Fermentation by gut microbiota cultured in a simulator of the human intestinal microbial ecosystem is improved by probiotic Enterococcus faecium CRL 183

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Submission date: September 05, 2011; Acceptance date: October 07, 2011; Publication date: October 08, 2011

Abstract

Background: Enterococci are used in a large number of dairy products, such as starter cultures in food supplements and in foods considered functional. In vitro gut fermentation models present an unmatched opportunity of performing studies frequently allenged in humans and animals owing to ethical concerns. A dynamic model of the human intestinal microbial ecosystem (SHIME) was designed to better simulate conditions intestinal microbiota.

Methods: The SHIME model was used to study the effect of Enterococcus faecium CRL 183 on the fermentation pattern of the colon microbiota. Initially, an inoculum prepared from human feces was introduced into the reactor vessels and stabilized over 2 wk using a culture medium. This stabilization period was followed by a 2-wk control period during which the microbiota were monitored. The microbiota were then subjected to a 4-wk treatment period by adding $10^8$ CFU/mL of the Enterococcus faecium CRL 183 to vessel one (the stomach compartment).

Results: The addition resulted into an overall increase of bacterial marker populations (Enterobacteriaceae, Lactobacillus spp., Bifidobacterium spp. and Clostridium spp.), with a significant increase of the Lactobacillus sp. and Bifidobacterium sp populations. The short-chain fatty acid (SCFA) concentration increased during the supplementation period; this was due mainly to a significant increase in the levels of acetic, butyric and propionic acids. Ammonium concentrations increased during the supplementation period.

Conclusions: Results showed that the major effect of E. faecium CRL 183 was found in the ascendant and transverse colon.
Key words: Gut microbiota, *Enterococcus*, Gastrointestinal resource management, Simulator of Human Intestinal Microbial Ecosystem (SHIME)