RNA detection: A single-tube RT-nPCR test was performed to detect CSF-virus RNA in tissue samples (7).

2.3 Freedom of CSF-virus

The commonly used methods described by Cannon and Roe (2) or by Cameron and Baldock (1) for calculating the probability of freedom of disease in a population were not applicable, because of a lack of knowledge of the dynamics of CSF-virus in a wild-boar population. A minimal expected prevalence resulting from an introduction of CSF-virus could not be selected and justified. As an alternative, the posterior probability of freedom of CSF-virus (*F*) given the observed test results (*T*) was derived, using Bayes theorem:

$$P(F|T) = \frac{P(T|F)P(F)}{P(T)} \qquad \text{(a)}$$

When the observed test results are obtained by applying a diagnostic test to a survey sample, one can estimate the probability of freedom of CSF-virus (*F*), the prevalence given the population is not free (*prev*), and the sensitivity (*Se*) and specificity (*Sp*) of the diagnostic test given the data. Equation (a) can than be extended:

$$P(F, prev, Se, Sp|T) = \frac{P(T|F, prev, Se, Sp)P(F, prev, Se, Sp)}{P(T)}$$

Using Bayesian inference, the posterior probability distributions for parameters *F*, *prev*, *Se* and *Sp* are estimated by a multinomial likelihood function and by including prior information on the four parameters. The multinomial likelihood for a positive test result can be written as:

$$P(T|F, prev, Se, Sp) = (1-F)(prev \times Se + (1-prev)(1-Sp) + F(1-Sp) \qquad \text{(b)}$$

The likelihood function based on (b) takes into account that the observed prevalence only occurs when the population is not free of CSF-virus and can be extended to a test result based on 3 test methods.

In our study, the prevalence was calculated based on the samples that were collected from wild boars within the surveillance programme from October 1999 to December 2001 (and analysed by all three diagnostic methods). Any qualitative superiority of one of the methods to the two others was ignored (no-gold standard method). Using the three diagnostic methods in parallel, 8 different combinations of test results could be obtained, when assuming that results of all diagnostic methods are independent conditional on the infection status of the tested animals. For each of 8 test result combinations, the likelihood function to observe a given test result combination was formulated, based on the sensitivity (Se_i) and specificity (Sp_i) of each of the three testing methods, the probability of freedom of CSF-virus (*F*) and the CSF-prevalence (*prev*) in the population when it would not be free of the virus (Table 1). This resulted in 8 equations with 8 unknown parameters. Posterior densities for the 8 unknown parameters (Se_i and Sp_i for i= 1 to 3; *F*, and *prev*), were obtained applying Bayesian inference using Gibbs sampling (5) in the WinBugs software (version 1.4). The model had 7 degrees of freedom while a total of 8 parameters had to be estimated. This made it unidentifiable without prior information on at least one parameter. No clear prior information on the parameters could be obtained from literature or reliable sources. Therefore different combinations of prior information for the different parameters were used to analyses the sensitivity of the obtained posterior distributions to the choice of their priors.

3. RESULTS

3.1 Descriptive statistics

A total of 1,282 animals was sampled from October 1999 to December 2001 (1,201 from the screening zone and 81 from the surveillance zone). Blood samples of 889 animals were analysed using the described serological methods. Nine samples were positive for antibodies against CSF-virus, 850 samples were negative (for 30 samples, no distinct test result could be derived). Tissue samples of 1,183 animals were examined by the inoculation method and all were CSF-virus negative. Tissue samples from all 1,282 animals were examined by the single tube RT-nPCR test and all were negative. Samples of 789 animals were examined by all 3 diagnostics methods. Nine (of the 789) were sero-positive but all other diagnostic results were negative.

3.2 Parameter estimations and sensitivity analysis

Seven different combinations of prior information for the sensitivity and specificity of the diagnostic methods and for the prevalence, given de Belgian wild boar population was CSF-infected, where chosen to run the model. For the prior distribution, the likelihood and the posterior distribution when choosing the least informative prior information (Se & $Sp \geq 0.5$; non-informative prior for *prev*; combination 1), the posterior median probability for freedom of disease was estimated at 0.970 with a 95% credibility interval of 0.149 to 1.000.

4. DISCUSSION

The method that was used to estimate probability of freedom of CSF-virus required prior knowledge to be included for the model to convert. The posterior distributions of most parameter were insensitive to the choice of prior information for the sensitivity and specificity of the diagnostics methods. Only the posterior distributions of the sensitivity of the diagnostic methods depended highly on its prior distributions. This was expected since almost all test results in the survey sample were negative. The choice of the prior distribution for the prevalence, given the population is free of CSF-virus had an influence on the posterior distribution of the probability of freedom of disease. Choosing a more informative prior narrowed the 95% credibility interval of the posterior distribution and pushed the median towards 1. This can be explained by the fact that we assumed that the CSF-prevalence in the population equals the prevalence given that the population is not free of CSF-virus (*prev*) times the probability that the population is not-free of CSF-virus (F). Under this assumption, any increase of *prev* would result in an increase of F since the CSF-prevalence in the population is constant.

The aim of the surveillance programme is to provide evidence for the East-Belgian wild-boar population to be free of CSF-virus. As an alternative to the methodology proposed in a report of the European Commission concerning CSF in wild boar (3), we calculated the probability of freedom of CSF-virus, without assuming a minimal expected prevalence when CSF would be present in the population. Independent on the choice of the prior information, all posterior distributions for the probability of freedom of CSF-virus are lying close to the upper boundary of 1. This represents a big gain of knowledge since we did not use any prior information for the probability of freedom of CSF-virus and took the uncertainty about the accuracy of the diagnostic methods into account.

5. REFERENCES

1. Cameron A.R. and Baldock F.C. A new probability formula for surveys to substantiate freedom from disease. *Prev Vet Med* 1998; 34: 1-17.
2. Cannon R.M. and Roe R.T. *Livestock disease surveys: a field manual for veterinarians.* Australian government publishing service, 1982.
3. Cec *Classical swine fever in wild boar.* Report XXIV/B3/R09/1999 European Commission, Brussels, Belgium, 1999.
4. Fritzemeier J., Teuffert J., Greiser-Wilke I., Staubach C., Schluter H. and Moennig V. Epidemiology of classical swine fever in Germany in the 1990s. *Vet Microbiol* 2000; 77: 29-41.
5. Gelfand A.E. and Smith A.F.M. Sampling-based approaches to calculating marginal densities. *J Amer Statist Assoc* 1990; 85: 398-409.
6. Koenen F., Van Caenegem G., Vermeersch J.P., Vandenheede J. and Deluyker H. Epidemiological characteristics of an outbreak of classical swine fever in an area of high pig density. *Vet Rec* 1996; 139: 367-371.
7. Mcgoldrick A., Bensaude E. and Paton D.J. Closed one-tube reverse transcription nested polymerase chain reaction for the detection of pestivirial RNA with fluerescent probes. *J Virol Methods* 1999; 79: 85-95.

THE RELATION BETWEEN *SALMONELLA* OCCURRENCE IN SOWS AND PIGLETS: A LONGITUDINAL STUDY

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ABSTRACT

The aim of the present study was to investigate the relationship between *Salmonella* occurrence in sows and their offspring. In 3 Belgian farrow-to-finish herds, a group of 34, 40 and 32 sows, respectively was selected. From each of the sows, 3 piglets were randomly selected. Relative risk ratios (RR) were calculated to evaluate the relation between *Salmonella* excretion and *Salmonella* seropositivity in the sows during late gestation and/or lactation and *Salmonella* excretion and *Salmonella* seropositivity in their offspring during the nursery period. Piglets originating from sows seropositive during lactation had a significant lower risk to be *Salmonella* culture positive during the nursery period (RR=0.25 (0.09-0.93)). Piglets originating from *Salmonella* excreting sows during late gestation or lactation did not have a significant higher risk for *Salmonella* excretion during the nursery period (RR=0.52 (0.00-1.90)). Under the present conditions, it could not be shown that sows play a major role in the direct transmission to their offspring.

SAMENVATTING

Het doel van dit onderzoek was het verband na te gaan tussen het voorkomen van *Salmonella* bij zeugen en haar nakomelingen. Op 3 gesloten Belgische varkensbedrijven werd een groep van respectievelijk 34, 40 en 32 zeugen geselecteerd. Van elk van die zeugen werden 3 biggen geselecteerd. Het verband tussen uitscheiding van *Salmonella* en het voorkomen van antistoffen tegenover *Salmonella* bij de zeugen gedurende de late dracht en/of de lactatie, en *Salmonella* uitscheiding en het voorkomen van *Salmonella* antistoffen bij de nakomelingen tijdens de batterijperiode werd berekend aan de hand van het relatief risico (RR). Uit de resultaten bleek dat biggen afkomstig van seropositie zeugen tijdens de lactatie een significant kleinere kans hadden om *Salmonella* uit te scheiden tijdens de batterijperiode (RR=0.25 (0.09-0.93)). Biggen afkomstig van *Salmonella* uitscheidende zeugen tijdens de late dracht of lactatie hadden geen significant hoger risico om *Salmonella* uit te scheiden tijdens de batterijperiode (RR=0.52 (0.00-1.90)). Gebaseerd op deze resultaten kon de rol van de zeug in de directe overdracht van *Salmonella* naar de biggen niet aangetoond worden.

1. Introduction

Since many years, *Salmonella* is recognized as one of the most important foodborne pathogens (Tauxe, 1997) causing yearly more than 10,000 human infections in Belgium (Annual Reports Scientific Institute of Public Health, un-published data). As pork is one of the major sources for human infection, many research has focused on the epidemiology and the control of *Salmonella* in finishing pigs and different routes of infection have been revealed. *Salmonella enterica* is known to survive well in the environment (Sandvang et al., 2000) and the direct and/or indirect transmission of *Salmonella* from the environment to the pigs is believed to play an important role in the infection of pigs. As demonstrated in other studies (Davies et al., 1998; Funk et al., 2001; Beloeil et al., 2003), *Salmonella* shedding can also be detected in sows and the role of the sow in the direct transmission to the piglets has been investigated. In Belgium, many pig herds are single site herds in which all production stages, from the sows (mating unit, gestation unit, farrowing units) until the finishing pigs (nursery, growing and finishing unit) are located at the same site. One can suggest that, if sows are excreting *Salmonella*, they might be an important source for direct transmission of *Salmonella* infections to the piglets and thereby introduce the infection in the finishing pigs.

2. Materials and methods

2.1 Selection of the herds and study population

In 3 Belgian farrow-to-finish herds, a group of 34, 40 and 32 sows, respectively were selected. The herds had a minimum herd size of 250-500 sows, were using a group management system in sows and were subclinically infected with *Salmonella*. The latter was detected by preliminary analysis of pooled faecal samples. The sows of the selected group had the same expected farrowing date but were of different parities. From each of the sows, the following data were collected: individual sow number, breed, parity and date of farrowing.
Three piglets from each sow were randomly selected and ear-tagged the day before weaning, with exclusion of the sick and weak piglets.

2.2 Collection of the samples and sample analysis

Individual faecal samples, using rectal gloves, and blood samples were taken from all sows during late gestation and lactation. Rectal swabs and blood samples were taken individually from all piglets the day before and 7 days after weaning, halfway the nursery period and the day before moving to the growing (herd B) or finishing unit (herd A and C).
The blood samples were centrifuged at 3,000 r.p.m. for 10 minutes and the serum samples were stored at -20°C until further analysis. Antibodies against *Salmonella* were detected in a commercial indirect mix-ELISA, following the instructions of the manufacturer (Idexx Laboratories, Inc., Maine, USA). Samples were considered positive if the Optical Density (OD%) was equal to or higher than 10%.
Salmonella was isolated from faecal samples and rectal swabs using a qualitative isolation method. Briefly, faecal samples were weighed and diluted 1:9 (w/w) with Buffered Pepton Water (BPW). Ten ml of BPW was added to the rectal swabs. All samples were incubated for pre-enrichment during 16-20 hours at 37°C, followed by selective enrichment on Modified Semisolid Rappaport-Vassiliadis (MSRV) agar plates for 24 hours at 42°C. If migration zones were present on the MSRV plates, a loopful of the culture edge of the migration zones was streaked on a Xylose Lysine Desoxycholate (XLD) agar plate and plates were incubated for 24h at 37°C. XLD plates were examined for the presence of typical colonies. After biochemical confirmation of suspected colonies, one colony of each *Salmonella* positive identified sample was randomly picked and subcultured on Tryptone Soya Broth (TSB) (Oxoid, CM131) and stored at -20°C.

2.3 Statistical analysis

Relative risk ratios (RR) were calculated to evaluate the relation between *Salmonella* excretion and *Salmonella* seropositivity in the sows during late gestation, lactation and during one of both periods and *Salmonella* excretion and *Salmonella* seropositivity in their offspring during the nursery period. The offspring (litter) of each sow was defined as positive if one of the 3 piglets sampled was positive during the nursery period. Because the expected counts in crosstab-cells were less than 5, exact 95% confidence intervals (C.I.) were calculated using multinomial parametric bootstrapping (@risk 4.5).

3. Results

Table 1: Relative risk ratios (RR) with 95% C.I. for a *Salmonella* culture positive and a *Salmonella* seropositive litter given the respective sow was culture positive or seropositive during late gestation and / or lactation.

	RR for a *Salmonella* culture positive litter	RR for a *Salmonella* seropositive litter
Salmonella culture positive sow during late gestation	-	0.90 (0.00-1.68)
Salmonella culture positive sow during lactation	1.18 (0.00-5.05)	1.21 (0.00-2.69)
Salmonella culture positive sow during late gestation or lactation	0.52 (0.00-1.90)	0.79 (0.22-1.53)
Salmonella seropositive sow during late gestation	-	4.12 (0.85-7.79)
Salmonella seropositive sow during lactation	0.25 (0.09-0.93)*	1.30 (0.51-3.16)
Salmonella seropositive sow during late gestation or lactation	-	-

The results for the RR are shown in Table 1. In case one of the cells in the cross-tabs was empty, no RR could be calculated. Piglets originating from sows seropositive during lactation had a significant (*) lower risk to be *Salmonella* culture positive during the nursery period. These piglets also had a higher probability, although not significant, to be seropositive during the nursery period.

4. Discussion

The results indicate that piglets originating from sows seropositive during lactation are at lower risk for excreting *Salmonella* during the nursery period. The same conclusion was made in a Danish longitudinal study and suggests the potential protection given by maternal antibodies (Kranker et al., 2003). These antibodies can persist for more than 8 weeks, still giving the pigs protection during part of the nursery period (Beloeil et al., 2003). Although there was a slight tendency, piglets originating from *Salmonella* excreting sows during late gestation or lactation did not have a significant higher risk for *Salmonella* excretion during the nursery period. Similar to the results described in the study by Kranker et al. (2003), the increase in *Salmonella* excretion during the nursery period was probably caused by horizontal transmission, triggered by weaning stress.
Under the present conditions, it could not be shown that sows play a major role in the direct transmission to their offspring. On the other hand, they may partially protect them by maternal antibodies. To clarify the possible relation between *Salmonella* excretion in sows and offspring, further research is going on analysing genetic similarities and/or differences between the *Salmonella* isolates found in the sows and the piglets.

5. References

1. Beloeil P.A., Chauvin C., Proux K., Rose N., Queguiner S., Eveno E., Houdayer C., Rose V., Fravalo P., Madec F., Longitudinal serological responses to *Salmonella enterica* of growing pigs in a subclinically infected herd, *Prev. Vet. Med.* 60 (2003) 207-226.
2. Davies P.R., Bovee F.G.E.M., Funk J.A., Morrow W.E.M., Jones F.T., Deen J., Isolation of Salmonella serotypes from feces of pigs raised in a multiple-site production system, *J. Am. Vet. Med. Assoc.* 212 (1998) 1925-1929.
3. Funk J.A., Davies P.R., Nichols M.A., Longitudinal study of *Salmonella* Enterica in growing pigs reared in multiple-site swine production systems, *Vet. Microbiol.* 83 (2001) 45-60.
4. Kranker S., Alban L., Boes J., Dahl J., Longitudinal study of Salmonella enterica serotype Typhimurium infection in three Danish farrow-to-finish swine herds, *J. Clin. Microbiol*. 41 (2003) 2282-2288.
5. Sandvang D., Jensen L.B., Baggesen D.L., Baloda S.B., Persistence of a *Salmonella enterica* serotype Typhimurium clone in Danish pig production units and farmhouse environment studied by pulsed field gel electrophoresis, *FEMS Microbiol. Lett.* 187 (2000) 21-25.
6. Tauxe R.V., Emerging foodborne diseases: an evolving public health challenge, *Emerg. Infect. Dis.* 3 (1997) 425-434.

OPTIMISING THE SAMPLING STRATEGY FOR AN EARLY CLASSICAL SWINE FEVER DETECTION

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ABSTRACT

In the control of classical swine fever, an early detection is crucial. In this study, the number of animals to be sampled to detect an infected pen using virus isolation and virus neutralisation was calculated with the hypergeometric distribution. In the primary infected pen (fattening pigs), infection could be detected from 3 days post inoculation (dpi) onwards. Between 3 and 16 dpi all animals of this pen are to be sampled to be 99% certain infected animals are included. From day 17 onwards, a priori selection was possible based upon apathy, which makes it possible to drastically reduce the sample size. In the adjacent pen, infection could only be detected at 23 dpi. When an ad random sampling procedure is used, a selection of samples for VI can be based upon the leukocyte count. This results in a reduction of the samples from 15 dpi onwards. Therefore, it is concluded that as long as there are no clinical signs present, almost all animals in a pen are to be sampled to be sure that an infection is present or not. Once diseased animals are present, an a priori selection based on apathy is the most appropriate method to assure an early detection.

Bij de bestrijding van klassieke varkenspest is een vroege detectie essentieel. In deze studie werd met de hypergeometrische distributie het aantal dieren berekend om een geïnfecteerd hok te detecteren (virus isolatie en virus neutralisatie). Het eerst geïnfecteerde hok (mestvarkens) kon vanaf 3 dagen na inoculatie (dni) gedetecteerd worden. Tussen 3 en 16 dni moesten alle varkens van het hok bemonsterd worden om met 99% zekerheid ten minste 1 dier te detecteren. Vanaf 17 dni maakte a priori selectie op basis van apathie een reductie van de bemonsteringsgrootte tot één dier mogelijk. In het naastliggende hok kon infectie pas gedetecteerd worden 23 dni. Wanneer willekeurig varkens worden bemonsterd kan men de te analyseren stalen (VI) selecteren op basis van de leukocyten telling, met een reductie vanaf 15 dni. Algemeen kan men besluiten dat wanneer geen klinische symptomen aanwezig zijn, bijna alle dieren bemonsterd moeten worden. Eenmaal wel symptomen aanwezig, is een selectie op basis van apathie de meest geschikte manier om een vroege detectie te bekomen.

1. INTRODUCTION

An early detection of a classical swine fever (CSF) epidemic is crucial to limit the duration of the high risk period (HRP). During this HRP the virus can spread almost unhindered and therefore, the length of this period is directly related to the extent of an outbreak (Horst et al., 1998). For early detection of the CSF virus, virus isolation (VI) or RT-nPCR are necessary (Dewulf et al., 2004). Yet both techniques are labour intensive and time consuming. Therefore, it is crucial to limit the number of samples by appropriate selection of the animals that are to be sampled or by selection of the blood samples that are to be tested in the lab.

In addition, early detection, if it proves to be efficient, may be an alternative for preventive emptying of herds in the neighbourhood of an infected herd. The concept of this control method is that when pigs are detected at an early stage of infection, the infection pressure is still insufficient for between herd spread. This procedure would result in a drastic reduction of the number of herds that are to pre-emptively emptied.

2. MATERIALS AND METHODS

In this analysis, the minimal required sample size was calculated to be able to detect infection in a pen with at least 99% certainty. Data from an experiment in fattening pigs (Dewulf et al., 2001) were used. In this experiment, two pens with susceptible pigs were present within the same compartment (pen 1, n=14 and pen 2, n=15). In pen 2 one pig was inoculated with CSF and subsequently the infection spread within and between the pens in a natural way. An individual pig was defined as infected when either this pig was viraemic (VI whole blood) or antibodies were detected using virus neutralisation (VN).

In a second part of the study it is evaluated whether it is possible to reduce the number of animals to be sampled without reducing the probability of detection, using a priori selection criteria.
First an a priori selection with non specific symptoms of the animals to be sampled was made. Pigs were selected on the presence of apathy. In this group, the probability that at least one of the selected animals with apathy was detected as infected was calculated.
Secondly, it was investigated if the leukocyte count would be a successful method to further decrease the number of samples that are to be analysed using VI. Leukopenia was defined as <10 000 WBC/ml in fattening pigs.

The probability of finding at least one positive pig in a pen from the moment the first pig in a pen became viraemic in whole blood and when varying numbers of randomly selected pigs or pigs with apathy were sampled was calculated using the hypergeometric distribution (Murray, 2004). The probability of having one positive VI or VN test after selecting the blood samples based upon the presence of leukopenia was calculated in a similar way. This probability distribution is calculated with following formula:

$$P(x=0|n,S,N)=\frac{\binom{S}{x}\binom{N-S}{n-x}}{\binom{N}{n}} \text{ and } P(x>0|n,S,N)=1-P(x=0|n,S,N)$$

The parameters are: *x*= the number of successes in the sample; *n*= the sample size; *S*= the number of successes in the population; *N*= the population size.

3. RESULTS

3.1. Random sampling methods and a priori selection of animals based on apathy

In the primary infected pen infection could be detected starting 3 dpi (VI). Only 17 dpi, the symptom apathy was observed for the first time. Before the presence of clinical symptoms, only a random sampling method was possible. Until 12 dpi, all animals had to be sampled to be able to detect at least one infected animal with 99% certainty. From 13 dpi, sample size reduced with an increasing number of infected animals in the pen (figure 1). The number of animals to be sampled became substantially smaller when the pigs were selected based on the presence of apathy (from 17 dpi onwards). Infection spread from the infected pen towards the adjacent pen, with first detection of infection 23 dpi. Selection on apathy was first possible 25 dpi and the decrease in sample size was similar as in the other pen.

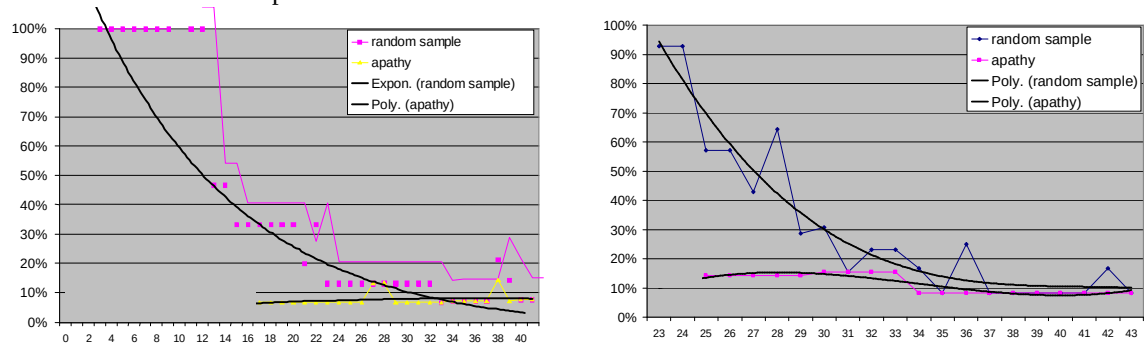

Figure 1: Sample size to detect at least one infected (VI or VN) animal per pen (99% certainty). left: primary infected pen; right: adjacent pen; X-axis: days post inoculation; Y-axis: % pigs.

3.2. Selection of samples to be analysed using the leucocyte count

First samples with leucopenia were present from 15 dpi. When using this selection criteria the number of samples that were to be analyzed reduced from 5 to 1.

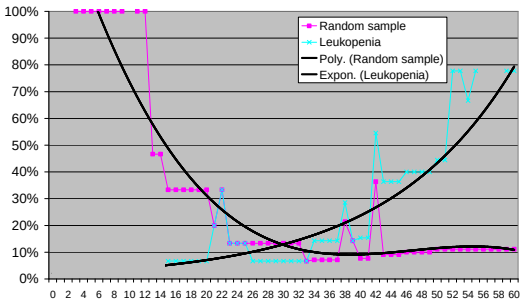

Figure 2: Sample size determination to select samples with leucopenia for analysis with VI or VN (pen 2).

4. DISCUSSION

In this paper, a sampling scheme intended to maximise the probability of detecting a CSF infected animal as soon as possible was developed. In the dataset used, inoculation of one pig corresponded to the introduction of the virus in a naïve herd. At an early stage of infection the prevalence of infected pigs per pen is low and there are not yet obvious clinical symptoms available. This inevitably leads to a high proportion of the present animals to be sampled in order to be sure that the present infection can be detected. At the herd level, this is practically unfeasible. In extension, as long as there are no clinical symptoms present to guide the sample selection almost the whole herd has to be sampled to be able to detect the limited number of first infected pigs.

Once clinical symptoms become apparent, which can take up to 14 days, the selection of animals that are to be sampled has to be based upon the presence of these symptoms. Within the group of clinical diseased animals a limited sample is already sufficient to be able to detect the disease. Yet, it has to be mentioned that the symptom we used (apathy), is not very specific. Therefore it is especially useful in times of an epizootic or suspicion of an epizootic.
Selection of the pigs based upon fever (data not shown in this paper) resulted in a comparable but slightly less efficient reduction of the number of pigs to be sampled. Moreover, in the field selecting pigs on body temperature is sometimes difficult to achieve.

When a random sampling scheme is used, a selection of blood samples to be analyzed on the basis of leukopenia can be useful to reduce the workload in the lab. This selection procedure gives a reduction of the number of samples to be analysed from 14 dpi onwards. When comparing this to the on herd selection based upon clinical symptoms, it only results in a 2 day gain. This again leads to the conclusion that selection on clinical symptoms is the most efficient.

Finally it has to be mentioned that when the selection of the animals that are to be sampled is not based upon clinical symptoms, the VI must always be combined with an antibody detection test since it may be possible that some animals are already infected for some time without showing apparent clinical symptoms and can already be virological negative and serologically positive at the moment of sampling.

It is concluded that as long as there are no clinical signs present (in the beginning of infection), almost all animals in a pen are to be sampled to be sure that an infection is present or not. Once there are diseased animals present, an a priori selection of animals based on apathy is the most appropriate method to assure an early detection.

5. ACKNOWLEDGEMENTS

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6. REFERENCES

Dewulf, J., Laevens, H., Koenen, F., Mintiens, K., en de Kruif A. An E2 sub-unit marker vaccine does not prevent horizontal or vertical transmission of classical swine fever virus. *Vaccine* 2001; 20: 86-91.

Dewulf, J., Koenen, F., Mintiens, K., Denis, P., Ribbens, S., de Kruif, A. Analytical performance of several classical swine fever laboratory diagnostic techniques on live animals for detection of infection. *J. Virol. Methods* 2004; 119: 137-43.

Horst, H.S., Dijkhuizen, A.A., Huirne, R.B., de Leeuw, P.W. Introduction of contagious animal diseases into the Netherlands: elicitation of expert opinions. *Livestock production Science* 1998; 53: 253-264.

Murray, N. *Handbook on Import Risk Analysis for Animals and Animal Products*. OIE, Paris, 2004.

AN EXPERIMENTAL INFECTION TO EVALUATE THE INDIRECT TRANSMISSION OF CLASSICAL SWINE FEVER BY PERSON CONTACTS

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ABSTRACT

Transmission of classical swine fever (CSF) by persons has been proposed as a route of virus spread. The objective of the current study was to examine the indirect transmission of CSF virus through persons wearing contaminated boots, gloves and coveralls in an experimental setting. Therefore, a carefully followed visitation scheme between experimentally inoculated and susceptible weaner pigs was used. The inoculated and susceptible pigs were housed in separated compartments, between which airborne transmission of the virus was made impossible. A worst-case scenario with an intensive visiting protocol and without any form of disinfection or hygiene was mimicked in this experiment. Fifteen days post inoculation, infection was detected in one contact pig. Therefore it is concluded that under these circumstances, transmission through person contacts is important.

Overdracht van klassieke varkenspest (KVP) door persoonscontacten wordt beschreven als een mogelijke weg van virusverspreiding. In deze studie werd de indirecte overdracht van het KVP virus door middel van gecontamineerde laarzen, handschoenen en overalls nagegaan. Hiervoor werd nauwgezet een bezoekprotocol tussen experimenteel geïnoculeerde en gevoelige varkens gevolgd. De geïnoculeerde en de gevoelige dieren werden gehuisvest in gescheiden compartimenten waartussen virustransmissie via de lucht onmogelijk was. Een worst-case scenario met intensieve visites zonder enige vorm van desinfectie en hygiëne werd nagebootst Vijftien dagen na inoculatie werd infectie gedetecteerd bij één van de contactdieren. Algemeen kan besloten worden dat onder deze omstandigheden, virusoverdracht door persoonscontacten belangrijk is.

INTRODUCTION

Because the importance of several transmission routes of classical swine fever (CSF) remains unclear, an investigation of the different routes is necessary. Person contacts and fomites (clothing, footwear and instruments, …) have been described as a possible route of virus transmission (Terpstra, 1988). Based upon the data of the 1997-1998 CSF-epidemic in the Netherlands, Elbers et al. (2001) conducted an epidemiological study that indicated that hygienic measures before entering pig premises reduced the risk of an infection. Stegeman et al. (2002) estimated the inter-herd transmission rate for persons as 0.0068 per contact.

The objective of this study was to examine whether person contacts can transmit classical swine fever virus from infectious to susceptible pigs.

MATERIALS AND METHODS

The experiment was performed in an isolation unit that consisted of 2 compartments (Figure 1). In compartment A, 6 weaner pigs were housed in one pen (pen 1). In compartment B, 3 pens were built (pens 2, 3 and 4). Each of the 3 pens housed 3 weaner pigs. The 6 weaner pigs in compartment A (pen 1) were experimentally infected (‘souche Lorraine’). From inoculation onwards, a strict visiting protocol was followed.

The isolation unit was entered with clean, disposable coveralls, disposable latex gloves and disinfected boots. At first, the 6 experimentally infected animals were clinically inspected. Afterwards, 2 pigs were trapped and blood was collected. Without changing clothes (coverall, boots and gloves) nor disinfection of boots, contact pigs in pen 2 in compartment B were examined and blood sampled. This was the first attempt of transmission. Hereafter, compartment B was left and in the corridor of the unit, clothes (coverall and gloves) were changed and boots were disinfected. Then again, the infected compartment was visited and the same actions were

performed with two other pigs of compartment A and the 3 contact pigs of pen 3. This action was a repetition of the first attempt of transmission. After this, without changing clothes the 2 remaining pigs of pen 1 were sampled. Just before the last pen (pen 4) was entered, clothes were changed (coverall, gloves and boots). This last pen was included as a control group where no transmission should occur. Pens with infected and susceptible animals were located in compartments with separated ventilation systems. There was no airflow from A to B.

Blood samples were taken every other day for virus, antigen and antibody detection. Rectal temperature was monitored daily. Samples of fomites were taken with moist sterile swabs. Places for sampling fomites were gloves, coveralls and boots. In total 36 samples of fomites were gathered.

In all blood samples, presence of virus was tested using virus isolation (VI) in whole blood. Swabs of fomites were used for VI.

RESULTS

Inoculation succeeded in all 6 experimentally infected animals. The average time between infection and start of viraemia was 2.8 days. At 15 dpi, one contact pig in pen 3 was detected viraemic: it was considered viraemic starting 14 dpi. At 17 dpi, all remaining pigs were euthanized.

In all samples of fomites except one, VI was unsuccessful. At 11 dpi, sampling of one glove used in the infected compartment was positive.

DISCUSSION AND CONCLUSION

Fifteen dpi, one pig in pen 3 was detected positive. It is assumed transmission took place 9 or 11 dpi (during the 4^{th} or 5^{th} visit). This is based on the minimum incubation time of 2 -4 days in weaner pigs (Laevens et al., 1998, Dewulf et al., 2002, Ribbens et al., in press). At the moment of presumed transmission, all inoculated pigs were viraemic for at least one week and a considerable infection pressure was built up. Moreover, at 11 dpi also the only positive fomite sample was found. This was consistent with a detected peak in excretions and secretions between 9 and 11 dpi (Ribbens et al., in press).

It is impossible to distinguish whether it was the frequent repetition of visits that resulted in a sufficient high infection pressure in the contact pens or whether infection was caused by only one successful transmission on a moment that the infection load was high enough. In our opinion, the latter is the most likely.

For several reasons, results of this transmission experiment cannot be extrapolated directly to field conditions. First, the experiment was designed as a worst-case scenario setting. In this setting, people did not use any hygienic measures at all. Visits of the infected pigs were immediately followed by visits of the susceptible pigs, using the same coveralls, gloves and without disinfection of the boots. In normal practice, such an intensive indirect contact is seldom present. Also contributing were the repeated visits between the inoculated pigs and the susceptible pigs. No attempts were made to investigate the effectiveness of used biosecurity protocols. Therefore, further research is required to evaluate the efficacy of different biosecurity measures.

In conclusion, it can be stated that without hygienic precautions, transmission of CSFV is possible by person contacts or fomites. Therefore, strict biosecurity protocols are crucial to prevent introduction and spread of CSF.

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REFERENCES

Dewulf, J., Laevens, H., Koenen, F., Mintiens, K. & de Kruif, A. An experimental infection to investigate the indirect transmission of classical swine fever virus by excretions of infected pigs. *J. Vet. Med. B* 2002; 49: 452-456.

Elbers, A.R., Stegeman, J.A. & de Jong, M.C. Factors associated with the introduction of classical swine fever virus into pig herds in the central area of the 1997-1998 epidemic in the Netherlands. *Vet. Rec.* 2001; 149: 377-382.

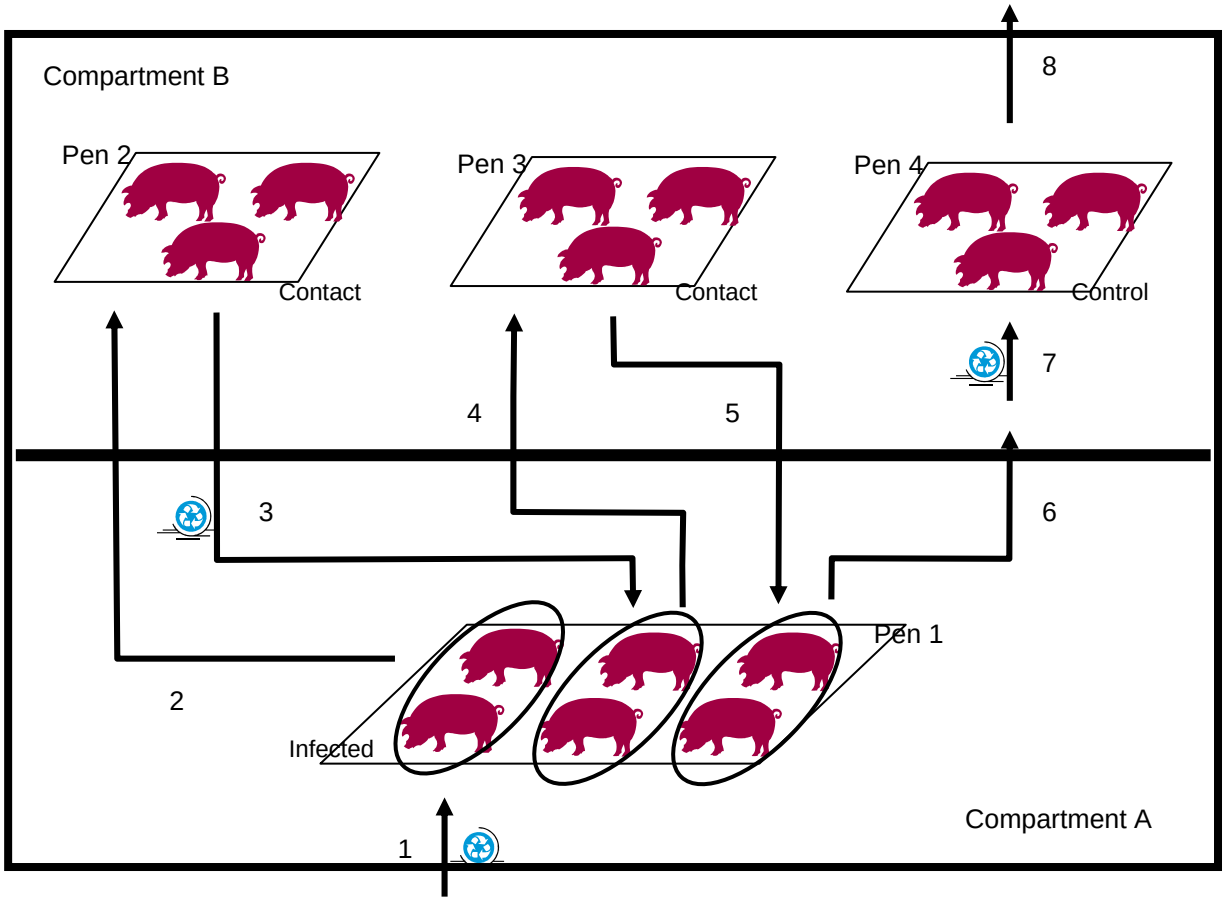
Laevens, H., Koenen, F., Deluyker, H. & Berkvens, D. An experimental infection with classical swine fever virus in weaner pigs. I. Transmission of the virus, course of the disease, and antibody response. *Vet. Q.* 1998; 20: 41-45.

Ribbens, S., Dewulf, J., Koenen, F., Laevens, H., Mintiens, K. & de Kruif, A. An experimental infection (II) to investigate the indirect classical swine fever transmission by excretions and secretions in weaner pigs. *J. Vet. Med. B.* 2004; in press.

Stegeman, J. A., Elbers, A. R. W., Bouma, A. & De Jong, M.C.M. (2002) Rate of inter-herd transmission of classical swine fever virus by different types of contact during the 1997–1998 epidemic in The Netherlands. Epid. and Infect. **128,** 285-291.

Terpstra, C. (1988) Epizootiology of Hog-Cholera. In: Classical swine fever and related viral infections. Editors: Liess B., Martinus Nijhoff Publishing, Dordrecht, The Netherlands, pp. 201-216.

Figure 1: Schematic presentation of the visiting and sampling scheme.



1: Entering isolation unit with new coverall, gloves and disinfected boots. **2**: Sampling 2 weaner pigs in the infected compartment A (pen 1), then sampling all contact pigs of pen 2 (**transmission 1**). **3**: New coverall, gloves and disinfection of boots. **4**: Sampling 2 weaner pigs of pen 1, then sampling all contact pigs of pen 3 (**transmission 2**). **5**: Returning to pen 1. **6**: Sampling of 2 remaining weaner pigs of pen 1. **7**: Just before sampling control pigs (pen 4) new coveralls, gloves and new disinfected boots. **8**: Leaving isolation unit.

: new coveralls, gloves and disinfection of boots/new boots.

MOLECULAR AND MATHEMATICAL EPIDEMIOLOGY OF BOVINE MASTITIS

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ABSTRACT

In this presentation, some recent developments in the molecular and mathematical epidemiology of bovine mastitis are used as examples to show the progress made in combining molecular and mathematical approaches to relevant research questions. Three examples are highlighted in some detail. Firstly, the arguments leading to the conclusion that in certain herds *S. uberis* infections may behave as a contagious form of mastitis are outlined. Secondly, the pathobiology of chronic coliform intramammary infections is discussed in some detail. The data appear to indicate that some reservoir of coliform bacteria in the mammary gland is necessary to be able to give rise to the observed data. Finally, the population dynamics and interaction of major and minor pathogenic bacterial species are examined. It is concluded that widespread infections of minor pathogens may lead to a reduction in transmission potential of major pathogens.

SAMENVATTING

In deze presentatie worden een aantal recente ontwikkelingen in the moleculaire en mathematische epidemiologie van bovine mastitis gepresenteerd. De combinatie van deze beide methoden leidt tot een snellere progressie bij het beantwoorden van belangrijke onderzoeksvraagstellingen. Drie voorbeelden worden in detail besproken. Ten eerste, gebaseerd op zowel mathematische modellen alswel op moleculaire fingerprint technieken wordt geconcludeerd dat S.uberis zich kan gedragen als een contagieuze pathogeen. Als tweede voorbeeld wordt aangehaald de pathogenese van chronische E.coli infecties. De besproken technieken leiden tot de conclusie dat intracellulaire overleving van bacterien zeer waarschijnlijk is. Tenslotte wordt de populatie dynamiek van major en minor pathogenen besproken. De conclusie is dat de verspreiding van minor pathogenen in de uier kan leiden tot een reductie van infecties met major pathogenen.

1. INTRODUCTION

Epidemiological research in bovine mastitis has been performed for many years with very early studies relying mostly on clinical observations and linking certain pathogenic bacteria to the clinical signs that were typically produced in the cow by these bacteria (e.g. *Streptococcus agalactiae* and *Arcanobacterium pyogenes*). In the last decade, two additional techniques have been added to the toolkit of the mastitis epidemiologists: mathematical modelling and molecular diagnostics. These new tools have added a lot of opportunities to contribute to a better understanding of the pathobiology of intramammary infections in the dairy cow. Molecular diagnostic tools allow the distinction between strains in the same bacterial species (9). Amongst other things, this does allow for more precise longitudinal follow up studies of infection occurrences in populations. Mathematical models have contributed especially in the area of contagious disease dynamics (1), both in terms of explaining observed infection (and/or disease) frequencies and predicting or simulating infection frequencies under a given set of preventive measures (1).

The objective of this presentation is to review a number of recent studies attempting to answer mastitis research questions using molecular and mathematical methods. Using these examples, we will also attempt to formulate some general experiences and suggestions that we have come to appreciate during the execution of these studies. The three areas of research are the epidemiology of *Streptococcus uberis* infections, the chronicity of *Escherichia coli* intramammary infections and the impact of minor pathogens on the risk of new infections with major pathogens.

1.1 Epidemiology of S. uberis infections

The underlying question with regard to the epidemiology of *S. uberis* infections was whether they originate from other cows or whether they originate from the environment of the cow. The origin of infections must be known so that appropriate control measures for mastitis prevention in dairy herds can be chosen. The question was approached with mathematical and molecular tools. The null-hypothesis that was tested in the mathematical approach to this study was that the number of new infections of *S. uberis* in a population does not depend on the number of existing shedders in that population. In statistical terminology, the infection dynamics are described

by: $I_{\Delta t} = \theta P_{t-1}$, where I = incidence, P = prevalence, Δt = a given period of time, t-1 = beginning of time period, θ = regression parameter. The null hypothesis assumes $\theta = 0$. The alternative hypothesis indicates that $\theta > 0$ (possibly $\theta <> 0$). A similar model was previously used by Lam et al. (4) to model the dynamics of *Staphylococcus aureus* infections in a dairy herd.

Data were from a dairy farm with 95 ± 5 lactating animals (mean ± s.d.) where an outbreak of *S. uberis* infections was observed (10). Data were collected during an 18-month observation period with 27 farm visits at 3-week intervals. Initially, a low prevalence and very low incidence of *S. uberis* infections was evident. At approximately sampling period 10, the start of an exponential growth of new infections could be seen. This outbreak halted around sampling 16. The prevalence remained high for a while, but then dropped to a much lower level. Towards the end of the observation period, the prevalence was still approximately three times as high as at the start of the study. To model these data in a biologically meaningful way, it was necessary to assess whether spread of one specific strain has occurred. It has been described that multiple strains of *S. uberis* co-exist within a given dairy herd (8). An outbreak consisting of cases from multiple molecularly distinguishable strains would indicate that spread did not occur from cow to cow, that is, would favour the null hypothesis. Typing of the strains in the outbreak using random amplified polymorphic DNA (RAPD) fingerprinting techniques resulted in strong evidence for clonal spread (11). One large clonal outbreak with the strain named 'B' was observed (Figure 1).

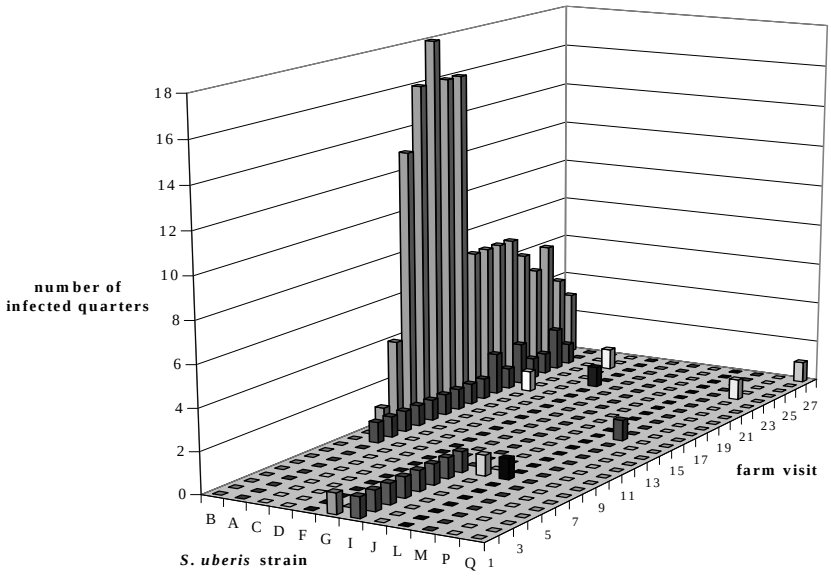

Figure 1 Frequency of infected quarters by farm and strain of *Streptococcus uberis*. Strains were typed by random amplified polymorphic DNA (RAPD) fingerprinting.

In addition, a number of single infections with a variety of different strains were observed on the farm. The data were modelled in a Poisson logistic regression model:

$$\varepsilon [\ln(IMI)] = \ln(\beta') + \ln (S/N) + \theta_1 * \ln(I) + \theta_2 * y + \theta_3 * U_m \quad (1)$$

where, ε = expected value, IMI = number of new intramammary infections with *Streptococcus uberis* in current time interval, β' = transmission parameter for model with ln(S/N) as offset, S = number of quarter-days susceptible in current time interval, N = total number of quarter-days in current time interval, I = number of quarter-days infected in preceding time interval, y = dummy variable for phase (y = 0 for early phase of the study up to and including the outbreak, y = 1 for the late phase of the study), U_m = dummy variable for compartment (U_m = 0 for R, U_m = 1 for U_1) and θ_i = regression coefficients. The estimates, standard errors and *P*-values for ln(β') and the three regression coefficients are shown in Table 1. Of specific interest is parameter θ_1 because this parameter tests the hypothesis that existing shedders contribute to the incidence of new infections.

Table 1. Estimates, standard errors and *P*-values for ln(β') and regression coefficients. U_1 = never before infected with *Streptococcus uberis*; R = recovered from infection with *S. uberis*

Model	Parameter	Coefficient	Estimate	Standard error	*P*-value

U_1 vs. R	ln(β')		0.11	0.78	0.8793
	ln(I)	θ_1	0.68	0.15	< 0.0001
	study phase	θ_2	-1.55	0.35	< 0.0001
	compartment	θ_3	-2.06	0.42	< 0.0001

The regression results indicated that θ_1 was significantly different from 0, and hence the initial null hypothesis was rejected implying that the number of new infections was not independent of the number of existing infections. Therefore, the alternative hypothesis, indicating contagious transmission of *S. uberis*, appeared to best fit the data.

1.2 Chronicity of E. coli intramammary infections

In recent publications, the occurrence of chronic *E. coli* intramammary infections was reported (2). Using DNA fingerprinting, the presence of indistinguishable isolates from repeated cases of clinical mastitis in the same quarter of the same cow was shown. An example of such an infection is shown in Figure 2. The isolates in lanes 2-14 were repeated cases of clinical coliform mastitis from the same quarter of the same cow and the isolates in lanes 16 to 19 came from a different quarter in the same cow.

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

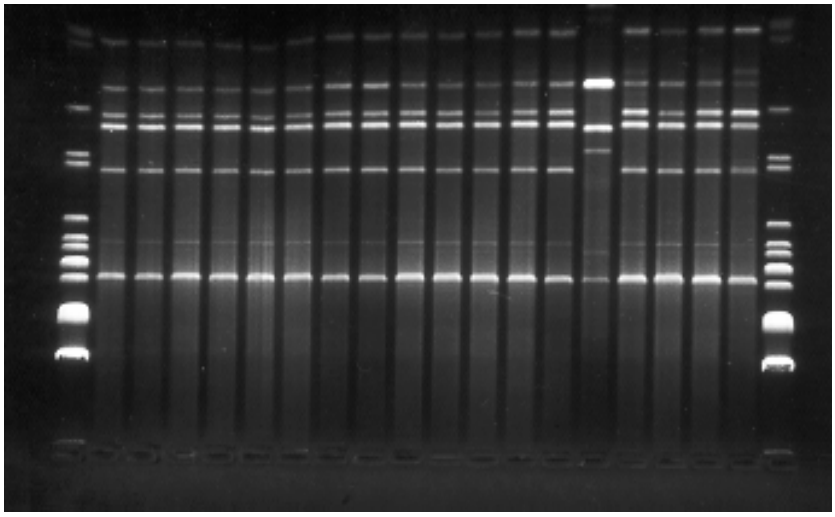

Figure 2. Genetically indistinguishable isolates (evaluated by DNA fingerprinting using PCR-REP and ERIC primers) from recurrent clinical *E. coli* mastitis cases. Lanes 1 and 20: molecular size marker. Lanes 2-14: Cow 1, quarter A; Lane 15: Cow 2; Lanes 16-19: Cow 1, quarter B.

Because of the high number of *E. coli* strains in the dairy environment, it is unlikely that recurrent isolation of one strain from the same quarter was the result of recurrent new infections. However, it is not impossible. To determine whether the infection was really persistent, longitudinal data on a single chronically infected cow were collected. In colony forming units and somatic cell concentrations, an apparent inverse cyclicity (with a Pearson correlation of -.36, $p<0.05$) was observed. These data, although relatively sparse, provide initial evidence that milk leukocytes and bacteria show a dynamic behaviour. Similar behaviour has been suggested for *S. aureus*. Such dynamic behaviour may be modelled using 'predator-prey' type modelling techniques:

$dR/dt = rR(1-R/K) - ENR^2/(R_0^2 + R^2)$ (2)

$dN/dt=N[-d+cER^2/(R_0^2 + R^2)]$ (3) where:

R = *E. coli* density in cfu per ml, t = time, r = growth rate of *E. coli* (logistic growth), K = carrying capacity of the system, E = somatic cell count (SCC) saturation level of 'consuming' *E. coli*, N = SCC density in cells per ml, R_0 = half-saturation density of *E. coli* (where $R > R_0$), d = per capita rate at which SCC die out when no *E. coli* are present, c = 'conversion efficiency' of *E. coli* to SCC - this may be considered as feeding efficiency.

To incorporate the concept of an intracellular reservoir for the bacteria, the model may be extended by including an additional state variable, Z, governed by the ODE's. Equations 4 and 5 are identical to equations 2 and 3, except for equation 4, where ϕZ, the release of bacteria from the third state, Z, at a rate ϕ per day, is added to and πR, the intracellular invasion of bacteria, R, at a rate π per day, is subtracted from dR/dt.

$dR/dt = rR(1-R/K) - ENR^2/(R_0^2 + R^2) + \phi Z - \pi R$ (4)

$dN/dt=N[-d+cER^2/(R_0^2 + R^2)]$ (5)

$dZ/dt= - \phi Z + \pi R$ (6)

The model with the intracellular reservoir fitted the data considerably better compared with a model without such a reservoir. Several potential reservoirs (i.e. dormant bacteria) may be envisaged. For example, leukocytes that contribute to the somatic cell count (SCC) ingest *E. coli* and a subsequent failure to kill the coliform bacteria, creates a reservoir. Studies have also shown that mammary epithelial cells may act as a reservoir (3).

1.3 Impact of minor pathogens on the risk of new infections with major pathogens

The bacterial pathogens responsible for infection of the mammary gland may be split into two main categories, major and minor. Infection with major pathogens generally results in clinical illness or strong inflammatory responses and reduced milk yields, whereas minor pathogen infection is usually subclinical with a less severe SCC increase or yield loss. Experimental evidence has in some cases shown cross-protection between species of pathogens. A mathematical model for the transmission of both major and minor pathogens along with their interaction via the host was developed by White et al. (7) to consider various methods for controlling the incidence of major pathogen infection (Figure 3). A stability analysis of the model equilibria provide explanations for observed phenomena. Previous modelling results focused on one bacterial species only. However, this multi-species model structure has provided a basis for quantifying the extent of cross protection between species and for assessing possible control strategies against the disease.

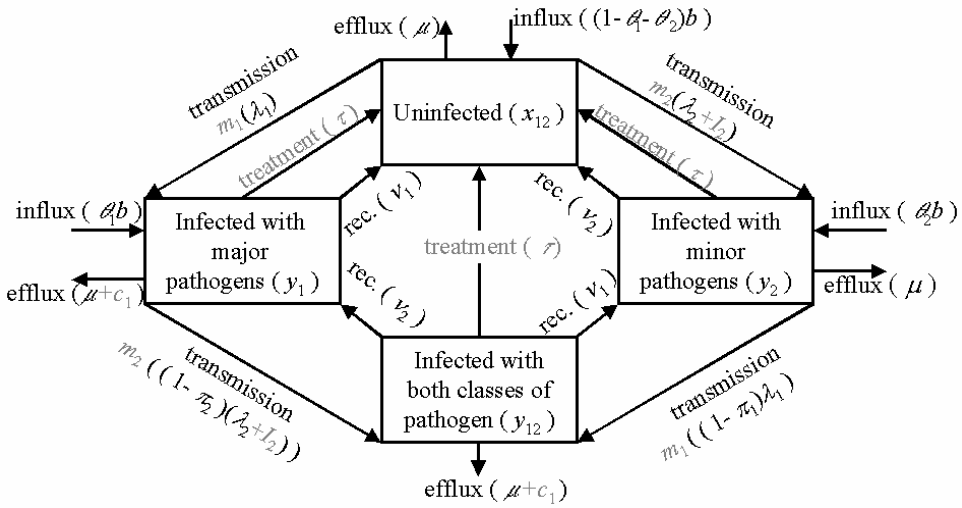

Figure 3. Multi-species infection transmission model (7).

This analysis extends the work of Lam et al. (4) who modelled mastitis transmission in cattle using SIS (susceptible-infectious-susceptible) models that were fitted to prevalence and incidence data from herds of dairy cows. The results suggested some interaction in the transmission of the different pathogen species. The results indicated that, where both minor and major pathogens were being transmitted, the basic reproduction number of *S. aureus* (a major pathogen) decreased during the course of an outbreak of mastitis. This result could not be explained using decoupled (no interaction between species) models. The objective of the extended work was to develop a simple multi-species model, where there is some cross-protection provided by infection by one class of pathogens (minor pathogens) against infection by another class (major pathogens) and to examine the dynamic consequences of the interaction (7). The multi-species model that was used is presented in Figure 3. Other symbols in Figure 3 represent interventions: m_i represents a decrease in transmission by post milking teat disinfection, c_i additional culling, τ treatment of infections and I_i inoculation of quarters. The model was fitted to the data observed by Lam et al. (4) using the computer package, Facsimile. The raw data were in the form of spreadsheets for each of eighteen samplings. The number of colony forming units of each pathogen for each quarter of each cow was given. The system equations (without intervention) are given by:

$$\left.\begin{aligned}
\dot{x}_{12} &= (1-\theta_1-\theta_2)b-(\lambda_1+\lambda_2+\mu)x_{12}+\nu_1 y_1+\nu_2 y_2\\
\dot{y}_1 &= \theta_1 b+\lambda_1 x_{12}+\nu_2 y_{12}-((1-\pi_2)\lambda_2+\nu_1+\mu)y_1\\
\dot{y}_2 &= \theta_2 b+\lambda_2 x_{12}+\nu_1 y_{12}-((1-\pi_1)\lambda_1+\nu_2+\mu)y_2\\
\dot{y}_{12} &= (1-\pi_1)\lambda_1 y_2+(1-\pi_2)\lambda_2 y_1-(\nu_1+\nu_2+\mu)y_{12}
\end{aligned}\right\}\ \text{where:}\ \left\{\begin{aligned}
1 &= x_{12}+y_1+y_2+y_{12}\\
b &= \mu\\
\lambda_1 &= \beta_1(y_1+y_{12})\\
\lambda_2 &= \beta_2(y_2+y_{12})
\end{aligned}\right\} \quad (7)$$

Steady state analysis has produced a 'cross-protection curve' that has a similar form to those produced from other multistrain/species models (6). A similar analysis on the model equations extended to include various control procedures has given some theoretical insight into their possible effects.

2. DISCUSSION

The known udder pathogenic bacterial species show such a large variability within species that valid modelling of observed events is only possible with knowledge of the particular clones present in the data. This was shown to be important in the analysis of the observed *S. uberis* outbreak in a dairy herd. Several of the strains obtained from infected cows showed behaviour typical of single isolated infections without transmission between animals. However, one of the strains showed a very different epidemiology, with abundant evidence for clonal spread according to the laws of mass action. Modelling of these data was very helpful in providing quantitative evidence for contagious behaviour of this *S. uberis* strain. Using statistical testing, a formal argument can be made that this particular strain showed a rate of new infection that was dependent on the number of shedders. The argument still continues, because it is not impossible that a surge of growth of this particular *S. uberis* strain occurred in the environment of the cows. Several quantitative and non-quantitative arguments favour the contagion hypothesis but the undisputed proof of that may turn out to be impossible.

Using molecular fingerprinting techniques, it was shown beyond doubt that chronic coliform infections occur in dairy cows. The observed data suggest a predator-prey type of cyclical system. Using fairly simple Lotka-Volterra type models, the observed data were reasonably well reproduced. Therefore, the initial models suggest that an intracellular reservoir explains the observed data slightly better than a model without an intracellular reservoir of bacteria.

The multi-species model is an extension of previous modelling work. It extended the specific modelling work of Lam et al. (4) on the transmission of mastitis pathogens as well as providing some validation of a standard multi-species model structure (5). When complex relationships between species exist, modelling is virtually the only option to look at the ecology of the organisms in the population. Using this multi-species modelling approach, it has become clear that competition between species may be an important control option with regard to the transmission of clinically important pathogens (6).

Some important developments for modern epidemiology are becoming evident when the results of these population studies on mastitis in cows are combined. Without a confirmation that clonal spread occurs through a population of animals, it is difficult to be persuasive in novel arguments (paradigm shifts) about the epidemiology of strains (10,11). Use of mathematical modelling to further explain the epidemiology and pathogenesis of intramammary infections has great potential. The examples presented all show an important additional understanding of the biology of infection in the population or in the host due to the additional tool of mathematical modelling.

REFERENCES

1. Anderson, R.M. and May, R.M. (1985). Infectious diseases of humans: Dynamics and control. Oxford University Press, Oxford.
2. Döpfer, D., Barkema, H.W., Lam, T.J.G.M., Schukken, Y.H. and Gaastra, W. (1999). Recurrent clinical mastitis caused by *Escherichia coli* in dairy cows. *J. Dairy Sci*. 82, 80-85
3. Döpfer, D., Almeida, R., Lam, T.J.G.M., Nederbragt, H., Oliver, S.P. and Gaastra, W. (2000). Adhesion and invasion of *E. coli* from recurrent clinical cases of bovine mastitis *in vitro*. *Vet. Microbiol*. 74, 331-343
4. Lam, T.G.M., De Jong, M.C.M., Schukken, Y.H. and Brand, A. (1996a). Mathematical modelling to estimate efficacy of post milking teat disinfection in split-udder trials of dairy cows. *J. Dairy Sci*. 79, 62-70
5. Lipsitch, M. (1997). Vaccination against colonising bacteria with multiple serotypes. Proc. Nat. Acad. Sci. 94, 6571-6576
6. White, L.J., Cox, M.J. and Medley, G.F. (1998). Cross immunity and vaccination against multiple parasite strains. *IMA J. Math. Appl. Med. Biol.* 15, 211-233
7. White, L.J., Evans, N.D., Lam, T.J., Schukken, Y.H., Medley, G.F., Godfrey, K.R. and Chappell, M.J. (2002). The structural identifiability and parameter estimation of a multispecies model for the transmission of mastitis in dairy cows with postmilking teat disinfection. *Math. Biosci.* 180, 275-291
8. Wang, S.M., Deighton, M.A., Capstick, J.A. and Gerraty, N. (1999). Epidemiological typing of bovine streptococci by pulsed-field gel electrophoresis. *Epidemiol. Infect.* 123, 317-324
9. Zadoks, R., van Leeuwen, W., Barkema, H., Sampimon, O., Verbrugh, H., Schukken, Y.H. and van Belkum, A. (2000). Application of pulsed-field gel electrophoresis and binary typing as tools in veterinary clinical microbiology and molecular epidemiologic analysis of bovine and human *Staphylococcus aureus* isolates. *J. Clin. Microbiol.* 38, 1931-1939
10. Zadoks, R.N., Allore, H.G., Hagenaars, T.J., Barkema, H.W. and Schukken, Y.H. (2002). A mathematical model of *Staphylococcus aureus* control in dairy herds. *Epidemiol. Infect.* 129, 397-416
11. Zadoks, R.N., Gillespie, B.E. Barkema, H.W. Sampimon, O.C. Oliver, S.P. and Schukken, Y.H. (2003). Clinical, epidemiological and molecular characteristics of *Streptococcus uberis*. *Epidemiol. Infect*. 130:335-49

RISK FACTORS ASSOCIATED WITH TETRACYCLINE RESISTANCE IN LACTOSE-POSITIVE ENTERIC COLIFORMS FROM FATTENING PIGS

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ABSTRACT

Antimicrobial drug use is considered to be the most important factor in the development of antimicrobial resistance, though it is probably not the only influencing factor. The aim of this study was to investigate the link between tetracycline resistance in lactose-positive enteric coliforms originating from fattening pigs, the antimicrobial drug use and other potential risk factors, under field conditions. Multivariable analysis revealed that the degree of tetracycline-resistance was influenced by the production system (All-in/All-out > continuous) ($P<0.01$), the inside pen hygiene (dirty < clean) ($P<0.05$) and the treatment with tetracyclines (yes>no) ($P<0.05$).

SAMENVATTING

Het toedienen van antibiotica aan dieren wordt aanzien als de belangrijkste oorzaak van resistentie ontwikkeling bij bacteriën. Toch bestaan er waarschijnlijk nog andere factoren die het voorkomen van resistentie beïnvloeden. In deze veldstudie werd het verband tussen de tetracycline-resistentie bij lactose-positieve coliformen van vleesvarkens en mogelijke beïnvloedende factoren, waaronder het antibioticumgebruik onderzocht. Aan de hand van multivariabele analyse bleek dat de graad van tetracycline-resistentie beïnvloed wordt door enerzijds het productiesysteem (All-in/All-out > continu) ($P<0.01$), de hygiëne binnen het hok (vuil < proper) ($P<0.05$) en het al dan niet behandeld zijn met tetracyclines (ja>nee) ($P<0.05$).

1. INTRODUCTION

Antimicrobial drugs are used in livestock production for the treatment and prevention of diseases, and to enhance growth of animals (Mathew et al., 2001). The selection pressure exerted by these antimicrobial drugs has caused the emergence of antimicrobial resistance, not only in pathogenic bacteria, but also in non-pathogenic bacteria of the commensal flora (Barbosa and Levy, 2000; van den Boogaard et al., 2000). Antimicrobial drug use is considered to be the most important factor in the development of antimicrobial resistance, though it is probably not the only influencing factor. Age, temperature, diarrhea, etc (Moro et al., 1998 & 2000; Mathew et al.,1999) are examples of other influencing factors. Most of them were determined under experimental conditions. The aim of this study was to determine influencing factors on the degree of tetracycline resistance in lactose-positive enteric coliforms originating from fattening pigs under field conditions.

2. MATERIALS AND METHODS

2.1. Selection of farms

Herds were selected from the Belgian farm animal identification and registration database (Sanitel, 2003). All herds (821) (a) had a closed or semi-closed production system, (b) were located in the most dense pig areas in Belgium and (c) had at least 150 sows and 600 fattening pigs. Cooperation was on a voluntary basis. To end up with 50 herds, 84 randomly selected herds needed to be contacted (response rate: 60%). During the visit, a questionnaire was filled in and faecal samples were collected.

2.2. Questionnaire

The questionnaire consisted of general herd data and specific data on management-, housing- and antimicrobial drug consumption factors for each production stage. General herd data pertained to the total number of animals in the herd and the weaning age. Housing factors included the number of animals per compartment, number of animals per m², ventilation type (ceiling, mechanical, door, flap and others) and floor type (fully slatted or partly slatted). Management factors pertained to production system (all-in all-out/continuous), cleaning and desinfection procedures (yes/no), inside pen hygiene (dirty or clean), recent relocation (yes/no) , type of feed (dry meal, dry pellets, wet meal, liquid feeding). The collected antimicrobial drug use data were evaluated using: (a) treatment incidences based on Used Daily Dose pig (DDDpig) and (b) Animal Daily Dose pig (ADDpig), and (c) the ratio UDDpig/ADDpig (Jensen et al., 2004; Timmerman et al., 2004). Using these data, two categorical factors were derived from the data for tetracycline use: tetracycline treatment (yes/no) and dose of tetracyclines (correct, under-or overdosed).

2.3. Sample collection and bacteriological analysis

Pooled rectal faecal samples were taken from pigs of three different production stages (16 per production stage): end of nursery period (10 ± 2 weeks), end of grower period (18 ± 2 weeks), end of finisher period (26 ± 2 weeks) and immediately transported to the laboratory for analysis.
The degree of tetracycline resistance (TETR) was determined using an agar dilution method (Timmerman et al., 2003).

2.4. Statistical analysis

TETR was analysed using multivariable linear mixed effects regression models with herd as random factor (S-plus; Verbeke en Molenberghs, 2000). First, bivariate Pearson's correlation coefficients were derived between the different potential risk factors. Next each potential risk factor was included alone as single fixed effect in a univariable model. Only risk factors with a P-value lower than 0.20 were included in the multivariable model.

3. RESULTS

Tetracycline resistant LPEC were found on every herd. The distribution of the average TETR for the fifty herds (150 production stages) is presented in Fig. 1. The overall TETR in LPEC was 56.8% (minimum 8.2%, median 56.9%, maximum 100.0%; 95% CI 53.2%-60.4% and standard deviation 22.4%).

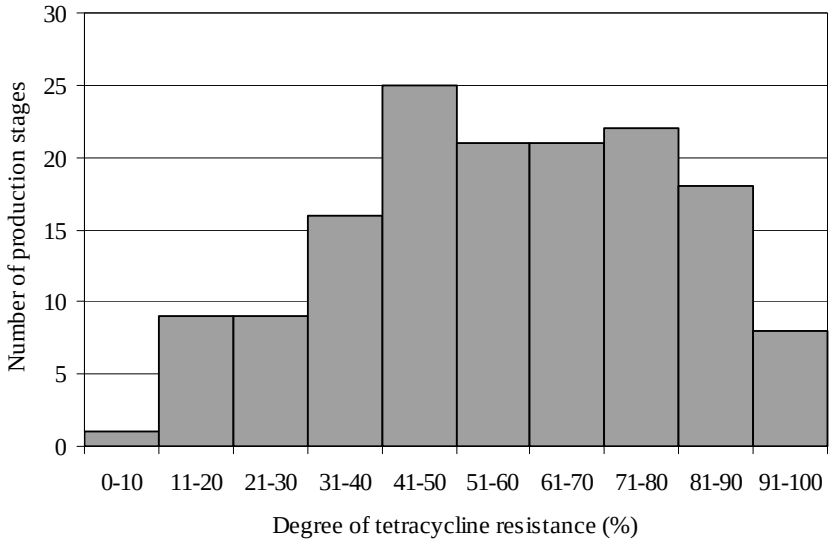

Figure 1: Distribution of the average TETR in fifty randomly selected closed or semi-closed pig herds (150 production stages).

Results of the univariable and multivariable analysis are shown in Table 1. After the multivariable analysis, three risk factors were identified: production system, inside pen hygiene and tetracycline treatment.

Table 1: Estimated herd-level TETR and 95% CIs from analyses based on the linear mixed model with herd as random factor. Only parameters with P<0.20 in the univariable analysis are shown and included in the multivariable model.

Parameter	TETR[a]	SD[b]	95% CI	P-value univariable	P-value multivariable
Categorical variables					
Production stage				0.1892	
End of nursery period	60.8	23.9	54.0-67.5		
End of grower period	56.1	21.6	50.0-62.2		
End of finisher period	53.6	21.5	47.5-60.0		
Production system				0.0093	0.0097
AIAO	60.7	21.8	56.2-65.2		
Continuous	50.4	22.7	44.2-56.7		
Recent relocation				0.0152	
<3 days ago	72.7	21.6	52.7-92.6		
3-10 days ago	60.9	19.1	46.2-75.6		
>10 days ago	55.9	22.7	51.9-59.8		
Inside pen hygiene				0.0049	0.0136
Dirty	52.9	22.2	48.4-57.3		
Clean	65.6	21.0	59.4-71.8		
Tetracycline treatment				0.0089	0.0353
Yes	66.6	20.0	60.5-72.6		
No	52.7	22.4	48.3-57.1		
Dose of tetracycline					
Not treated	52.7	22.3	48.4-57.1	0.0208	
Underdosed	78.1	6.3	68.1-88.0		
Correctly dosed	56.7	20.5	37.8-75.6		
Overdosed	67.6	20.6	60.2-74.9		
Continuous variables					
Number of animals per compartment				0.1333	
Number of animals per m²				0.1047	
Total number of animals per herd				0.0791	
Weaning age				0.1532	
Total UDDpig				0.0458	

DISCUSSION

These results confirm that the treatment with antimicrobial drugs is important in the development of resistance, but they also confirm that other factors can influence the development of resistance. Although the age of pigs has been significantly correlated with resistance in other studies (young animals had higher degrees of resistance), this was not found in our study, probably due to the minimal age difference of the sampled animals (max. 4 months). Moro et al. (2000) found that moving and mixing (relocation) of pigs was significantly correlated to tetracycline-resistance. These results were confirmed in the univariable analysis, but not in the multivariable analysis. Despite the fact that transfer of resistant bacteria in continuous housing systems has been suspected for vancomycin-resistant enterococci (Bager et al., 1999), these findings could not be confirmed for the widespread tetracycline-resistance in LPEC. Probably is the dilution of resistant bacteria with susceptible bacteria more important than the transfer of resistant bacteria. The fact that a lower degree of tetracycline-resistance was seen in dirty pens confirms this hypothesis.

ACKNOWLEDGEMENTS

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REFERENCES

A reference list can be obtained by the first auhor.

TEN YEARS OF BOVINE VIRUS DIARRHOEA VIRUS (BVDV) CONTROL IN NORWAY - A BENEFICIAL JOINT EFFORT IN THREE PARTS

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Abstract

The Norwegian control of BVDV started in 2002/2003. Initially the program was a cooperation between the cattle industry and official authorities, from 1998 the official authorities took over the program and in 2001 the cattle industry joined back in. By October 2004, there was 4 cattle herds left in the country were movement restriction due to BVDV suspicion have not yet been lifted. No new restrictions have been imposed in 2004. Hence, the Norwegian cattle population appears close to being cleared from BVDV.

The NPV of BVDV control in Norway discounting back to 1993 and using a 6% discount rate is estimated to 132 million NKr (16 mill Euro). The 5'th and 95'th percentiles of the NPV distribution being 22 and 264 million Nkr, respectively. Increased resources have been used in the late phase of control to 'mop up' the last infective sources in the population.

Materials and methods

Information regarding the program cost parameters was gathered from the participating parties, the cattle industry (TINE, GENO & Norwegian Meat), The National Animal Health Authorities (NAHA), and The National Veterinary Institute (VI). Only variable costs directly associated with the control program, and costs carried by the farmers as a consequence of the control program, were accounted for. No overhead costs have been included in the present calculations.

The benefit of the control program was estimated as the difference between the assumed losses without control, represented by static 1993 BVDV infection level through out the ten-year period, and the observed losses during the program period. The financial losses associated with BVDV infection were estimated based on input parameters gathered from studies of the herd level effects of BVDV on health, reproduction, and production in BVDV sero-converted (SC) herds (sero-conversion based on bulk tank milk samples) and herds with BVDV antibody positive young stock (YS) (Valle, 2000).

The calculations were performed in Microsoft Excel, and the add-in program @RISK was used to account for the uncertainty in the program cost and financial loss estimates. The annual net benefits over the ten years were discounted to a 1993 net present value (NPV) using a 6% discount rate.

Results

The total costs directly associated with the BVD program and costs associated with the respective parties, are presented graphically for the ten years in Figure 1, with corresponding figures in Table 1.

The industry and the farmers have supported about 64% of the total costs related to BVDV control over the ten-year period.

The observed and expected numbers of sero-converted and young stock positive herds used in the estimation of the national annual losses are shown in Figure 1. The numbers are to be seen in comparison with the national population of about 22,000 dairy herds and 4,000 beef herds. Currently 4 cattle herds are left with movement restrictions (a positive YS-sample is the background for imposing movement restrictions).

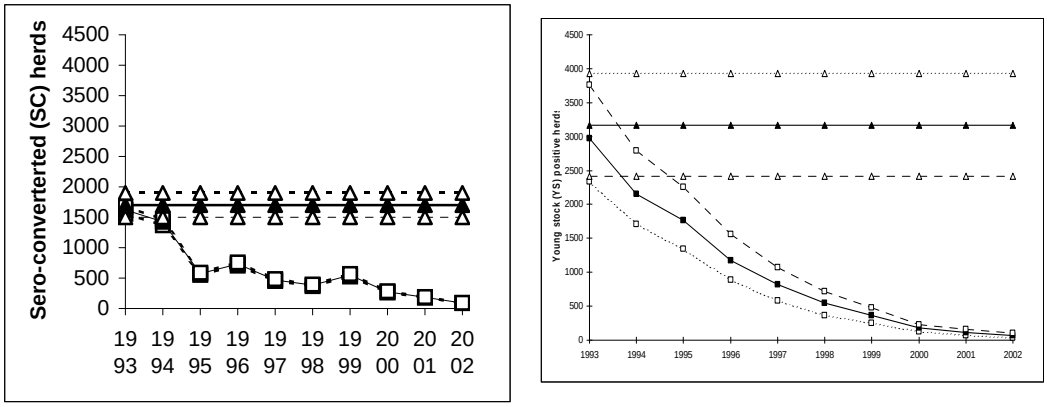

Figure 1. The annual number of bovine virus diarrhoea virus sero-converted dairy herds (left) and young stock positive dairy and beef herds (right) as observed under the Norwegian control program (■), and the reference level (▲) used for estimation of financial benefits of the program (i.e. a flat 1993 status). The 5'th and 95'th percentile for the uncertainty distributions are included as dotted lines.

When subtracting the total annual costs related to the BVDV control program, top line in Figure 2, left, from the annual animal health benefits, top line in Figure 2, right, we arrived at an annual net benefit, bottom line Figure 2, right, yielding a median NPV (1993) of 132 million NKr when using a 6% discount rate. The 5th and 95th percentiles of the NPV distribution were 22 and 264 million NKr, respectively.

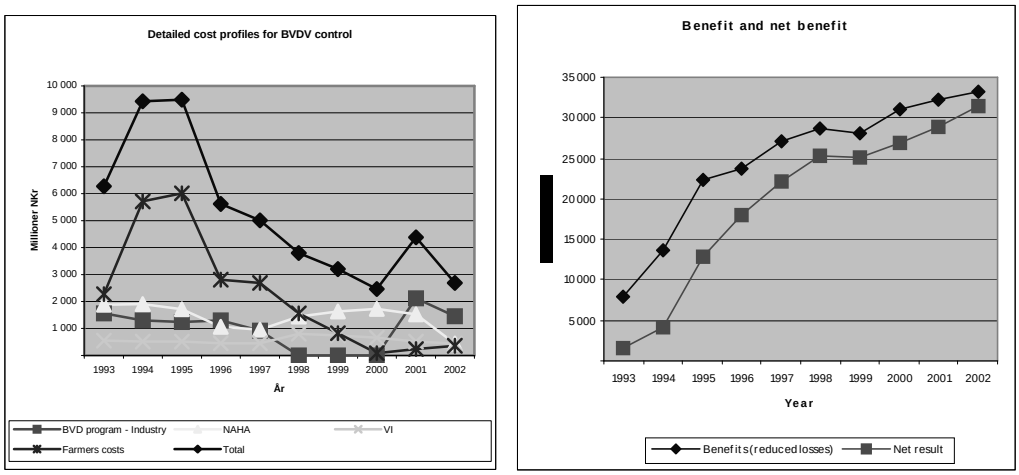

Figure 2, Total costs profiles and cost profiles for each of the institutions taking part in the BVDV control program, as well as for the farmers (left). Total and net benefit (costs subtracted) profiles (right).

Table 1, Cost in thousand Norwegian kroners (1$=8Nkr) separated into the institutions taking part in the control program, the farmers expenses related to herd screenings as well as the costs of lost options. The sum of these costs (Total costs) is subtracted from the calculated benefits (reduced losses) due to the program, yielding a net benefit (Net result).

Regarding	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002
Cattle industry	1 558	1 299	1 240	1 298	918	0	0	2 117	1 454	1 100
NAHA	1 886	1 902	1 715	1 057	955	1 383	1 577	1 706	1 453	390
VI	547	507	514	458	450	444	417	368	370	331
SUM program	3 991	3 708	3 470	2 813	2 322	1 827	1 994	4 191	3 277	1 821
Farmers costs	2 278	5 716	6 018	2 810	2 695	1 561	825	81	63	13
Total costs	6 269	9 423	9 487	5 623	5 017	3 388	2 818	4 271	3 340	1 834
Benefits	7 852	13 640	22 305	23 683	27 179	28 696	28 013	31 128	32 171	33 230
Net result	1 583	4 216	12 818	18 060	22 163	25 308	25 194	26 857	28 831	31 396

Discussion

The Norwegian control program shows cost-effectiveness already in the first year of the program. The identification and isolation of possible infected premises without massive individual animals testing together with the low initial BVDV herd prevalence, the efficiency of these measurements via bulk milk testing, the low cost test scheme and the co-operative nature using already existing resources were major factors contributing to keeping the total program costs down.

Sparse information was available for the assessment of the BVDV trend in Norway without a control program. However, based on the indications of an increasing prevalence and incidence of BVDV at the start of the program, in 1993, the chosen reference level was regarded as conservative choice.

The risk of re-infection has been one of the major arguments against zoo-sanitary control. Judging by the current situation i.e. after ten years with control in Norway, the risk of re-infection has not been sufficient to hamper the goal of eradicating BVDV from the Norwegian cattle population.

It should be noted that the low number of BVDV movement restrictions left in Norway in 2004 would not have been achieved without the increased intensity of the control program starting in 2001.

References

Valle P.S., 2000. Bovine virus diarrhoea virus – Epidemiological studies of the infection and the cost-benefit of control in Norway. Norwegian School of Veterinary Science, Thesis.

ANIMAL HEALTH AND ECONOMICS: FURTHER DIMENSIONS

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Eating offers pleasure at the risk of future pain
(Shogren, 2003)

1. Introduction

Economics is concerned with the allocation of scarce resources to competing uses, thereby providing the greatest benefit to society. The resource to be allocated is commonly money, but the other limiting resources (labour, land, management) can also be considered. The benefit can be interpreted in a number of ways, depending on the particular circumstances to which economic principles are applied. Both animal and human welfare benefit from the improvement of animal health (Morris, 1999).

Den Hartog stated that the health status of livestock has to be further improved, as more than 10 % of production capacity is lost due to sub clinical infection. Diseases have a cascade of effects on the productivity of affected animals. From the animal welfare point of view animal health is a part of sustainable livestock, taking into consideration the specific needs of the species. In this perspective animal health is priority as such and the economic objective and trade potentials are considered as a second goal.

The current paper is focussing on two further dimensions. First, the idea is to broaden the field from problems of animal disease to the animal health approach. Second, study and research is becoming quite deeper as the economic aspects of the animal welfare issue are implemented.

2. Economics and animal disease

The economic process of major interest to veterinary science involves transforming resources (grass, feed, labour, animals) into products (meat, milk, eggs, horse-rides, pet companionship etc.) that benefit people. From an economic point of view, disease is an intrusion into the resource transformation process. It reduces the products and services gained from any level of resource use and so lowers the level of benefits available to society. Disease is considered as an economic process in itself, because it consumes economic resources or generates negative benefits for society (Mc Inerney, 1988).

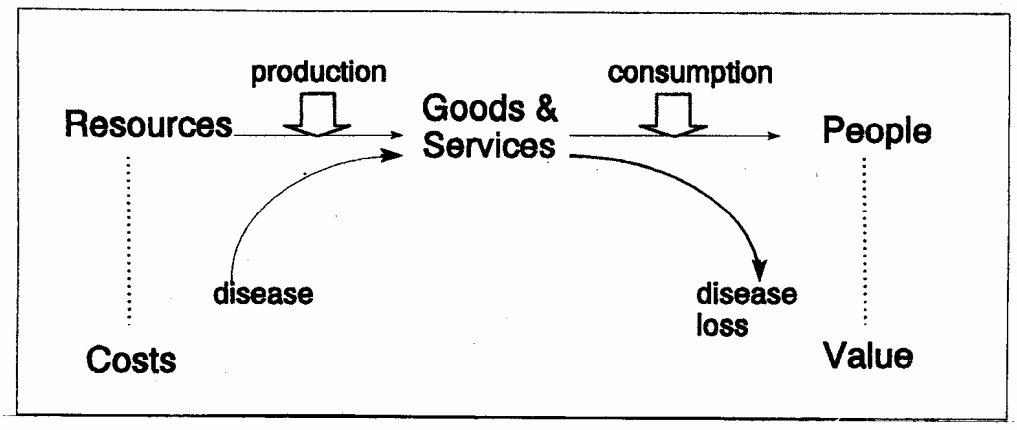

Figure 1: The impact of disease in an economic process

In this approach, livestock disease affects first people and second animals. This statement is true not just for zoonoses, but any disease condition about which society is sufficiently interested to do something.

The economic concepts go further and address questions about how best (most economically efficient) to undertake disease control and how far to pursue it.

Measurements of costs and benefits always involves applying appropriate monetary values to physical quantities of resources used and outputs gained. It is the difference in the relevant values to apply at farm

(prices) and at sector level (prices, taxes and subsidies) that give rise to the divergence between private and social valuations of any scheme.

3. Economic analysis techniques

Noordhuizen et al. (2001) indicates four economic techniques frequently applied in the veterinary domain.

First, partial budgeting can be defined as a method to quantify the economic consequences of a certain change carried at the farm. The suggested change should be implemented if the returns (A) and the cost reduction (B) is larger than the lost returns (C) and the additional costs (D):

$$A + B > C + D$$

Second, cost-benefit analysis is used to assess the value of a certain action programme over a given period of time. Three major components are addressed in cost-benefit analysis:

- specification of costs and benefits
- definition of the discount rate
- identification of a value decision criterion

The technique is often applied at groups of farms, at sector level or national level and not at the level of individual farms. Two major problems in the calculation may occur. First problem is when control programmes are complex and associated with a high degree of uncertainty. Another point regards the proper valuation of the benefits. Primary costs and benefits are those that are paid or come in favour to the farmers paying for the programme. Secondary benefits and costs are the so-called externalities of a programme. They come in favour to those people not directly responsible for the costs.

Third, decision tree analysis is a formal structured way to model chance events related to complex decisions. It uses a decision tree as a representation of the flow of events in a logical, time related and structured way. Further more, it helps in elucidating the probabilities and the outcomes of certain decision alternatives (Marsh, 1999).

Fourth, in Markovian chains simulation is made about individuals moving between classes according to a specified, fixed probability e.g. P_{si} (the probability that an animal moves from class S to class I). For example, the proportion of animals that is still in class S at time t+1 is given by the following formula:

$$S_{t+1} = (1-P_{si})\ S_{t-8} < P_{si} < 1$$

4. Extended decision support systems

In epidemiological simulation studies extended decision support systems are developed to reduce the impact of animal diseases. The main objective of these studies is to gain insight into the economic effects of different strategies to improve animal health and avoid animal diseases.

In the research of Van Der Gaag (2004) the focus was on the pork supply chain from piglet to carcass. To achieve the objective, the cost-effectiveness of control measures and strategies are estimated. In order to carry out these estimations, insight in the effect of control on the spread of Salmonella and the costs for control is needed as a basis. Two computer models were develop: first, an epidemiological model to stimulate the introduction and spread of Salmonella in the pork supply chain and the second, an economic model to evaluate the economic consequences of control measures in the pork supply chain. The promising strategies in the pork supply chain were formulated in relation to the cost-effectiveness of preventive and corrective measures used in control of Salmonella.

Vonk Noordegraaf (2002) developed and applied simulation models to support policy making in various phases of the decision-making process with respect to a national bovine herpesvirus 1 eradication programme in the Netherlands. More specifically, he studied the epidemiological and economic consequences of various control strategies. The thesis provided the insight into the cost-effectiveness of various strategies to control the virus and identified the gaps in knowledge about the virus spread that would have greatest impact on the progress and costs of the virus eradication. Finally, the model behaviour was developed with respect to associations between farm characteristics and the loss of the virus-free certificate during the simulated eradication programme.

Mangen (2002) discusses the possible emergency vaccination strategies, using an existing epidemiological simulation model. She analysed another macro-economic model that calculates the weekly flow of pigs and thus links the first model's outputs with a simulation model of the Dutch pig market (Dupima). With Dupima market prices and trade flows are calculated and the control programme costs and changes in producer surplus within a quarantine zone are quantified.

The Office International des Ēpizooties (OIE, 1999) publishes the examples of practical approaches to reduce of the impact of animal diseases. The study of Morris (1999) proposes the guide to the selection of the most suitable method for endemic diseases, which occur intermittently as local outbreaks, and for diseases, which have the potential to cause an epidemic. Since the information required for analysis at individual herd

level is much simpler than that required for national policy decisions and funding decisions by international agencies, an outline of the requirements for each level of analysis is provided. Issues surrounding the degree of risk of different choices are examined, and the application of decision analysis to higher-risk choices is introduced. Finally, procedures to provide confidence in the results of evaluations through sensitivity analysis are explained.

Saatkamp (1996) focused on the economic evaluation of national identification and recording (I&R) systems for pigs. He reviews four basic concepts of I&R systems. For the simulation of average epidemics of classical swine fever, the State-Transition model described by Saatkamp et. al. (1995) was used. This model simulates the spread of classical swine fever under various conditions with respect to I&R system, region and control strategy. The economic model is linked to the epidemiological simulation model, and uses the simulation classical swine fever epidemics as input for the economic calculations. Basically, all calculations are straightforward transformations of epidemiological outcomes into monetary terms. The economic model considered four categories of losses and costs as follow: cost elements of removal, cost elements of intervention, cosy elements of losses to Trade and Industry, and finally cost elements of institutional and operational costs.

5. Towards animal health economics

The importance of animal health and the minimisation of disease risks for animal and people is the current approach. From the economic point of view, the main objective is to support the decision-making process on a health program, which is feasible and payable (Dijkhuizen and Morris, 1997).

Three objectives are coming foreword:

- first, objective criteria for decision-making about preventive actions to improve the animal health status.
- second, to focus on health management of livestock products in the chain from farm to table.
- third, an economic oriented animal health care at regional or national level to prevent animal disease problems.

The emergence of new pathogens, changes in the food system, and increased food-product trade all led to increased attention to food-safety issues during the 1990s. Food-safety economics is a new research field, which needs a solid framework of concepts, procedures and data to support the decision-making process in food-safety improvement (Velthuis, et.al., 2003). Consumer health and welfare is the ultimate goal of food-safety improvement.

Future directions for research were identified in all four areas.

- Risk communication
- Developing guidelines for traceability systems
- Integrating economics into farm-to-table risk assessment
- Encouraging pro-active risk management in international trade

6. Animal Welfare and Economic Benefit

The concern humans show over animal welfare is based on their own perceptions of how animals are affected by the conditions under which they are kept. From a strictly economic point of view farm animals are no more than resources that are employed in economic processes, which generate benefits for people. Welfare considerations arise only because a possible side effect of gaining economically valuable output from animals can be that their well-being is to a greater or lesser extent ‘used up’. Further examination reveals that animal welfare is not at all outside the economic calculus. First, reductions in animal welfare at some stage start to represent a real economic cost to society.

Second, the reason we are drawn into husbandry practices that have negative effects on the welfare of animals is the pursuit of our own economic benefit – principally in the form of cheaper, better quality or more predictable food supplies. Any move to improve the welfare of animals, therefore, may involve giving up some of this benefit – i.e. impose an economic cost. The search for appropriate welfare standards involves economic choices about whether the benefits of cheaper food compensate for the costs in terms of unease over the animals’ welfare. Livestock producers have the incentive to identify specific markets. The expectation is that there is a genuine demand for a higher cost product with higher welfare characteristics.

7. Conclusion

Review of literature about animal health economics is leading to three conclusions.

First, from the economic point of view the traditional techniques of cost-benefit analysis are enlarged to simulation and decision-making models.

Second, the subject is changing towards a preventive approach, focusing on concerns for food safety, associated with the perceived consequences of intensive agriculture and international trade.

Third, animal welfare decisions relate to different systems of production and respond to the differential pattern of demands.

The economic analysis of animal health has always been driven by concerns to find efficient solutions to actual problems.

References

Bondt, N.; Jansen, L.F. (2001). Diergeneesmiddelengebruik en gezondheidskosten. Een eerste inventarisatie. Rapport 1.01.02, LEI, Den Haag, 35 p.

Bondt, N.; Jansen, L.F.; Hoste, R. (2001). Economie en welzijn op melkveebedrijven. Een verkennend onderzoek. Rapport 2.01.08, LEI, Den Haag, 35p.

Bos, E.J.; van Leeuwen, M.G.A.; de Vlieger, J.J. (2001). Bestrijdingsscenario's voor Mond- en Klauwzeer.Rapport 2.01.14, LEI, Den Haag, 30 p.

Brent, R.J. (2003). Cost-Benefit Analysis and Health Care Evaluations., Edward Elgar, Cheltenham, 373p.

Bunte, F.; Wolbrink, M.; van Rie, JP.; Burgers, S. (2001). Kiplekker. Een kosten-batenanalyse van een reductie in de besmetting van pluimveevlees met salmonella en campylobacter. Rapport 3.01.03, LEI, Den Haag, 75p.

Huirne, R. (1999). Strategie en risico. Inaugure rede uitgesproken op 30 september 1999, Wageningen Universiteit, Wageningen, 26p.

Huirne, R.B.M.; Mourits, M.; Tomassen, F. ; de Vlieger, J.J. ; Vogelzang, T.A. (2002). MKZ: Verleden, Heden en Toekomst. Rapport 6.02.14, LEI, Den Haag, 183p

Leslie, J. and Upton, M. (1999). The economic implications of greater global trade in livestock and livestock products. Revue Scientifique et Technique, Office International des Ēpizooties, 18 (2), 440-457.

Mangen, M.-J.J. (2002). Economic welfare analysis of simulated control strategies for Classical Swine Fever epidemics. PhD-Thesis Wageningen University, the Netherlands, ISBN: 90-5808-621-6.

Mangen, M.-J.J.; Jalvingh, A.W.; Nielen, M.; Mourits, M.C.M.; Klinkenberg, D.; Dijkhuizen, A.A. (2000). Spatial and stochastic simulation to compare two emergency-vaccination strategies with a marker vaccine in the 1997/1998 Dutch Classical Swine Fever epidemic. Preventive Veterinary Medicine 1561, 1-24.

McInerney, J.P. (2001). Part III: Economic aspects of the animal welfare issue. IN: Application of Quantitative Methods in Veterinary Epidemiology. Eds. J.P.T.M. Noordhuizen, K. Frankena, M.V. Thrusfield, E.A.M. Graat, Wageningen Pers, Wageningen, The Netherlands, ISBN: 9074134890.

Meuwissen, M.P.M.; Horst, H.S.; Huirne, R.B.M.; Dijkhuizen, A.A. (1997). Schade verzekerd ? Een haalbaarheidsstudie naar risico-kwantificering en verzekering van veewetziekten., Landbouwuniversiteit Wageningen, Vakgroep Agrarische Bedrijfseconomie, Wageningen, 164p.

Meuwissen, M.P.M.; Huirne, R.B.M.; Skees, J.R. (2003) Income Insurance in European Agriculture. EuroChoices, Spring 2003, Vol. 2, nr.1, 12-16.

Morris, R.S. (1999). The application of economics in animal health programmes: a practical guide. Revue Scientifique et Technique, Office International des Ēpizooties, 18 (2), 305-314.

Noordhuizen, J.P.T.M.; Frankena, K.; Thrusfield, M.V.; Graat, E.A.M. (2001). Application of Quantitative Methods in Veterinary Epidemiology. Wageningen Pers, Wageningen

OIE (1999). Office International des Ēpizooties. Revue Scientifique et technique. The economics of animal disease control. Vol. 18 (2), pp. 564.

Ribbens, S. (2004); Een epidemiologische evaluatie van het risico op de verspreiding van epidemische varkensziekten in vlaanderen toegepast op klassieke varkenspest., Vakgroep Voortplanting, Verloskunde en Bedrijfsdiergeneeskunde, Universiteit Gent, 13p.

Saatkamp, H.W. (1996). Simulation studies on the potential role of national identification and recording systems in the control of Classical Swine Fever. Wageningen Agricultural University, The Netherlands, ISBN: 90-6754-441-8.

Saatkamp, H.W.; Huirne, R.B.M.; Geers, R.; Dijkhuizen, A.A.; Noordhuizen, J.P.T.M.; Goedseels, V. (1995). State-transition modelling of Classical Swine Fever to evaluate national Identification and Recording systems – General aspects and model description. Agricultural Systems.

Shogren, J.F. (2003). Part 2: Food-safety economics: consumer health and welfare. In: New Approaches to Food-Safety Economics. Eds. A.G.J. Velthuis, L.J. Unnevehr, H. Hogeveen and R.B.M. Huirne. Kulwer Academic Publishers. The Netherlands, ISBN: 1-4020-1425-2.

Sikkema, A. (2002). Enten of ruimen. De psychologische en economische gevolgen van MKZ. Resource, Magazine van Wageningen Universiteit & Researchcentrum, Wageningen, oktober 2002, 16-19.

Tacken, G.M; van Leeuwen, M.G.A.; Koole, B.; van Horne, P.L.M.; de Vlieger, J.J.; de Bont, C.J.A.M. (2003). Ketenconsequenties van de uitbraak van vogelpest. Rapport 6.03.06, LEI, Den Haag, 53p.

Van Der Gaag, M.A. (2004). Epidemiological and economic simulation of Salmonella control in the pork supply chain. PhD-Thesis Wageningen University and Applied Research of Animal Sciences Group, The Netherlands, ISNB: 90-5808-973-8.

Velthuis, A.G.J.; Unnevehr, L.J.; Hogeveen, H.; Huirne, R.B.M. (2003). New Approaches to Food-Safety Economics. Kluwer Academic Publishers, London, 134p.

Vonk Noordegraaf, A. (2002). Simulation modelling to support national policy making in the control of bovine herpesvirus 1. PhD-Thesis Wageningen University, the Netherlands, ISBN: 90-5808-637-2.