

ABSTRACT

Lactobacillus plantarum is a highly flexible and versatile species, that can be isolated from a wide variety of niches, including the mammalian gut and fermented foods where it is present at high concentrations. Its ability to survive and persist in a wide variety of niches is reflected in its ability to use multiple carbohydrate sources and its high capacity for adaptation. For a long time, it has been exploited as starter cultures in fermentations, mainly of plant-derived raw materials. Currently, there is also a huge scientific interest in studying the potential probiotic properties of food-associated *Lactobacillus plantarum* strains for improving the human gastrointestinal health.

Recent studies have shown the similarities which exist between strains isolated from fermented foods and probiotic strains belonging to the same species isolated from the gastrointestinal tract. Considering this, it is thought that autochthonous *Lactobacillus plantarum* strains from fermented foods may have an impact on health, and could display the same properties as commercially renowned probiotic strains. Whilst *Lactobacillus plantarum* strains have been proposed as potential probiotic candidates, the ability of autochthonous strains consumed in fermented foods to interact with the host and the underlying mechanisms which govern this, are still unclear. This thesis describes methods for screening *Lactobacillus plantarum* strains for attributes commonly associated with probiotics through the establishment of *in silico* and *in vitro* models and utilizes an *ex vivo* fermentation model of gut microbiota to characterize the probiotic activity of selected food-borne strains.

Initially, a collection of food-borne *Lactobacillus plantarum* strains were evaluated for their potential to adhere to epithelial cells and mucus by *in vitro* assays. This first screening showed the high potential of food-borne *Lactobacillus plantarum* strains, and served as a cull

to select the most promising strains. Based on these results, the molecular mechanisms underlying the immunomodulatory properties of two selected *Lactobacillus plantarum* strains were evaluated by studying the early cytokine response modulated through the interaction with pattern-recognition receptors in murine macrophages. Results confirmed the ability of food-origin *Lactobacillus plantarum* strains to interact with host cells and modulate the immune response at the same level as probiotic strains.

The complete genome of three *Lactobacillus plantarum* strains were sequenced and putative probiotic genes were identified and annotated, allowing a better understanding of how *Lactobacillus plantarum* strains respond to different stresses and interact with the host. Moreover, the comparative genomic analysis showed how closely related *Lactobacillus plantarum* strains isolated from both fermented foods and the gut are. Finally, the ability of food-borne *Lactobacillus plantarum* to increase the diversity of the intestinal microbiota of patients with inflammatory bowel disease was confirming using a continuous faecal fermentation model.

All of the results obtained here highlight the potential of food-associated strains, and the need for in-depth studies of their genomes and potential functions. In particular, the properties investigated here lead us to consider fermented foods as a rich source of *Lactobacillus plantarum* strains with potential probiotic functions.