IAD 2016

17 & 18

MARCH 2016

PLOUFRAGAN - FRANCE

Proceedings

Xth Symposium of the French network for *Domestic Animal Immunology*

anses

French agency for food, environmental and occupational health & safety

Investigate, evaluate, protect

Towards the understanding of porcine cellular immune response to Chlamydia trachomatis and suis infections

T.Käser (1), J.A.Pasternak (1), M.Rieder (1), G.Hamonic (1), K.Lai (1), M. Delgado-Ortega (1), H.L.Wilson (1), V. Gerdts (1), **F.Meurens** (1,2,3)

(1)Vaccine and Infectious Disease Organization-InterVac, University of Saskatchewan, Saskatoon, Canada ; (2) LUNAM Université, Oniris, Nantes-Atlantic College of Veterinary Medicine and Food Sciences and Engineering, UMR BioEpAR, F-44307 Nantes, France ; (3) INRA, UMR1300 Biology, Epidemiology and Risk Analysis in Animal Health, CS 40706, F-4430 Nantes, France

Keywords: Pig, genital mucosa, T cell, Chlamydia, pre-clinical model

Chlamydia trachomatis (CT) infections cause serious diseases including infertility and trachoma. A vaccine against CT is not available but urgently needed. A recent study shows that pigs could serve as an affordable and relevant pre-clinical animal model but the porcine cellular immune response to the disease is poorly understood. Therefore, our aim was to establish a comprehensive analysis of porcine chlamydia-specific T-cell subsets. Pigs were synchronized and infected in standing estrus with 10^8 IFUs C. suis (CS) or CT intra-vaginally and intra-uterine. Then they were clinically monitored, and serum, swabs and blood were taken to analyse the humoral immune response, detect chlamydia, analyse immune cell counts and for PBMC isolation. Chlamydia-specific CD4+ T cells, CTLs, and gamma-delta-T cells were detected after in vitro restimulation of CFSE-labelled PBMC via flow cytometry while cytokine production was analysed via multiplex. Clinical scores, qPCR and serology confirm CS and CT infection with gross pathological changes in 3/4 CS-infected and 2/4 CT-infected animals. Proliferation analyses showed a chlamydia-specific CD4+ T-cell response while CTLs and gamma-delta-T cells responded less effectively. Multiplex analyses revealed IFNg and IL17 indicating a strong TH1 and TH17 responses. We incorporated recent advances regarding porcine toolbox to analyse the chlamydia-specific cellular immune response demonstrating the important role of a TH1 response upon in vivo CT infection of pigs. With the ability to comprehensively analyse not only the humoral but also the cellular responses, pigs can now serve as an important animal-model in chlamydia vaccine development bridging the gap between mice and primates.

Whole blood transcriptome analysis of Mycoplasma mycoides subsp. mycoides-infected cattle confirms immunosuppression but does not reflect local inflammation

V. Rodrigues (1,2), P. Holzmuller (1,2), C. Puech (2,1), H. Wesonga (3), F. Thiaucourt (1,2), L. Manso-Silván (1,2)

(1) CIRAD, UMR15 CMAEE, F-34398 Montpellier – France - (2) INRA, UMR1309 CMAEE, F-34398 Montpellier – France
(3) Kenyan Agricultural Research Institute, Nairobi – Kenya.

Keywords: cattle; contagious bovine pleuropneumonia; mycoplasma mycoides mycoides; whole blood transcriptome; immunosuppression.

Contagious bovine pleuropneumonia (CBPP), caused by Mycoplasma mycoides subsp. mycoides (Mmm), is a severe respiratory disease of cattle responsible for major economic losses in sub-Saharan Africa. Disease control relies mainly on the use of empirically attenuated vaccines that provide limited protection. Thus, understanding the virulence mechanisms used by Mmm as well as the role of the host immune system in disease development, persistence, and control is a prerequisite for the development of new, rationally designed control strategies. The aim of this study was to assess the use of whole blood transcriptome analysis to study cattle-Mmm interactions, starting by the characterization of the bovine response to Mmm infection during the acute form of the disease. For that purpose, we compared the transcriptome profile of whole blood from six cattle, before challenge by contact with Mmm-infected animals and at the appearance of first clinical signs, using a bovine microarray. Functional analysis revealed that 680 annotated genes were differentially expressed, with an overwhelming majority of down-regulated genes characterizing an immunosuppression. The main bio-functions affected were "organismal survival", "cellular development, morphology and functions" and "cell-to cell signaling and interactions". These affected functions were consistent with the results of previous in vitro immunological studies. However, microarray and qPCR validation results did not highlight pro-inflammatory molecules (such as TNFα, TLR2, IL-12B and IL-6), whereas inflammation is one of the most characteristic traits of acute CBPP. This global gene expression pattern may be considered as the result, in blood, of the local pulmonary response and the systemic events occurring during acute CBPP. Nevertheless, to understand the immune events occurring during disease, detailed analyses on the different immune cell subpopulations, either in vivo, at the local site, or in vitro, will be required. Whole blood transcriptome analysis remains an interesting approach for the identification of bio-signatures correlating to recovery and protection, which should facilitate the evaluation and validation of novel vaccine formulations.