

Abstract

Different pathogenic bacteria including the uropathogens have developed resistance against the antibiotics and have now become a constant threat for the humanity. This frightening situation constantly demands the development of new ways and methods that can cope with the menace of drug resistance and probiotics like *Lactobacillus plantarum* can be one of the effective ways to control these virulent antibiotic resistant uropathogens. In this study, potential *Lactobacillus plantarum* strains were isolated from fruits and vegetables, identified and next generation sequencing of these strains was done. Out of 105 isolated strains, five strains that showed the best results were selected. Four were identified as *Lactobacillus plantarum* while one strain was identified as *Lactobacillus paraplantarum* which is closely related to *L. plantarum* genotypically and also shows highly similar phenotypic properties. Stress related proteins encoding genes were also identified in the these strains. In-vitro studies were done in for checking the efficacy of *L. plantarum* strains against the three uropathogenic strains of *Escherichia coli*, one strain of *Klebsiella pneumoniae* and one strain of *Enterococcus faecalis* and their antimicrobial activity was speculated to be linked with the genes that encode for class II bacteriocin i.e. plantaricin. Next generation sequencing revealed the presence of plantaricin biosynthesis gene clusters in strains i.e. bacteriocin operons *plnEFI*, *plnABCD* and regulatory operon *plnA* in *L. paraplantarum* and *plnEFI*, *plnD* and *plnG* in rest of the four *L. plantarum* strains. The results obtained showed the effectiveness of these plantaricin producing strains as were speculated. This study can be helpful in developing probiotic therapy and can replace the antibiotic therapy hence eliminating the side-effects associated with the antibiotic uptake as well as controlling the drug resistant pathogens. Moreover, the genome sequence can give better insight to the adaptive stress response as well as the host interaction mechanisms.