Exploring the virulence genes expression of *Arcobacter butzleri* during simulated infection of human gut models

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*Arcobacter butzleri* is an emerging foodborne pathogen of the *Campylobacteraceae* family, often isolated from chicken, pork and bovine meat, which causes different gastrointestinal diseases in human and animals. However, pathogenicity of *A. butzleri* is still underestimated due to a substantial lack of information on its virulence mechanisms, metabolic and genomic features. The aim of this study is an increase, through the use of gut models and molecular biology methods, the knowledge about *A. butzleri* virulence mechanism.

**MATERIALS AND METHODS**

**Strain:** *A. butzleri* LMG 10828

**Cell line:**
- HT29 MTX
- Caco-2
- Mixed (Caco-2/HT29 MTX; 9/1)

**Study of:**
- Colonization
- Invasion
- Intestinal barrier permeability (TEER)
- Translocation

**Intact models**

**2D MODELS**

<table>
<thead>
<tr>
<th>Colonization (90 minutes after initial inoculum)</th>
<th>Invasion (90 minutes after initial inoculum)</th>
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<tr>
<td>Maximum colonization capability</td>
<td>Maximum invasion capability</td>
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**3D MODELS**

- Translocation on Caco-2
- TEER on Caco-2

- **Higher colonization on mixed cell lines**
- **Higher invasion capability** on Caco-2 models compared to Mixed models

**RT-qPCR set-up**

- Primer3-BLAST design followed by *in vitro* test to confirm absence of non-specifics, appropriate thermal cycle and right target amplification

**Gene expression preliminary results**

- Overexpression of adhesion- and invasion-related genes after 150 minutes from the addition of *A. butzleri* in the models.

**CONCLUSIONS**

- Higher colonization in the mixed models
- Translocation of the bacteria through the layer after 24 hours not linked with TEER decrease
- Obtainment of a RT-qPCR protocol to study *A. butzleri* virulence gene expression
- Overexpression of the virulence genes after 150 minutes form the bacteria inoculum

- The subsequent experiment will deepen the knowledge about gene expression of others genes attributed at the virulence