

# Unraveling potential probiotic features in the genome of *Lactobacillus paragasseri*

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## Abstract

The vaginal microbiota is dominated by lactobacilli, which exerts important health-promoting effects and prevention of bacterial vaginosis (BV). *Lactobacillus paragasseri* is a sister taxon related to *L. gasseri* and has been recently described in 2018 as a new species. Therefore, its role in the vaginal environment must be investigated. Moreover, previous studies suggest the vaginal ecosystem as a potential source of probiotic strains to be used in the treatment of other dysbiosis related diseases such as gastrointestinal disorders. Currently, comparative genomics studies have been shown as a promising tool in the prediction of the possible mechanisms related to their beneficial activity. In this work two *L. paragasseri* strains, CRI16 and CRI18 were recovered from healthy women of reproductive age. The strains were isolated from healthy subjects while CRI22 was isolated from a BV patient. The genomes were assembled with SPAdes and annotated via RAST. Eight genome sequences of *L. paragasseri* were obtained from NCBI and included in the comparative analysis. Genes involved in protective mechanisms, such as bacteriocins were predicted using BAGEL. The metabolic pathway of other health-promoting features such as vitamins and short-chain fatty acids and the adaptation to gastrointestinal stress conditions were characterized via PATRIC. The presence of genetic mobile elements such as plasmids and phages was evaluated in the strains to evaluate their safety for human use. In this context, antibiotic resistance genes and virulence factors were investigated using CARD and VFDB databases respectively. Our results revealed several beneficial features such as the presence of three and six bacteriocin genes in CRI16 and CRI18 respectively. Metabolic pathway analysis indicates both strains are able to produce vitamins K2, B1 and B9. Furthermore, they also seem to be able to produce Lactate and to degrade biogenic amines, including putrescine and spermidine although they may produce cadaverine as well. Interestingly, the strains present enzymes genes involved in bile salts deconjugation, suggesting adaptation to gastrointestinal conditions. Regarding safety issues, one intact prophage sequence was predicted in both strains and only CRI16 harbors a plasmid of 40kb, although no antibiotic resistance or virulence gene was found. Our study represents the first step in the characterization of the *L. paragasseri* strains CRI16 and CRI18 suggesting them as potential candidates for probiotic use.

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Link to Video: