cells (FDC) in lymphoid tissues before they infect the brain. In aged spleens PrPc expression and TSE agent accumulation upon FDC were reduced. Furthermore, the splenic marginal zone microarchitecture was substantially disturbed adversely affecting the delivery of immune complexes to FDC. This study is the first to suggest that the effects of aging on the microarchitecture that the function of the splenic marginal zone significantly influence the pathogenesis of an important pathogen.[2]

Figure 1: http://www.eventure-online.com/parthen-uploads/6/12PRI/img1_188549.jpg

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PO-068: Transcriptome changes of ovine medulla oblongata during presymptomatic natural scrapie and their association with prion-related lesions

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The pathogenesis of natural scrapie and other naturally prion diseases is still poorly understood. The determination of transcriptome variations in infected vs. control animals might clarify some molecular mechanisms of the prion induced pathology. In addition, it may allow the development of new tools for diagnostics and therapy. We presented here for the first time the natural scrapie associated alterations in the gene expression profiles in caudal medulla oblongata (MO) in ovine affected by the resymptomatic phase of the disease using a custom microarray platform. A total of 86 significant probe sets displayed expression changes greater than 2-fold. From these probes we identified 32 genes with known function, those genes encode proteins that are involved in immune response, cell adhesion, and transcription. Our results confirm earlier published regulated genes found in murine models with induced scrapie. Moreover, we have identified new genes that show diferential expression in scrapie and could be involved in prion neuropathology. Finally, we have investigated the relationship between gene expression profiles and the appearance of the main scrapie related lesions: Prion protein deposition, gliosis and spongiosis. In this context, the potential impacts of these gene expression changes in MO on scrapie development are discussed.

PO-069: Glial cells and scrapie progress

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Transmissible Spongiform Encephalopathies (TSEs) are a group of neurodegenerative disorders affecting animals and humans and for which no effective treatment is available to date. Vacuolization, neuronal and neurite degeneration, deposit of pathological prion protein (PrPsc) and gliosis, are changes typically found in TSE affected individuals. However, the actual role of this last feature, microgliosis and astrocytosis, has not been precisely determined.

The objective of this work is to deal with this role by assessing the involvement of the glial cells in natural Scrapie affected animals at different stages of the disease. To analyze the possible correlation between the glial reaction and the progress of the disease is proposed here. In order to achieve this aim, immunohistochemical techniques are performed to be applied on Scrapie samples from different sources and corresponding to different genotypes. With this specific aim, a descriptive study about the distribution and/or the morphology of glial cells in transversal cerebellum sections differs according to the clinical stage is developed here.

All advances achieved in the frame of this approach result especially relevant for the study about prion pathologies since some other components than PrPsc could be essential to the neurodegenerative progression associated with TSEs and therefore, other alternative strategies for their treatment could be considered.

Acknowledgments. This work was funded by a grant from the University of Zaragoza (UZ2010-BIO-10).

PO-070: Evaluation and quantification of prion infectivity of saliva by sPMCA, sheep and bank vole bioassay

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Scrapie is a prion disease of small ruminants that is transmitted horizontally or by contact with environmental reservoirs of infectivity. In Chronic Wasting Disease (CWD) saliva carries significant levels of infectivity contributing to disease spread.[1,2] We recently demonstrated that salivary glands of scrapie affected sheep accumulate PrP^{Sc}.[3] The aim of this study was to evaluate and possibly quantify the prion infectivity in saliva from scrapie affected sheep by using sPMCA, sheep and bank voles bioassay.