2011-11-25-190 Paratuberculosis databases updated (2011-11-23)
To: (08) Mycobacterial diseases; (23) Veterinary education; (27) Scientific information
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New publications in the PARATUBERCULOSIS database (1091-1092)

1091 Nakase, H., Tamaki, H., Matsuura, M., Chiba, T., Okazaki, K. (2011)
Involvement of Mycobacterium avium subspecies Paratuberculosis in TNF-alpha Production from Macrophage: Possible Link Between MAP and Immune Response in Crohn's Disease
Inflammatory Bowel Diseases, 17, Pages: E140-E142 DOI: 10.1002/ibd.21750 Published: NOV 2011

Evaluation of the risk of paratuberculosis in adult cows fed Mycobacterium avium subsp paratuberculosis DNA-positive or -negative colostrum as calves
American Journal of Veterinary Research, 72, 1456-1464

New publications in the CROHN'S DISEASE AND PARATUBERCULOSIS database (619-621)

619 Harris, J. (2011)
Autophagy and cytokines
Cytokine, 56, 140-144

Autophagy is a highly conserved homoeostatic mechanism for the lysosomal degradation of cytosolic constituents, including long-lived macromolecules, organelles and intracellular pathogens. Autophagosomes are formed in response to a number of environmental stimuli, including amino acid deprivation, but also by both host- and pathogen-derived molecules, including toll-like receptor ligands and cytokines. In particular, IFN-gamma, TNF-alpha, IL-1, IL-2, IL-6 and TGF-beta have been shown to induce autophagy, while IL-4, IL-10 and IL-13 are inhibitory. Moreover, autophagy can itself regulate the production and secretion of cytokines, including IL-1, IL-18, TNF-alpha, and Type I IFN. This review discusses the potentially pivotal roles of autophagy in the regulation of inflammation and the coordination of innate and adaptive immune responses. (C) 2011 Elsevier Ltd. All rights reserved
Nakase, H., Tamaki, H., Matsuura, M., Chiba, T., Okazaki, K. (2011) Involvement of Mycobacterium avium subspecies Paratuberculosis in TNF-alpha Production from Macrophage: Possible Link Between MAP and Immune Response in Crohn’s Disease
Inflammatory Bowel Diseases, 17, Pages: E140-E142 DOI: 10.1002/ibd.21750 Published: NOV 2011
Letter, abstract not available

Nature Genetics, 43, 1066-1U50

More than 1,000 susceptibility loci have been identified through genome-wide association studies (GWAS) of common variants; however, the specific genes and full allelic spectrum of causal variants underlying these findings have not yet been defined. Here we used pooled next-generation sequencing to study 56 genes from regions associated with Crohn's disease in 350 cases and 350 controls. Through follow-up genotyping of 70 rare and low-frequency protein-altering variants in nine independent case-control series (16,054 Crohn's disease cases, 12,153 ulcerative colitis cases and 17,575 healthy controls), we identified four additional independent risk factors in NOD2, two additional protective variants in IL23R, a highly significant association with a protective splice variant in CARD9 (P < 1 x 10(-16), odds ratio approximate to 0.29) and additional associations with coding variants in IL18RAP, CUL2, C1orf106, PTPN22 and MUC19. We extend the results of successful GWAS by identifying new, rare and probably functional variants that could aid functional experiments and predictive models.