2013-08-23-071 Paratuberculosis databases updated (2013-08-22)

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New publications in the PARATUBERCULOSIS database (1484-1489)

1484 Maattanen, P., Trost, B., Scruten, E., Potter, A., Kusalik, A., Griebel, P., Napper, S.

Divergent Immune Responses to Mycobacterium avium subsp paratuberculosis Infection Correlate with Kinome Responses at the Site of Intestinal Infection
Infection and Immunity, (2013) 81, 2861-2872
Mycobacterium avium subsp. paratuberculosis is the causative agent of Johne's disease (JD) in cattle. M. avium subsp. paratuberculosis infects the gastrointestinal tract of calves, localizing and persisting primarily in the distal ileum. A high percentage of cattle exposed to M. avium subsp. paratuberculosis do not develop JD, but the mechanisms by which they resist infection are not understood. Here, we merge an established in vivo bovine intestinal segment model for M. avium subsp. paratuberculosis infection with bovine-specific peptide kinome arrays as a first step to understanding how infection influences host kinomic responses at the site of infection. Application of peptide arrays to in vivo tissue samples represents a critical and ambitious step in using this technology to understand host-pathogen interactions. Kinome analysis was performed on intestinal samples from 4 ileal segments subdivided into 10 separate compartments (6 M. avium subsp. paratuberculosis-in fected compartments and 4 intra-animal controls) using bovine-specific peptide arrays. Kinome data sets clustered into two groups, suggesting unique binary responses to M. avium subsp. paratuberculosis. Similarly, two M. avium subsp. paratuberculosis-specific immune responses, characterized by different antibody, T cell proliferation, and gamma interferon (IFN-gamma) responses, were also observed. Interestingly, the kinomic groupings segregated with the immune response groupings. Pathway and gene ontology analyses revealed that differences in innate immune and interleukin signaling and particular differences in the Wnt/beta-catenin pathway distinguished the kinomic groupings. Collectively, kinome analysis of tissue samples offers insight into the complex cellular responses induced by M. avium subsp. paratuberculosis in the ileum and provides a novel method to understand mechanisms that alter the balance between cell-mediated and antibody responses to M. avium subsp. paratube rculosis infection.

1485 Liu, X.F., Zhang, L., Zeng, J., Gao, Y., Tang, Z.Y.

Superparamagnetic nano-immunobeads toward food safety insurance
Journal of Nanoparticle Research, (2013) 15, Article Number: UNSP 1796 DOI: 10.1007/s11051-013-1796-x Published: JUL 2013-In this work, superparamagnetic nano-immunobeads (SPM-NIBs) based on conjugation of superparamagnetic Fe3O4 nanoparticles with specific antibodies have been developed toward food safety insurance. The resultant SPM-NIBs exhibits excellent colloidal stability and reversible magnetic response. Vibrio parahaemolyticus, which is a main foodborne pathogenes from contaminated seafood, can be separated specifically and efficiently by the resultant SPM-NIBs. The results of bacteria separation demonstrate that the SPM-NIBs have a higher specific activity and sensitivity toward V. parahaemolyticus. About 80 % of V. parahaemolyticus cells can be captured when the concentration of the broth reaches 10(3) CFU/mL. Thus, the SPM-NIBs can effectively enhance the efficiency for target bacteria inspections by shortening the period of culture time. This work holds the promise of development of general technique to prepare effective SPM-

NIBs toward food safety inspections and other bio-related applications for target analyte separation and collection.

1486 Verdier, J. , Deroche, L., Allez, M., Loy, C., Biet, F., Bodier, C.C., Bay, S., Ganneau, C., Matysiak-Budnik, T., Reyrat, J.M., Heyman, M., Cerf-Bensussan, N., Ruemmele, F.M., Menard, S.

Specific IgG Response against Mycobacterium avium paratuberculosis in Children and Adults with Crohn's Disease
Plos One, (2013) 8, Article Number: e62780 DOI: 10.1371/journal.pone.0062780
Published: MAY 2 2013-Background and Aims: Presence of serum antibodies against Mycobacterium avium paratuberculosis (MAP) in Crohn's Disease (CD) as a disease characteristic remains controversial. In the present work, we assessed antibody reactivity of serum and intestinal fluid against four distinct MAP-antigens, including the recently identified MAP-specific lipopentapeptide (L5P). Methods: Immunoglobulin concentrations and specificity against 3 non MAP-specific antigens: glycosyl-transferase-d (GSD), purified protein derivative from MAP (Johnin-PPD), heparin binding haemagglutinin (MAP-HBHA) and one MAP-specific antigen: synthetic L5P were determined by ELISA in gut lavage fluids from adult controls or patients with CD, and in sera of children or adult controls or patients with CD, ulcerative colitis or celiac disease. Results: Total IgA and IgG concentrations were increased in sera of children with CD but were decreased in sera of adults with CD, thereof specificity against MAP antigens was assessed by normalizing immunoglobulin concentrations between samples. In CD patients, IgG reactivity was increased against the four MAP antigens, including L5P in gut lavage fluids but it was only increased against L5P in sera. By contrast, anti-L5P IgG were not increased in patients with ulcerative colitis or celiac disease. Conclusions: A significant increase in anti-L5P IgG is observed in sera of children and adults with CD but not in patients with other intestinal inflammatory diseases. Anti-L5P antibodies may serve as serological marker for CD.

1487 Sohal, J.S. , Singh, S.V., Singh, P.K., Singh, A.V., Kumar, N.

A new marker IS1311 L2 PCR-REA for identification of 'Indian Bison' type Mycobacterium avium subspecies paratuberculosis
Indian Journal of Biotechnology, (2013) 12, 204-207
Previously, a new biotype (Indian Bison type S5) of Mycobacterium avium subspecies paratuberculosis (MAP), genetically different from so Tar reported MAP genotypes, was identified. This biotype is widely distributed in different geographical regions in India among various host species including humans. Due to deletion of TG at 64th and 65th of IS1311 element at locus 2 (L2), there is a loss of BsaJI restriction site in Indian Bison type MAP S5. However, in non-Indian MAP (cattle type/sheep type/US Bison type), the site was intact. Taking advantages of these variations in the genome, authors optimized a new marker IS1311 L2 PCR-REA (Restriction Endonuclease Assay), capable of distinguishing Indian Bison type MAP S5 from other biotypes. To test the field applicability, newly optimized assay was applied on 66 DNA samples (27 from cultural isolates and 39 from clinical specimens) where it successfully distinguished the MAP of Indian Bison type from other MAPs. Hence, this assa y can be used to characterize MAP isolates in future molecular epidemiology investigations. Also the applicability of this assay on clinical DNA samples gives us freedom to have knowledge of the infecting MAP genotype prior to culture.

1488 Cook, K.L., Flis, S.A., Ballard, C.S.

Sensitivity of Mycobacterium avium subsp paratuberculosis, Escherichia coli and Salmonella enterica serotype Typhimurium to low pH, high organic acids and ensiling
Journal of Applied Microbiology, (2013) 115, 334-345
Aims: To evaluate the persistence of Mycobacterium avium subsp paratuberculosis (Myco.paratuberculosis), Salmonella enterica serotype Typhimurium (Salm.Typhimurium) and a commensal Escherichia coli (E.coli) isolate under the low pH and high organic acid (OA) conditions of ensiling of forages. Methods and Results: Decay rates and the time required to obtain a 90% reduction in cell concentration were calculated following (i) exposure to buffered OA (pH 4.0, 5.0, 6.0 or 7.0) (ii) exposure to silage exudates and (iii) survival through ensiling

of forage materials. Salm.Typhimurium had higher decay rates in silage exudates (-0.5601day(-1)) than did E.coli (-0.1265day(-1)), but both exhibited lower decay rates in silage than in OA or silage exudates. Myco.paratuberculosis showed no decrease in silage and decay rates in silage exudates were significantly lower (2-12 times) than for the other two organisms. Conclusions: Escherichia coli, Salm.Typhimurium and Myco.paratuberculosis exhibit marked differences in response to acidity. All three organisms show acid resistance, but Myco.paratuberculosis in particular, if present in manure and applied to forage grasses, may survive the low pH and high OA of the ensilaging process; silage may therefore be a potential route of infection if ingested by a susceptible animal. Significance and Impact of Study: This information contributes to the understanding of potential risks associated with silage preservation and contamination of livestock feed with manure-borne pathogens.

New publications in the CROHN'S DISEASE AND PARATUBERCULOSIS database (830)

830 Dall'Olio, F., Vanhooren, V., Chen, C.C., Slagboom, P.E., Wuhrer, M., Franceschi, C.

N-glycomic biomarkers of biological aging and longevity: A link with inflammaging
Ageing Research Reviews, (2013) 12, 685-698
Glycosylation is a frequent co/post-translational modification of proteins which modulates a variety of biological functions. The analysis of N-glycome, i.e. the sugar chains N-linked to asparagine, identified new candidate biomarkers of aging such as N-glycans devoid of galactose residues on their branches, in a variety of human and experimental model systems, such as healthy old people, centenarians and their offspring and caloric restricted mice. These agalactosylated biantennary structures mainly decorate Asn297 of Fc portion of IgG (IgG-G0), and are present also in patients affected by progeroid syndromes and a variety of autoimmune/inflammatory diseases. IgG-G0 exert a pro-inflammatory effect through different mechanisms, including the lectin pathway of complement, binding to Fey receptors and formation of autoantibody aggregates. The age-related accumulation of IgG-G0 can contribute to inflammaging, the low-grade pro-inflammatory status that characterizes elderly, b y creating a vicious loop in which inflammation is responsible for the production of aberrantly glycosylated IgG which, in turn, would activate the immune system, exacerbating inflammation. Moreover, recent data suggest that the N-glycomic shift observed in aging could be related not only to inflammation but also to alteration of important metabolic pathways. Thus, altered N-glycans are both powerful markers of aging and possible contributors to its pathogenesis. (C) 2012 Elsevier B.V. All rights reserved.

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