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Characterization of Erythromycin and Tetracycline Resistance in Lactobacillus fermentum Strains

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Abstract

© 2018 Elizaveta Anisimova and Dina Yarullina. Lactobacillus fermentum colonizing gastrointestinal and urogenital tracts of humans and animals is widely used in manufacturing of fermented products and as probiotics. These bacteria may function as vehicles of antibiotic resistance genes, which can be transferred to pathogenic bacteria. Therefore, monitoring and control of transmissible antibiotic resistance determinants in these microorganisms is necessary to approve their safety status. The aim of this study was to characterize erythromycin and tetracycline resistance of L. fermentum isolates and to estimate the potential transfer of resistance genes from lactobacilli to the other Gram-positive and Gram-negative bacteria. Among six L. fermentum strains isolated from human feces and commercial dairy products, five strains demonstrated phenotypic resistance to tetracycline. PCR screening for antibiotic resistance determinants revealed plasmid-located tetracycline resistance genes tet(K) and tet(M) in all strains and erythromycin resistance genes erm(B) in the chromosome of L. fermentum 5-1 and erm(C) in the plasmid of L. fermentum 3-4. All tested lactobacilli lacked conjugative transposon Tn916 and were not able to transfer tetracycline resistance genes to Staphylococcus aureus, Staphylococcus epidermidis, Listeria monocytogenes, Acinetobacter baumannii, Citrobacter freundii, and Escherichia coli by filter mating. Staphylococcus haemolyticus did not accept erythromycin resistance genes from corresponding Lactobacillus strains. Thus, in the present study, L. fermentum was not implicated in the spread of erythromycin and tetracycline resistance, but still these strains pose the threat to the environment and human health because they harbored erythromycin and tetracycline resistance genes in their plasmids and therefore should not be used in foods and probiotics.

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