2013-07-23-053 Paratuberculosis databases updated (2013-07-22)

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New publications in the PARATUBERCULOSIS database (163-1467)

1463 Dimareli-Malli, Z., Mazaraki, K., Stevenson, K., Tsakos, P., Zdragas, A., Giantzi, V., Petridou, E., Heron, I., Vafeas, G.

Culture phenotypes and molecular characterization of Mycobacterium avium subsp paratuberculosis isolates from small ruminants
Research in Veterinary Science, (2013) 95, 49-53
In this study the suitability of different solid media was investigated for the isolation of Mycobacterium avium subsp. paratuberculosis (Map) in order to identify the optimum single or combination of media to permit the isolation of all strain types from small ruminants. A subset of these Map strains was then further characterized by molecular typing methods to assess the genetic diversity of Map strains in the study area (Northern Greece). Map strains were isolated from tissues and faeces of infected goats (n = 52) and sheep (n = 8) and were analysed for polymorphisms in IS1311 to classify the strain type as Type C or S. The study found that M7H11 supplemented with mycobactin j, OADC and new born calf serum (M7H11+Mj) is the best single choice of medium for the primary isolation of Map of both Type C and S from small ruminants. The combination of M7H11+Mj and Herrolds egg yolk medium supplemented with mycobactin j and sodium pyruvate allowed the detection of all Map isolates in this study. Nineteen Map isolates were characterised by pulsed-field gel electrophoresis and the isolates demonstrated significant genetic diversity. Twelve different SnaBI and 16 distinct SpeI profiles were detected of which 25 have not been described previously and are new profiles. The combination of both enzyme profiles gave 13 different multiplex profiles. Ten different multiplex profiles were detected in goats and three in sheep. One ovine isolate gave the same multiplex profile as a caprine isolate and two different profiles were found within a single goat herd.

1464 Thirunayukkarasu, S., Plain, K.M., Eckstein, T.M., de Silva, K., Whittington, R.J.

Cellular and humoral immunogenicity of Mycobacterium avium subsp paratuberculosis specific lipopentapeptide antigens
Research in Veterinary Science, (2013) 95, 123-129
Paratuberculosis caused by Mycobacterium avium subsp. paratuberculosis (MAP) is a chronic infectious disease affecting domestic and wild ruminants. Antigens currently used for the diagnosis of paratuberculosis are whole-cell derived crude preparations. The identification of MAP-specific antigens for the specific and early diagnosis of this infection is strongly needed. This study assessed the ability of the MAP-specific synthetic lipopeptide antigen Para-LP-01 to invoke specific serum antibody (Ab) and cell-mediated immune (CMI) responses in sheep experimentally exposed to MAP S strain. Responses were compared to those elicited by the crude whole-cell derived MAP 316v antigen (316v). Para-LP-01 induced a significant serum Ab response in MAP-infected sheep in comparison with unexposed or uninfected sheep, but failed to induce detectable CMI responses including production of IFN-gamma, IL-10 and lymphoproliferation, unlike 316v which invoked both CMI and serum Ab responses in MAP-exposed sheep. Para-LP-01 is a suitable antigen for serodiagnosis of MAP-infection in sheep. The differential induction of humoral and CMI responses by lipid based antigens could enhance current understanding of the role played by cell-wall associated lipid antigens in the pathogenesis of MAP-infection.

1465 Singh, P.K., Singh, S.V., Saxena, V.K., Singh, M.K., Singh, A.V., Sohal, J.S.

Expression Profiles of Different Cytokine Genes in Peripheral Blood Mononuclear Cells of Goats Infected Experimentally with Native Strain of Mycobacterium Avium Subsp Paratuberculosis

Animal Biotechnology, (2013) 24, 187-197

Paratuberculosis (ParaTB), caused by Mycobacterium avium subspecies paratuberculosis (MAP) is a chronic enteritis of ruminants and may contribute to Crohn's disease in humans. Key features of host immunity to MAP infection include an early pro-inflammatory (Th1-like) response that eventually gives way to a predominant anti-inflammatory (Th2-like) response. Many studies have been conducted to understand the underlying mechanism of misdirected host immune response, however, these studies mainly focused on cattle. The present study is the first attempt to test the hypothesis of shift in Th1 to Th2 like responses during the progression of ParaTB in caprine species (small ruminant). Ten healthy male kids (<6 months old) of the same breed were selected for this study. Of the 10 kids, 6 were experimentally infected with native strain (S5) of MAP (Indian Bison Type) and the remaining 4 kids were control. Kids were monitored for a period of 12 months post infection (MPI) and were tested for establishment of infection. Expression levels of IFNG, IL2, IL12, IL4, and IL10 genes were estimated before infection and at 4, 8, and 12 MPI in stimulated peripheral blood mononuclear cells (PBMCs) of infected and control kids. The study demonstrated the expression of IFNG and IL2 as classic Th1-like pro-inflammatory signatures; whereas, IL10 exhibited itself as classical Th2-like signature. The study also reports unexpected lowered expression of the IL12 gene simultaneously with increased expression of IFNG, lowered expression of the IL2 gene (compared to IFNG), and suppressed expression of the IL4.

1466 Marfell, B.J., O'Brien, R., Griffin, J.F.T.

Global gene expression profiling of monocyte-derived macrophages from red deer (Cervus elaphus) genotypically resistant or susceptible to Mycobacterium avium subspecies paratuberculosis infection

Developmental and Comparative Immunology, (2013) 40, 210-217

Mycobacterium avium subspecies paratuberculosis (MAP) can cause a chronic inflammatory bowel disease, Johne's disease OD), in ruminant animals. This study has explored the molecular basis of resistance and susceptibility to this disease in red deer breeds previously confirmed to express polarised phenotypes by experimental infection trials and following natural infection. Monocyte-derived macrophage cultures were obtained from uninfected red deer selected for either a resistant or susceptible phenotype. Cells were infected with MAP in vitro and gene expression analysed by RNA-Seq. Transcriptome analysis revealed a more disrupted gene expression profile in macrophages from susceptible animals compared with cells from resistant animals in terms of the number of genes up- or downregulated. Highly upregulated genes were related to chemotaxis (CXCL10, CSF3, and CCL8) and type I interferon signalling (RSAD2, IFIT1, IFIT2, ISG12, ISG15, USP18, and HERC6). Upregulation of these genes was observed to be greater in macrophages from susceptible animals compared to cells from resistant animals in response to in vitro MAP infection. These data support the use of transcriptomic approaches to enable the identification of markers associated particularly with susceptibility to MAP infection. (C) 2013 Elsevier Ltd. All rights reserved.

1467 Sa, L.D.E., de Oliveira, J.M.B., Santos, G.R., Brandespim, D.F., da Silva, J.L., Mota, R.A., Pinheiro, J.W.

Serological evaluation and risk factors for Mycobacterium avium subsp paratuberculosis infection in dairy herds of Microregion Garanhuns, Pernambuco

Pesquisa Veterinaria Brasileira, (2013) 33, 310-314

The present study aimed to conduct an epidemiological investigation of Mycobacterium avium subsp. paratuberculosis (MAP) infection in dairy cattle of the Garanhuns microregion, in Pernambuco, Brazil. Blood samples were collected from 408 animals from 19 herds located in 15 cities. Serological tests were performed by indirect immunoenzymatic assay (ELISA) for antibodies against MAP. In all farms, a questionnaire to investigate risk factors was used, and Global Position System (GPS) receivers were used to collect geographic coordinates to show the spatial distribution of the animals. The prevalence of MAP infected cattle was 2.7% (11/408; I.C. 1.4-4.9). The rate of infection was 47.4% (9/19). An annual birth rate over 51

calves/year (OR 3.8; I.C. 1.1-13.1) was identified as a risk factor in logistic regression analysis. Thus, it is concluded that MAP infection is present in dairy cattle of the microregion studied here, and control measures based on the identified risk factors should be implemented in order to reduce the sources of infection **PDF NOT AVAILABLE**.

New publications in the CROHN'S DISEASE AND PARATUBERCULOSIS database (815-816)

815 Greaves, R.B., Read, M., Timmis, J., Andrews, P.S., Butler, J.A., Gerckens, B.O., Kumar, V.

In silico investigation of novel biological pathways: The role of CD200 in regulation of T cell priming in experimental autoimmune encephalomyelitis
Biosystems, (2013) 112, 107-121
The use of simulation to investigate biological domains will inevitably lead to the need to extend existing simulations as new areas of these domains become more fully understood. Such simulation extensions can entail the incorporation of additional cell types, molecules or molecular pathways, all of which can exert a profound influence on the simulation behaviour. Where the biological domain is not well characterised, a structured development methodology must be employed to ensure that the extended simulation is well aligned with its predecessor. We develop and discuss such a methodology, relying on iterative simulation development and sensitivity analysis. The utility of this methodology is demonstrated using a case study simulation of experimental autoimmune encephalomyelitis (EAE), a murine T cell-mediated autoimmune disease model of multiple sclerosis, where it is used to investigate the activity of an additional regulatory pathway. We discuss how application of this methodology guards against creating inappropriate simulation representations of the biology when investigating poorly characterised biological mechanisms. (C) 2013 Elsevier Ireland Ltd. All rights reserved.

816 Kobayashi, K.S.

Shaping Intestinal Bacterial Community by TLR and NLR Signaling
Guarino A_Quigley EMM_Walker WA (eds): Probiotic Bacteria and Their Effect on Human Health and Well-Being.World Rev Nutr Diet.Basel_Karger_2013, vol 107, pp 32-42 (DOI:10.1159/000346493), (2013) 107, 32-42
Human intestines harbor a diverse microbial community composed of a large number of bacteria and other microorganisms. These intestinal microbiota have evolved to achieve a symbiotic relationship with the host. In addition to aiding host metabolic pathways by breaking down foods and supplying nutrients to their host, microbiota play an important role in the development and maintenance of the host immune system. At the same time, the detection of microorganisms and their products by innate immune receptors such as TLRs (Toll-like receptors) and NLR (nucleotide-binding domain, leucine-rich repeats, or NOD-like receptor) proteins are critical for maintaining intestinal homeostasis by shaping microbial communities. This review summarizes recent progress about the role of TLRs and NLRs in the regulation of intestinal microbiota. Accumulating evidence suggest that intestinal microbiota have a large impact on both intestinal and systemic diseases. Therefore, understanding the mechanism of microbial regulation by TLRs and NLRs is important for the advancement of therapeutic interventions against digestive and other diseases. Copyright (c) 2013 S. Karger AG, Basel. **PDF NOT AVAILABLE**.

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