2011-08-25-139 Paratuberculosis databases updated (2011-08-25)
To: (08) Mycobacterial diseases; (23) Veterinary education; (27) Scientific information
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New publications in the PARATUBERCULOSIS database (1047-1051)


Consumer demand for food safety and quality improvements, combined with new regulations, requires determining the processor’s confidence level that processes lowering safety risks while retaining quality will meet consumer expectations and regulatory requirements. Monte Carlo calculation procedures incorporate input data variability to obtain the statistical distribution of the output of prediction models. This advantage was used to analyze the survival risk of Mycobacterium avium subspecies paratuberculosis (M. paratuberculosis) and Clostridium botulinum spores in high-temperature short-time (HTST) milk and canned mushrooms, respectively. The results showed an estimated 68.4% probability that the 15 sec HTST process would not achieve at least 5 decimal reductions in M. paratuberculosis counts. Although estimates of the raw milk load of this pathogen are not available to estimate the probability of finding it in pasteurized milk, the wide range of the estimated decimal reductions, reflecting the variability of the experimental data available, should be a concern to dairy processors. Knowledge of the C. botulinum initial load and decimal thermal time variability was used to estimate an 8.5 min thermal process time at 110 degrees C for canned mushrooms reducing the risk to 10(-9) spores/container with a 95% confidence. This value was substantially higher than the one estimated using average values (6.0 min) with an unacceptable 68.6% probability of missing the desired processing objective. Finally, the benefit of reducing the variability in initial load and decimal thermal time was confirmed, achieving a 26.3% reduction in processing time when standard deviation values were lowered by 90%

1048 Meikle, V., Bianco, M.V., Blanco, F.C., Gioffre, A., Garbaccio, S., Vagnoni, L., Di Rienzo, J., Canal, A., Bigi, F., Cataldi, A. (2011) Evaluation of pathogenesis caused in cattle and guinea pig by a Mycobacterium bovis strain isolated from wild boar Bmc Veterinary Research, 7, Background: In many regions of the world, wild mammals act as reservoir of Mycobacterium bovis, a situation that prevents the eradication of bovine tuberculosis. In order to observe whether a strain isolated from a wild boar, previously tested as highly virulent in a mice model, is also virulent in cattle, we performed cattle experimental inoculation with this strain Results: Groups of Friesian calves were either infected with the wild boar strain M. bovis 04-303 or with the bovine strain NCTC10772 as a control. We found that antigen-specific IFN-gamma release in whole blood samples occurred earlier in animals infected with M. bovis 04-303. Both M. bovis strains resulted in a positive skin test, with animals infected with the wild boar isolate showing a stronger response. These results and the presence of more severe organ lesions, with granuloma and pneumatic areas in cattle demonstrate that the wild boar isolate is more virulent than the NCTC10772 strain. Additionally, we tested the infectivity of the M. bovis strains in guinea pigs and found that M. bovis 04-303 had the highest pathogenicity. Conclusions: M. bovis strains isolated from wild boars may be pathogenic for cattle, producing TB lesions

The immune response of ruminants to Johne’s disease has been long associated with a cell mediated immune (CMI) response in the early stages of infection with a switch to an antibody response later as the disease manifests. This study examines the immune response in sheep to Mycobacterium avium subspecies paratuberculosis (Map) infections, specifically the antigen-specific interferon gamma (IFN-gamma) and antibody responses as surrogates of T helper-1 (Th1) and Th2 immunity. The difference in IFN-gamma production between paucibacillary and multibacillary diseased animals was also examined. The results show that sheep are more likely to have a combined antibody and IFN-gamma response (seen in 50% of the animals) rather than a switch from an IFN-gamma to antibody response (39%). Multibacillary diseased animals were found to have a decrease in functional ability to produce IFN-gamma from cells stimulated with MAP-specific antigens and non-specific mitogens. This indicates that the immune responses to Map infections are more complex than thought, where both antibody and cellular immunity may play key roles in the early stages of disease manifestation or resistance. The loss of the cellular response in multibacillary animals may be an indication that the entire immune response is dysfunctional, with the cell mediated responses becoming affected first. (C) 2010 Elsevier GmbH. All rights reserved

Intestinal amebiasis and gastrointestinal tuberculosis can mimic inflammatory bowel disease and its exacerbations clinically, pathologically, radiologically and endoscopically. In the existence of IBD and/or either one of these two pathogens, early identification and prompt treatment can improve the clinical course of the patients. The aim of this study was to investigate the presence of Entamoeba histolytica and/or Mycobacterium spp. in biopsy specimens of patients with inflammatory bowel disease in Turkey. As the differentiation of pathologic Entamoeba histolytica must be based on isoenzymatic, immunologic or molecular analysis and PCR is a rapid and reliable method for the identification of Mycobacterium spp., we investigated the presence of these pathogens in the biopsy specimens of 20 patients who were suspected to have IBD and nine controls, by using PCR-based detection methods. All of them were histopathologically diagnosed as Crohn's disease and none of the specimens contained these two pathogens. We thought that the low prevalence of both infections in Crohn's disease patients may have caused our negative findings and loss of pathogens could have lowered the sensitivity. Further studies with larger number of patients are needed to determine the misdiagnosis rate and coexistence of these three diseases.

Genetics of animal health and disease in cattle
Irish Veterinary Journal, 64, There have been considerable recent advancements in animal breeding and genetics relevant to disease control in cattle, which can now be utilised as part of an overall programme for improved cattle health. This review summarises the contribution of genetic makeup to differences in resistance to many diseases affecting cattle. Significant genetic variation in susceptibility to disease does exist among cattle suggesting that genetic selection for improved resistance to disease will be fruitful. Deficiencies in accurately recorded data on individual animal susceptibility to disease are, however, currently hindering the inclusion of health and disease resistance traits in national breeding goals. Developments in 'omics' technologies, such as genomic selection, may help overcome some of the limitations of traditional breeding programmes and will be especially beneficial in breeding for lowly heritable disease traits that only manifest themselves following exposure to pathogens or environmental stressors in adulthood. However, access to large databases of phenotypes on health and disease will still be necessary. This review clearly shows that genetics make a significant contribution to the overall health and resistance to disease in cattle. Therefore,
breeding programmes for improved animal health and disease resistance should be seen as an integral part of any overall national disease control strategy.

New publications in the CROHN'S DISEASE AND PARATUBERCULOSIS database (580-583)


Investigating the proteolytic activity of the recombinant Mycobacterium leprae Heat Shock Protein of 65 kDa (rHsp65), chaperonin 2 (cpn2), we observed that it displays high instability. The fragmentation process starts at the C-terminus followed by progressive degradation of the N-terminus, which leads to a stable fragment comprising the middle region of the molecule. Urea was able to prevent autolysis, probably due to its denaturing action, while EDTA increased degradation levels indicating the need for metal ions. Peptides originated from autolysis were purified and analyzed by mass spectrometry, generating a continuous map. Since the bacteria and mammalian Hsp60 are known to be targets of the immune response and have been implicated in autoimmune diseases and chronic inflammation, the in vivo effect of rHsp65 peptides was evaluated in the spontaneous Systemic Lupus Erythematosus (SLE) model developed by the (NZB/NZW)F(1) mouse hybrids, and their individual anti-rHsp65 IgG2a/IgG1 antibody titer ratio was determined. The results showed orientation toward a T(H)1 responsiveness, and the treatment with the rHsp65 peptides diminished the environmental variance of the survival time of treated animals. These results outline the fact that environmental factors may also act through the modified stability expression of Heat Shock Proteins intervening during autoimmune processes. (C) 2011 Elsevier Ltd. All rights reserved


Inflammation and immune response play an important role in the pathogenesis of atherosclerosis. In this prospective study we tested the hypothesis of whether polymorphic variations in the NOD2/CARD15 gene may influence the risk of developing clinically evident coronary artery disease (CAD). ARG702TRP, GLY908ARG, and Leu1007fsinsC NOD2/CARD15 polymorphisms were analyzed in 109 consecutive patients with angiographically documented CAD and in 109 age- and sex-matched healthy controls. The ARG702TRP, GLY908ARG, and Leu1007fsinsC polymorphisms were analyzed by polymerase chain reaction followed by restriction digestion. The prevalence of the Leu1007fsinsC polymorphism was significantly increased in CAD patients compared with controls (11.9% vs 1.8%; odds ratios (OR) 7.2, 95% confidence interval (95% CI) 1.5-32.9; p = 0.01), especially in those presenting with an acute coronary syndrome (OR 5.7; 95% CI 1.1-39.7; p = 0.034 vs stable angina). In CAD patients the frequency of GLY908ARG polymorphism was significantly lower (1.8% vs 6.4% in controls; OR 0.05, 95% CI 0.01-0.69; p = 0.031, at multivariable analysis) and the prevalence of the ARG702TRP polymorphism was higher compared with controls (10.1% vs 3.7%; OR 2.9, 95% CI 0.91-9.6; p = 0.07). We report in a Caucasian population that NOD2/CARD15 polymorphisms influence the development of clinically evident and angiographically documented coronary artery disease. In particular, the Leu1007fsinsC polymorphism was associated with an increased risk of clinically evident and
angiographically documented coronary atherosclerosis and clinical destabilization of coronary plaques, whereas the GLY908ARG polymorphism demonstrated a protective effect on coronary atherogenesis. These correlations were independent of cardiovascular risk factors at multivariable analysis. These findings may contribute to the identification of a novel genetic approach for the stratification of cardiovascular risk profile. (C) 2011 American Society for Histocompatibility and Immunogenetics. Published by Elsevier Inc. All rights reserved

Yeh, I., George, E., Jokinen, C.H. (2011) **Cutaneous Mycobacterial Spindle Cell Pseudotumor: A Potential Mimic of Soft Tissue Neoplasms**
American Journal of Dermatopathology, 33, E66-E69

A 55-year-old man with scleroderma treated with prednisone and etanercept presented with enlarging sporotrichoid nodules on the forearm. Microscopically, there were large circumscribed dermal and subcutaneous nodules of spindled and epithelioid cells, resembling a spindle cell neoplasm. Small foci of neutrophils were also present, and a subsequent Ziehl-Neelsen stain highlighted beaded acid-fast bacilli in the interstitium. Tissue culture demonstrated Mycobacterium chelonae. Cutaneous mycobacterial spindle cell pseudotumor is an exceedingly rare lesion, with only 6 previously reported cases. Although these included patients with autoimmune disease receiving immunosuppressive therapy, this is the first case reported in association with a tumor necrosis factor alpha inhibitor, etanercept. Furthermore, this represents the first mycobacterial spindle cell pseudotumor described in association with M. chelonae. Mycobacterial spindle cell pseudotumor should be considered in the differential diagnosis of cutaneous spindle cell proliferations, especially in immunocompromised patients

Gastroenterology, 141, 642-U750

BACKGROUND & AIMS: Mycobacterium bovis Bacillus Calmette-Guerin (BCG), killed by extended freeze-drying (EFD), induces secretion of interleukin-10 and reduces lung inflammation in a mouse model of asthma. We investigated the effects of EFD BCG in mouse models of inflammatory bowel disease. METHODS: EFD BCG was administered subcutaneously to mice with colitis induced by dextran sodium sulfate (DSS), oxazolone, or adoptive transfer of CD4(+)CD45RB(high)Foxp3(-) T cells from C57Bl/6 Foxp3GFP mice to RAG2(-/-) mice. RESULTS: EFD BCG, administered either before induction of DSS and oxazolone colitis or after development of acute or chronic DSS-induced colitis, reduced symptom scores, loss of body weight, and inflammation. Although transfer of CD4(+)CD45RB(high)Foxp3(-) cells induced colitis in RAG2(-/-) mice, administration of EFD BCG at the time of the transfer converted Foxp3(-) T cells to Foxp3(+) T cells and the mice did not develop colitis. EFD BCG protected mice from colitis via a mechanism that required expansion of T regulatory cells and production of interleukin-10 and transforming growth factor beta. EFD BCG activated the retinoid X receptor (RXR)-alpha-peroxisome proliferator-activated receptor (PPAR)-gamma heterodimer, blocked translocation of nuclear factor kappa B to the nucleus, and reduced colonic inflammation; it did not increase the number of colon tumors that formed in mice with chronic DSS-induced colitis. CONCLUSIONS: EFD BCG controls severe colitis in mice by expanding T regulatory cell populations and PPAR-gamma and might be developed to treat patients with inflammatory bowel disease