Epigenetic mechanisms are thought to be involved in perinatal programming, the concept that early-life exposures have long-lasting consequences on adult phenotype and disease susceptibility. In order to study long-term impacts of inflammation during the perinatal period, we investigated the effects of postnatal exposure to the bacterial endotoxin lipopolysaccharide (LPS) on the adult immune response and methylation of immune response genes in mice. The *in vivo* and *in vitro* characterization of the mice primed with an early-life LPS challenge showed significant long-lasting down-regulation of several pro-inflammatory cytokines (TNF-α, IL-6, MCP-1) to an adult LPS infection, confirming the programming of the immune system.

The global methylation measured by LUMA and concurrently methylation levels of the repetitive B1 element increased in splenic PBMCs, suggesting genuine genome-wide methylation changes in mice primed with an early-life LPS challenge.

Methylation analysis, using bisulfite pyrosequencing, of particular genes involved in the LPS-TLR4 pathway revealed no differences in IFNγ, TNFα, IL-1R or MD2 promoter methylation upon early-life LPS treatment.

Genome-wide MeDIP-chip analysis allowed us to establish a list of candidate genes that might be involved in the programming mechanism. These genes are being validated by methylation specific PCR (MSP) and bisulfite pyrosequencing.

Our results will contribute to demonstrate that perinatal infections have an impact on functions of the immune system by (de)regulation of epigenetic DNA modifications of immune response genes.