Introduction: Tea is the second most commonly consumed beverage in the world. Its forecasted growing consumption is driven by consumer demand for new flavors and recognition of the health benefits, which results in the emergence of innovative herbal tea and tea blends with the addition of herbs and spices. Currently, no legislation specifies microbiological criteria for tea in Europe. However, available guidelines require the absence of pathogenic Salmonella spp. in finished products.

Methods: Information relating to the prevalence of Salmonella spp. in curtain environments was collected following searches of electronic databases, scientific journals, books, technical reports, and company internal data. The search strategy included keywords “microbiology”, “tea”, “prevalence”, “quality”, “Salmonella”.

Results: An exhaustive search of the literature (over 2,150 publications screened) and internal data yielded 17 publications. The overall analysis indicated low prevalence of positive samples of total 2,336 (identified) of Salmonella at the level of 2%, with no study reporting pathogens in black and green tea. All positive samples were in bacterial teas (e.g., jasmine, lemon, bergamot, rooibos, peppermint or lemon verbena tea).

Significance: Findings of this review align with a history of safe use of tea over thousands of years and equally confirm that control of Salmonella spp. within factory facilities manufacturing black and green tea should rely on preventative approaches, e.g., ingredient quality programs, Good Manufacturing Practices, Hazard Analysis Critical Control Points and environmental monitoring programs, rather than final product testing. Considering that the pathogens have been sporadically isolated from herbal teas, robust sampling plans aligned to final product testing based on statistical methods are suitable to control the risk of Salmonella spp. associated with tea blends containing herbs, dried flowers, fruit pieces, and spices.

P2-38 Survival of Listeria monocytogenes in Food Residues on Packaging Materials for Dairy Products

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Introduction: Listeria monocytogenes is known for causing foodborne infections often associated with high mortality rates. Survival under adverse conditions of L. monocytogenes for extended periods of time has been reported. L. monocytogenes contamination
Exploring the Virulence Gene Expression of *Arcobacter butzleri* during Simulated Infection of Human Gut Models

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**Introduction:** *Arcobacter butzleri* is an emerging foodborne pathogen often isolated from pork, chicken and beef meat, which causes different gastrointestinal diseases in human due to its invasive behaviour. However, the pathogenicity of *A. butzleri* is still underestimated due to a substantial lack of information on its virulence mechanisms, metabolic and genomic features.

**Purpose:** This study aims to explore, in simulated host-pathogen interactions, the expression of nine genes that are currently correlated with virulence traits of *A. butzleri*.

**Methods:** After the *ex novo* design of primers for the nine genes (*cadF, ciaB, cj1349, irgA, hecA, hecB, mviN, pldA, tlyA*) on an *A. butzleri* reference genome (type strain LMG 10828\(^1\)), their relative expression was quantified by quantitative RT-PCR under simulated host-pathogen interaction conditions. Briefly, In Vitro gut models of mucus-producing (HT29–MTX) and non-producing (HT29, Caco-2) human cells were co-incubated with the pathogen and total bacterial RNA was recovered at different time points. At the same time, bacterial counts were performed to describe the colonization and translocation capabilities of *A. butzleri*, by using two dimensional and three dimensional gut models, respectively.

**Results:** As the first outcome, an RT-qPCR protocol, suitable to quantify the relative expression of the nine virulence genes of *A. butzleri* in the presence of human cells, was optimized. Applying this protocol, an upregulation of part of those genes along the co-incubation time was observed. In addition, a favourable role of the mucus for the pathogen colonization was observed whereas the data from the three-dimensional models suggested an intracellular passage of *A. butzleri* through the epithelial barrier.

**Significance:** The results of this study represent a first step in the understanding of *A. butzleri* pathogenicity and are important to explain its role in gastrointestinal diseases.
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