New publications in the **PARATUBERCULOSIS database** (1198-1210)

1198  
**Heat treatment of colostrum on commercial dairy farms decreases colostrum microbial counts while maintaining colostrum immunoglobulin G concentrations**  
Journal of Dairy Science, 95, 2697-2702  
This study was conducted on 6 commercial dairy farms in Minnesota and Wisconsin to describe the effect of heat treatment (at 60 degrees C for 60 min) on colostrum, on colostrum bacteria counts, and immunoglobulin G concentrations. First-milking colostrum was collected each day, pooled, divided into 2 aliquots, and then 1 aliquot was heat treated in a commercial batch pasteurizer at 60 degrees C for 60 min. Frozen samples of pre- and post- heat-treated colostrum were submitted for standard microbial culture (total plate count and total coliform count, cfu/mL) and testing for immunoglobulin G concentrations (mg/mL). Data were analyzed from 266 unique batches of colostrum. Linear regression showed that heat treatment decreased colostrum total plate counts (-2.25 log(10)) and coliform counts (-2.49 log(10)), but, overall, did not affect colostrum IgG concentration. Though higher-quality batches of colostrum did experience a greater magnitude of loss of IgG as a result of heat treatment as compared with lower- or intermediate-quality batches of colostrum, the colostral IgG concentrations in these batches remained high overall, and within acceptable limits for feeding. This study demonstrates that batch heat treatment of colostrum at 60 C for 60 min can be successfully conducted on commercial dairy farms by farm staff to decrease colostrum microbial counts while maintaining colostrum IgG concentrations.

1199  
**Heritability estimates for Mycobacterium avium subspecies paratuberculosis status of German Holstein cows tested by fecal culture**  
Journal of Dairy Science, 95, 2734-2739  
The objective of this study was to estimate genetic manifestation of Mycobacterium avium ssp. paratuberculosis (MAP) infection in German Holstein cows. Incorporated into this study were 11,285 German Holstein herd book cows classified as MAP-positive and MAP-negative animals using fecal culture results and originating from 15 farms in Thuringia, Germany involved in a paratuberculosis voluntary control program from 2008 to 2009. The frequency of MAP-positive animals per farm ranged from 2.7 to 67.6%. The fixed effects of farm and lactation number had a highly significant effect on MAP status. An increase in the frequency of positive animals from the first to the third lactation could be observed. Threshold animal and sire models with sire relationship were used as statistical models to estimate genetic parameters. Heritability estimates of fecal culture varied from 0.157 to 0.228. To analyze the effect of prevalence on genetic parameter estimates, the total data set was divided into 2 subsets of data into farms with prevalence rates below 10% and those above 10%. The data set with prevalence above 10% show higher heritability estimates in both models compared with the data set with prevalence below 10%. For all data sets, the sire model shows higher heritabilities than the equivalent animal model. This study demonstrates that genetic variation exists in dairy cattle for paratuberculosis infection susceptibility and furthermore, leads to the conclusion that MAP detection by fecal culture shows a higher genetic background than ELISA test results. In conclusion, fecal culture seems to be a better trait to control the disease, as well as an appropriate feature for further genomic analyses to detect MAP-associated chromosome regions.

1200  
Genome-wide association study to identify chromosomal regions associated with antibody response to Mycobacterium avium subspecies paratuberculosis in milk of Dutch Holstein-Friesians

Journal of Dairy Science, 95, 2740-2748

Heritability of susceptibility to Johne's disease in cattle has been shown to vary from 0.041 to 0.159. Although the presence of genetic variation involved in susceptibility to Johne's disease has been demonstrated, the understanding of genes contributing to the genetic variance is far from complete. The objective of this study was to contribute to further understanding of genetic variation involved in susceptibility to Johne's disease by identifying associated chromosomal regions using a genome-wide association approach. Log-transformed ELISA test results of 265,290 individual Holstein-Friesian cows from 3,927 herds from the Netherlands were analyzed to obtain sire estimated breeding values for Mycobacterium avium subspecies paratuberculosis (MAP)-specific antibody response in milk using a sire-maternal grandsire model with fixed effects for parity, year of birth, lactation stage, and herd; a covariate for milk yield on test day; and random effects for sire, maternal grandsire, and error. For 192 sires with estimated breeding values with a minimum reliability of 70%, single nucleotide polymorphism (SNP) typing was conducted by a multiple SNP analysis with a random polygenic effect fitting 37,869 SNP simultaneously. Five SNP associated with MAP-specific antibody response in milk were identified distributed over 4 chromosomal regions (chromosome 4, 15, 18, and 28). Thirteen putative SNP associated with MAP-specific antibody response in milk were identified distributed over 10 chromosomes (chromosome 4, 14, 16, 18, 19, 20, 21, 26, 27, and 29). This knowledge contributes to the current understanding of genetic variation involved in Johne's disease susceptibility and facilitates control of Johne's disease and improvement of health status by breeding.

Unexpected high responses to tuberculin skin-test in farmed red deer: Implications for tuberculosis control

Preventive Veterinary Medicine, 104, 327-334

Tuberculosis (TB) in deer is a serious zoonotic disease of worldwide distribution. Detection of infected animals is usually performed using single or comparative skin-testing (SST/CST), although false responses due to sensitization to other mycobacteria may occur, hampering diagnostic specificity. We describe the evolution of the responses to the SST, CST and to an in-house serological assay in a red deer farm subjected to regular TB testing in southern Spain in an attempt to understand the dynamics of possible non-specific reactions occurring under field conditions. We performed 2288 skin-tests and ELISAs in nine sampling periods between May 2009 and January 2011. In May 2010, a strong increase in skin fold thickness in response to avian purified protein derivative (PPD) (mean = 4.0 mm, 95% CI = 3.5-4.5) and bovine PPD (mean = 1.8 mm, 95% CI = 1.6-2.0) was observed in yearling deer hinds (n = 150), compared to values recorded for the same individuals in November 2009 (avian PPD: mean = 0.7 mm, 95% CI = 0.6-0.8 and bovine PPD: mean = 0.7 mm, 95% CI = 0.6-0.7) and in January 2011 (avian PPD: mean = 2.2 mm, 95% CI = 1.9-2.4 and bovine PPD: mean = 1.1 mm, 95% CI = 1.0-1.2). Using SST, 54 animals (36%) of the yearlings tested in May 2010 would have been classified as positive reactors, while none of them was positive in the CST. The five animals with highest skin fold increases to mycobacterial antigens were culled and subjected to post-mortem analysis, which confirmed the absence of Mycobacterium tuberculosis complex (MTBC) infection but demonstrated the presence of environmental mycobacteria and closely related bacteria in four out of the five analyzed animals. Our results demonstrated how non-specific responses to mycobacterial antigens can adversely affect the specificity of TB diagnosis based on the SST. Thus, once TB infection has been ruled out using confirmatory techniques, application of comparative diagnostic tests is highly advisable to maximize test specificity and avoid the slaughter of false positive reactors. (c) 2011 Elsevier B.V. All rights reserved

Cloning and expression of AhpC gene of Mycobacterium avium sub sp paratuberculosis

The present study was undertaken to amplify, clone and express AhpC gene from *Mycobacterium avium* sub sp. *paratuberculosis* (MAP). Primers specific for AhpC gene with restriction enzyme sites, viz. NdeI and XhoI were designed. AhpC gene was amplified using DNA from MAP culture with designed primers by polymerase chain reaction (PCR). An amplicon of size 588 bp was obtained. The AhpC gene was first cloned into TOPO vector pCR2.1 and subcloned into prokaryotic expression vector pET22b. Colony PCR was carried out for the selection of the recombinant clones and further confirmed by restriction enzyme digestion. The recombinant clone was induced with 0.3 mM final concentration of isopropyl-beta-D-thiogalactopyranoside (IPTG) for the expression of the recombinant AhpC gene. The expressed protein was analysed by 12% SDS-PAGE. As AhpC gene exist as a homodimer, 2 protein fractions of 24 KDa and 45 KDa were obtained after induction. The specificity of the protein was determined by immunoblot analysis with polyclonal MAP antibodies.

1203 Chiodini, R.J. (2012)  
*The image of mass destruction inevitably leads to intellectual mass distraction*  
Journal of Crohns & Colitis, 6, 388-389  
Abstract not available.

1204 Chamberlin, W.M. (2012)  
*Much is still to be learned about pathogenic Mycobacteria*  
Journal of Crohns & Colitis, 6, 390-391  
Abstract not available.

1205 Van Kruiningen, H.J. (2012)  
*Much is still to be learned about pathogenic Mycobacteria Reply*  
Journal of Crohns & Colitis, 6, 392-392  
Abstract not available.

*Mycobacterium avium paratuberculosis and Crohn’s Disease: An association requiring more research*  
Journal of Crohns & Colitis, 6, 393-393  
Abstract not available.

*Meta-Analysis of Two Genome-Wide Association Studies of Bovine Paratuberculosis*  
Plos One, 7, Article Number: e32578 DOI: 10.1371/journal.pone.0032578 Published: MAR 2 2012-Background: Bovine paratuberculosis (ParaTB) also known as Johne’s disease, is a contagious fatal disease resulting from infection by *Mycobacterium avium* subspecies *paratuberculosis* (MAP). Previous studies have identified loci associated with ParaTB using different measurements to define cases and controls. The objective of this study was to combine the data from two recent studies to identify genetic loci associated with MAP tissue infection and humoral immune response, defined by MAP ELISA-positive cattle, by comparing cases and control animals for one or both measures of infection. Methodology/Principal Findings: The two populations used for the association analyses were a cohort of MAP tissue infected animals and control Holstein cows from the USA and the second cohort composed of ELISA-positive and ELISA-negative Holstein cows from Italy. Altogether 1190 cattle were genotyped with the illumina BovineSNP50 BeadChip. SNP markers were removed if the minor allele frequency <0.01 or genotyping failure was 5%. Animals were removed with >5% genotyping failure. Whole genome association analyses were conducted with the GRAMMAR-CG method using two different definitions of control populations. Conclusion/Significance: The analyses identified several loci (P < 5 e-05) associated with ParaTB, defined by positive ELISA and presence of bacteria in tissue compared to ELISA and tissue negative animals, on chromosomes 1, 12 and 15 and one unassigned SNP. These results confirmed associations on chromosome 12 and the unassigned SNP with ParaTB which had been found in the Italian population alone. Furthermore, several additional genomic regions were found associated with
ParaTB when ELISA and tissue positive animals were compared with tissue negative samples. These loci were on chromosomes 1, 6, 7, 13, 16, 21, 23 and 25 (P < 5 e-05). The results clearly indicate the importance of the phenotype definition when seeking to identify markers associated with different disease responses.

1208 Masala, S., Paccagnini, D., Cossu, D., Brezar, V., Pacifico, A., Ahmed, N., Sechi, L., Mallone, R. (2012) Antibodies directed against mycobacterium avium paratuberculosis show a crossed reactivity with antigen beta-cellular ZnT8 in Sardinian type 1 diabetic patients. Diabetes & Metabolism, 38, A4-A4 Meeting presentation, abstract or full text will not be available. For similar paper published by the same team see 686_Paccagnini_PTB or 1094_Masala _PTB.

1209 Wenzel, C. (2012) Paratuberculosis in a 80 male goat. Tierarztliche Umschau, 67, 80-81 A case of paratuberculosis (Johne's disease) in a male goat is reported. Clinical signs and course of illness are described. Cachexia rather than diarrhoea was observed. Mycobacterium paratuberculosis was detected by faeces culture.

1210 Ghosh, P., Hsu, C.Y., Alyamani, E.J., Shehata, M.M., Al-Dubaib, M.A., Al-Naeem, A., Hashad, M., Mahmoud, O.M., Alharbi, K.B.J., Al-Busadah, K., Al-Swailem, A.M., Talaat, A.M. (2012) Genome-Wide Analysis of the Emerging Infection with Mycobacterium avium Subspecies paratuberculosis in the Arabian Camels (Camelus dromedarius). Plos One, 7, Article Number: e31947 DOI: 10.1371/journal.pone.0031947 Published: FEB 29 2012 Mycobacterium avium subspecies paratuberculosis (M. ap) is the causative agent of paratuberculosis or Johne's disease (JD) in herbivores with potential involvement in cases of Crohn's disease in humans. JD is spread worldwide and is economically important for both beef and dairy industries. Generally, pathogenic ovine strains (M. ap-S) are mainly found in sheep while bovine strains (M. ap-C) infect other ruminants (e.g. cattle, goat, deer), as well as sheep. In an effort to characterize this emerging infection in dromedary/Arabian camels, we successfully cultured M. ap from several samples collected from infected camels suffering from chronic, intermittent diarrhea suggestive of JD. Gene-based typing of isolates indicated that all isolates belong to sheep lineage of strains of M. ap (M. ap-S), suggesting a putative transmission from infected sheep herds. Screening sheep and goat herds associated with camels identified the circulation of this type in sheep but not goats. The current genome-wide analysis recognizes these camel isolates as a sub-lineage of the sheep strain with a significant number of single nucleotide polymorphisms (SNPs) between sheep and camel isolates (similar to 1000 SNPs). Such polymorphism could represent geographical differences among isolates or host adaptation of M. ap during camel infection. To our knowledge, this is the first attempt to examine the genomic basis of this emerging infection in camels with implications on the evolution of this important pathogen. The sequenced genomes of M. ap isolates from camels will further assist our efforts to understand JD pathogenesis and the dynamic of disease transmission across animal species.

New publications in the CROHN’S DISEASE AND PARATUBERCULOSIS database (DDDDD)


682 Chamberlin, W.M. (2012) Much is still to be learned about pathogenic Mycobacteria Journal of Crohns & Colitis, 6, 390-391 Abstract not available.
**Much is still to be learned about pathogenic Mycobacteria Reply**
Journal of Crohns & Colitis, 6, 392-392
Abstract not available.

**Mycobacterium avium paratuberculosis and Crohn's Disease: An association requiring more research**
Journal of Crohns & Colitis, 6, 393-393
Abstract not available.
A cross-sectional study was undertaken (October 2010 to August 2011) to estimate the prevalence of paratuberculosis in the small ruminant dairy industries in Ontario, Canada. Blood and feces were sampled from 580 goats and 397 sheep. A cross-sectional study was undertaken (October 2010 to August 2011) to estimate the prevalence of paratuberculosis in the small ruminant dairy industries in Ontario, Canada. Blood and feces were sampled from 580 goats and 397 sheep (lactating and 2 y of age or older) that were randomly selected from 29 randomly selected dairy goat herds and 21 convenience herds.