New publications in the PARATUBERCULOSIS database (1392-1401)

1392 Smith, S.L. , West, D.M., Wilson, P.R., de Lisle, G.W., Collett, M.G., Heuer, C., Chambers, J.P.

The prevalence of disseminated Mycobacterium avium subsp paratuberculosis infection in tissues of healthy ewes from a New Zealand farm with Johne's disease present
New Zealand Veterinary Journal, (2013) 61, 41-44

AIM: To determine the prevalence of disseminated Mycobacterium avium subsp. paratuberculosis (Map) infection in healthy ewes in a flock with a history of clinical Johne's disease. METHODS: Twenty-four healthy ewes, from a large sheep and cattle farm with a history of clinical Johne's disease in the ewe flock, were randomly selected, euthanased, blood sampled, and examined at necropsy. BACTEC (TM) radiometric culture for Map was performed on samples of faeces, ileum, mesenteric lymph node, biceps femoris muscle and mononuclear cells in peripheral blood. Serum antibody ELISA tests were performed. Histological sections and Ziehl Neelsen (ZN) stains of impression smears of ileum and mesenteric lymph node were examined for pathological lesions characteristic of Johne's disease and acid fast organisms (AFO). Indirect quantification of Map was performed, using BACTEC radiometric growth indices measuring the time taken for the production of 14CO2. RESULTS: No histological evidence of Johne's disease or AFO was found in the ileum and mesenteric lymph nodes. Twelve of the 24 ewes (50%) had Map cultured from the ileum (n=6) and/or mesenteric lymph nodes (n=8) while none had Map cultured from the faeces, biceps femoris muscle or blood mononuclear cells. One of the 12 Map culture positive ewes was serum ELISA positive. The culture growth rates in liquid medium suggest low numbers of Map were present in the tissues of the culture positive ewes. CONCLUSION: Fifty per cent of clinically healthy ewes exposed to Map within a Johne's infected flock were Map culture positive in the ileum and/or mesenteric lymph node(s), while the ELISA was positive in 8% of those animals (n=1). There was no faecal shedding of Map and no Map was cultured from skeletal muscle or from blood mononuclear cells suggesting that systemic Map infection, defined as positive culture of Map from skeletal muscle and/or blood, may be uncommon in healthy mixed age ewes without clinical Johne's disease. CLINICAL RELEVANCE: ELISA serology detected 1 of 12 ewes infected with Map whilst none were detected from faecal BACTEC radiometric culture, suggesting biosecurity measures used to control the spread of Map may be of limited use. Map was not cultured from blood mononuclear cells or skeletal muscle, indicating that meat from healthy ewes, from farms where Johne's disease is present, is an unlikely source of Map exposure for humans. Further research is warranted to establish the prevalence and dissemination of Map in tissues outside the alimentary tract of healthy ewes from farms throughout New Zealand where Map is present.

1393 Karthik, K. , Das, P., Murugan, M.S., Singh, P.

Evaluation of bioelectronics sensor compared to other diagnostic test in diagnosis of Johne's disease in goats
Small Ruminant Research, (2013) 109, 56-63

A bioelectronics sensor has been developed and it is evaluated for the diagnosis of paratuberculosis in goats. Initially hematite nanoparticles were prepared and using this nanoparticles as core, electrically active polyaniline coated magnetic (EAPM) nanoparticles are synthesized from aniline monomer (made electrically active by acid doping). These EAPM nanoparticles were fabricated with rabbit anti-goat IgG for the detection of goat antibodies on the capture pad. The protoplasmic antigen of Mycobacterium avium subspecies paratuberculosis (MAP) immobilized onto the capture pad will detect the antibody against MAP in the goat sera samples. This bound goat antibody will be detected by the anti-goat IgG
previously bound to EAPM. Upon detection the EAPM nanoparticles bridges an electric circuit between the silver electrodes, flanking the capture membrane. The electrical conductance, caused by EAPM, was measured as direct charge transfer between the electrodes. Testing of the biosensor with known Johne’s disease (JD) positive and negative serum samples gave significant difference in the electrical conductance value. Further the efficacy of this biosensor was compared with other serological tests like agar gel immunodiffusion (AGID) and absorbed ELISA using field sera. Out of 265 goat sera tested, positive results recorded were: AGID 36 (13.59%), bioelectronics sensor 49 (19.14%), and absorbed ELISA 51 (19.25%). This biosensor was also compared in live animals using intradermal Johnin test and nested PCR (detecting mycobacterial DNA in feces) in 65 animals. Of which, positive results recorded in animals were: Johnin test 21 (32%), biosensor 26 (40%) and fecal PCR detected mycobacterial DNA in 28 (43%) animals. Though the nanobioelectronics sensor was slightly less sensitive (not statistically significant) compared to absorbed ELISA and fecal nested PCR for mycobacterial DNA but it was simple to perform in field conditions and requires less time. 

The speed of detection and the equipment involved would support its application toward the various point-of-care opportunities aimed at control and management of Johne’s disease in goats. (C) 2012 Elsevier B.V. All rights reserved.

**Update on Johne's disease programme**

Veterinary Record, (2012) 171, 604-604

Abstract not available.

**Bioexclusion of diseases from dairy and beef farms: Risks of introducing infectious agents and risk reduction strategies**


Infectious disease represents a major threat to the productivity and welfare of cattle herds throughout the world. The introduction of infectious agents into dairy and beef farms may be through direct transmission (purchased cattle, reintroduced resident cattle and contact with contiguous cattle) or indirect transmission (fomites, visitors, other species, and biological materials) and this article reviews the evidence supporting these transmission routes. In the absence of eradication programmes for many endemic infectious diseases, bioexclusion is the key management process for risk reduction. Various ameliorative bioexclusion strategies have been recommended and the evidence supporting these protocols is considered. (c) 2012 Elsevier Ltd. All rights reserved.

**Genomics of complex traits**


The analysis of complex genetic traits, including mapping and identification of causative genes, has long been an enigma of genetic biology, whether in the animal sciences or in medical sciences. Traits of agricultural interest and traits of medical interest are often under the influence of both environmental factors and multiple genes, each with modest contributions to the total variance in the trait. Although the number of known mutations underlying complex traits is still relatively small, advances in genomics have greatly enhanced traditional pathways to their analysis and gene mining. The candidate gene approach, linkage analysis, and association studies are all significantly more powerful with recent advances in genome mapping, sequencing, and analysis of individual variation. Avenues to gene discovery are discussed with emphasis on genome wide association studies (GWAS) and the use of single nucleotide polymorphisms (SNPs) as revealed by increasingly powerful commercially available microarrays. PDF WILL NOT BE AVAILABLE.

**Identification of potential biomarkers to distinguish Mycobacterium colombiense from other mycobacterial species**

Molecular and Cellular Probes, (2013) 27, 46-52

Mycobacterium avium complex (MAC) consists of 9 species of slow-growing mycobacteria with differing degrees of pathogenicity, host preference and environmental distribution.
Mycobacterium colombiense is a novel member of MAC that is responsible for disseminated infections in HIV-infected patients in Colombia and lymphadenopathy cases in Europe. At present, methods to easily differentiate novel members of MAC are lacking. In this study, we identified possible biomarkers that are potentially useful for the detection of M. colombiense by PCR or chromatography. The Randomly Amplified Polymorphic DNA (RAPD) technique was used to amplify genomic fragments of M. colombiense CECT 3035 that were subsequently used in the development of a direct colony-specific PCR assay using specific primers. The designed primers amplified a 634-bp fragment of DNA from M. colombiense, which included a 450-bp genomic region that encodes a hypothetical protein of 149 amino acids that is exclusive to M. colombiense. Bioinformatic analyses revealed that this hypothetical protein had no signal peptide, active sites or functional domains to aid its identification or classification. In addition, using thin-layer chromatography, we identified a different profile of mycolates for M. colombiense strains. The test developed in this study has potential applications in the routine identification of M. colombiense and in molecular assays designed for the surveillance of MAC strains. (C) 2012 Elsevier Ltd. All rights reserved.


Previous investigations suggest that the prevalence of Mycobacterium avium subsp. paratuberculosis (MAP) in Swedish cattle is low and all recent cases have been linked to imported animals. The aim of this study was to evaluate the surveillance system for MAP infection in Swedish cattle and to estimate the probability that the Swedish cattle population is free from this infection. Calculations of surveillance sensitivities and probability of freedom were made using stochastic scenario-tree modelling, which allows inclusion of information from several different sources, of complex surveillance data including results from non-representative sampling, as well as of documentations of differences in risk of being infected. The surveillance components included in the model were: (1) clinical surveillance, (2) fallen stock investigations, (3) the national surveillance programme (mainly beef herds), (4) a survey involving dairy herds and (5) a risk-based survey targeting herds with imported cattle. Previous or current presence of imported animals and participation in the on-going control programme was specified for each tested herd, in order to adjust for differences in risk. Calculations were made for each year from the start of 2005 to the end of 2008, and this formed the basis for a final estimate covering the whole study period and predictions of future probabilities of freedom from MAP. Results show that when applying a design prevalence of one animal in 0.1% of the herds, the probability of freedom at the end of 2008 was 0.63. At the design prevalence of one animal in 0.5% of herds, the estimated probability is >95% and it is demonstrated that the prevalence of MAP in Swedish cattle is below this level or absent. In order to increase the annual surveillance sensitivity in the future and thereby improve the probability of freedom, new surveillance activities or an intensification of current ones are needed. (C) 2012 Elsevier B.V. All rights reserved.

Menten, J., Boelaert, M., Lesaffre, E. An application of Bayesian growth mixture modelling to estimate infection incidences from repeated serological tests Statistical Modelling, (2012) 12, 551-578

Diagnoses of infectious diseases are often performed using antibody detection through enzyme-linked immunosorbent assay techniques. These data are usually dichotomized into positive and negative samples using a fixed cut-off and prevalences of infection are subsequently estimated assuming perfect correspondence between the dichotomized test results and infection status. In contrast to this approach, in this case study, we estimate the effect of distributing insecticide impregnated bednets to prevent Leishmania infection through mixture modelling of the original continuous data. We analyze the data from a cluster randomized intervention trial using a generalized latent variable model consisting of a longitudinal mixture model for the observed outcome and a Hidden Markov model for the underlying unobserved disease status to estimate the effect of an intervention. The response and structural models are jointly estimated in a Bayesian framework. This model has the advantage that it avoids the need to choose an arbitrary cut-off and allows for uncertainty in
the infection status. In this paper, we describe the development of the model and selection of priors, the application to the motivating data, model checking and simulation results. PDF WILL NOT BE AVAILABLE.


**Effects of vaccination against paratuberculosis on tuberculosis in goats: diagnostic interferences and cross-protection**

Bmc Veterinary Research, (2012) 8, Article Number: 191 DOI: 10.1186/1746-6148-8-191 Published: OCT 16 2012-Background: Most countries carrying out campaigns of bovine tuberculosis (TB) eradication impose a ban on the use of mycobacterial vaccines in cattle. However, vaccination against paratuberculosis (PTB) in goats is often allowed even when its effect on TB diagnosis has not been fully evaluated. To address this issue, goat kids previously vaccinated against PTB were experimentally infected with TB. Results: Evaluation of interferon-gamma (IFN-gamma) secretion induced by avian and bovine tuberculins (PPD) showed a predominant avian PPD-biased response in the vaccinated group from week 4 post-vaccination onward. Although 60% of the animals were bovine reactors at week 14, avian PPD-biased responses returned at week 16. After challenge with M. caprae, the IFN-gamma responses radically changed to show predominant bovine PPD-biased responses from week 18 onward. In addition, cross-reactions with bovine PPD that had been observed in the vaccinated group at week 14 were reduced when using the M. tuberculosis complex-specific antigens ESAT-6/CFP-10 and Rv3615c as new DIVA (differentiation of infected and vaccinated animals) reagents, which further maintained sensitivity post-challenge. Ninety percent of the animals reacted positively to the tuberculin cervical comparative intradermal test performed at 12 weeks post-infection. Furthermore, post-mortem analysis showed reductions in tuberculous lesions and bacterial burden in some vaccinated animals, particularly expressed in terms of the degree of extrapulmonary dissemination of TB infection. Conclusions: Our results suggest a degree of interference of PTB vaccination with current TB diagnostics that can be fully mitigated when using new DIVA reagents. A partial protective effect associated with vaccination was also observed in some vaccinated animals.

1401 Severins, M.

**A modeller's perspective on infection dynamics within and between hosts**

Veterinary Quarterly, (2012) 32, 169-178 The goal of this case-series was to increase our understanding of some complex within and between-host infection dynamics through the creation of mathematical and computational models that are able to capture the existing host and/or parasite heterogeneity. This goal was reached through a series of research projects (regarding experimental autoimmune encephalomyelitis (EAE) in mice, Mycobacterium avium subspecies paratuberculosis infection in cattle, Eimeria acervulina infection in chicken and human malaria) that gradually build up in complexity of both the system modelled and the modelling techniques used. In this case-series, the vast majority of model components have a direct link with reality. The results have shown some detailed examples of the valuable contribution that models have in understanding infection processes. The most satisfying achievements have come from those models that were able to, in hindsight, make complicated experimental results seem obvious and logical, and where the process of building the model was as insightful as the final results. The models created in these projects help to explain a wide range of sometimes contradictory experimental results and are used to predict the effect of control measures. In addition, they generate ideas for the development of new methods of control. PDF WILL NOT BE AVAILABLE.

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2013-04-02-019 Paratuberculosis databases updated (2013-03-20 last part)
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1394  Brigstocke, T.

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Veterinary Record, (2012) 171, 604-604
Abstract not available.


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1396  Womack, J.E., Jang, H.J., Lee, M.O.

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1397  Leguizamon, J., Hernandez, J., Murcia, M.I., Soto, C.Y.

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Surveillance system sensitivities and probability of freedom from Mycobacterium avium subspp. paratuberculosis infection in Swedish cattle
Preventive Veterinary Medicine, (2013) 108, 47-62

Previous investigations suggest that the prevalence of Mycobacterium avium subspp. paratuberculosis (MAP) in Swedish cattle is low and all recent cases have been linked to imported animals. The aim of this study was to evaluate the surveillance system for MAP infection in Swedish cattle and to estimate the probability that the Swedish cattle population is free from this infection. Calculations of surveillance sensitivities and probability of freedom were made using stochastic scenario-tree modelling, which allows inclusion of information from several different sources, of complex surveillance data including results from non-representative sampling, as well as of documentations of differences in risk of being infected. The surveillance components included in the model were: (1) clinical surveillance, (2) fallen stock investigations, (3) the national surveillance programme (mainly beef herds), (4) a survey involving dairy herds and (5) a risk-based survey targeting herds with imported cattle. Previous or current presence of imported animals and participation in the on-going control programme was specified for each tested herd, in order to adjust for differences in risk. Calculations were made for each year from the start of 2005 to the end of 2008, and this formed the basis for a final estimate covering the whole study period and predictions of future probabilities of freedom from MAP. Results show that when applying a design prevalence of one animal in 0.1% of the herds, the probability of freedom at the end of 2008 was 0.63. At the design prevalence of one animal in 0.5% of herds, the estimated probability is >95% and it is demonstrated that the prevalence of MAP in Swedish cattle is below this level or absent. In order to increase the annual surveillance sensitivity in the future and thereby improve the probability of freedom, new surveillance activities or an intensification of current ones are needed. (C) 2012 Elsevier B.V. All rights reserved.

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Statistical Modelling, (2012) 12, 551-578

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