Evaluation of Aliarcobacter butzleri transcriptome during simulated infection of a human intestinal model

Aliarcobacter butzleri is a Gram negative bacterium of the *Campylobacteraceae* family often isolated from fecal samples from different animals and human clinical cases. In the last years, they are increasingly being isolated from different types of meats (in particular pork, chicken) and have been associated with symptoms such as diarrhea, vomiting, abdominal pain in humans. This study led to evaluate the invasion and colonization ability of 3 *A. butzleri* strains isolated from human on *in vitro* intestinal cell models obtaining transcriptomic data of *A. butzleri* in virulence conditions.

The RNAseq analysis of the strains LMG10828^T, LMG11119 and 31 has been performed with the use of a mixed mucus producer cell models (Caco-2 + HT29 MTX, 9/1 ratio) at 30 and 90 minutes from the inoculum jointly at an evaluation of the colonization/invasion ability of the strains. The RNA obtained has been sequenced with Illumina technology and the number of reads, mapped on the gene sequences, have been elaborated with the software edgeR to allowing the determination of differentially expressed genes (DEGs).

The data shown greater expression of genes related to TonB protein (intracellular growth), membrane protein and oxidoreductase activity (energy supply) in conditions of virulence in the strains tested. Moreover, the Inner membrane protein YjcH gene results overexpressed at 30 and 90 minutes from the inoculum, jointly with the gene codify for Cation/acetate symporter ActP at 90 minutes. Genes related to *tonB* function, *exbB and exdB* result overexpressed at 90 minutes together only in the strain LMG 11119 (greater colonization than the other two strains, $p < 0.05$), resulting not DEGs or underexpressed in the strains 31. Moreover, recently the urease pathway has been linked to the *A. butzleri* virulence, a part of these genes result underexpressed in the strains 31 that showed a lower colonization.