

Faecal shedding and gene expression profile suggest suppression of the immunity in calves after an oral infection with *Escherichia coli* O157:H7.

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- Background

Enterohaemorrhagic *Escherichia coli* (EHEC), like *E. coli* O157:H7 are frequently detected in bovine faecal samples in slaughter houses, as cattle are the main natural reservoir of EHEC. They do not show clinical symptoms upon infection, but for humans the consequences can be severe. After ingestion and subsequent colonization of the human colon, EHEC releases verocytotoxins causing microvascular endothelial injuries which might lead to haemorrhagic colitis and haemolytic uremic syndrome.

EHEC infection can persist in herds for longer periods. The immune response against EHEC in cattle can not clear the infection rapidly as infected animals can secrete the bacteria over a period of months. The reason why some animals stop shedding is unknown. We performed different infection trials, observing a first infection eliciting a primary immune response which was unable to protect cattle from an experimental re-infection. Furthermore, the duration of the first infection was mostly shorter (<14 days, n=32) compared to the duration of the second infection (>28 days, n=21). We hypothesized that these results may reflect a suppression of certain pathways of the immune system, making cattle more prone to persistent colonization after re-infection.

- Methods

To test the former hypothesis, the RNA-Seq technology and bioinformatics were used to quantify changes in the recto-anal junction (RAJ) and ileal Peyer's patches transcriptome of nine Holstein-Friesian calves in response to a primary (n=3) and secondary infection (n=3) with EHEC O157:H7 in comparison to non-infected control calves (n=3).

- Results

A total of 21,046 genes were detected at least once in one of the nine RAJ samples or ileal Peyer's patches samples. In the RAJ, fourteen genes were found to be affected by a first infection with EHEC whereas nine genes were affected after a second infection with EHEC compared to the control group ($\log_2(\text{fold change}) \neq 0$; q-rate $< 0,1$). In the ileal Peyer's patches 1152 genes were influenced by a first infection compared to the control group and ten genes were affected by the reinfection compared to the same control. Here, we could observe a general downregulation of immunostimulatory genes and a suppression of immune suppressing genes.

- Conclusion

Although the RAJ is a major site of colonization, this area does not seem to be significantly modulated upon infection. The gene-expression in the ileal Peyer's patches is far more influenced by EHEC infection showing that a first EHEC infection modulates the immune response promoting the colonization during a second infection.