Transcriptional response to Staphylococcus aureus challenge in mammary epithelial cells isolated from genetically selected ewes on milk somatic cell score

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The milk somatic cell score (SCS) is an indirect indicator of mastitis, currently used as a selection criterion of dairy cattle and sheep. The lower the SCS, the less susceptible to mastitis animals are. To assess the effectiveness of SCS-based selection, two divergent lines of dairy sheep were created. As Mammary Epithelial Cells (MEC) are numerous and present as the first line of defence, they may play a crucial role in the early host-pathogen interaction. The present study focuses on transcriptomic profiling of MEC co-cultured with living ovine *S. aureus* or with their secretory products.

MEC were prepared from six ewes of each genetic line. RNA's were extracted from cells without stimulation, or after one or five hours of culture. RNA's were hybridised with an ovine oligonucleotid microarray. Data from living *S. aureus* stimulation and from supernatant stimulation, obtained from its culture, were analyzed separately.

Both stimuli caused large changes in MEC gene expression patterns, especially after 5 hours stimulation. IL-8 and SAA3 were strongly over-expressed in MEC after stimulation. Secretion of IL-8 was also confirmed by ELISA in the MEC culture supernatant. 242 genes were differentially expressed (BH5%) between ewes of the high and low SCS lines in both experiments. Most of these genes are involved in Biological Process, Cellular Compartment and Molecular Function of GO analysis. Differences in gene expression of mammary epithelial cells isolated from mastitis resistant and susceptible dairy sheep provide insights into genetically determined divergent responses to *S. aureus* in the mammary glands of ruminants.

Mammary Epithelial Cells, mastitis, divergent selection, dairy sheep, transcriptomic