## Real-time PCR Analysis of Intestinal Microbiota in Peritoneal Dialysis Patients

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Abstract

Bifidobacterium and Lactobacillus can beneficially affect the host by producing acetic acid

and lactic acid which lower pH and thereby inhibits the growth of pathogens or by competing

with pathogens for epithelial adhesion sites and nutrients. The transmural migration of enteric

organisms into the peritoneal cavity can cause peritonitis in peritoneal dialysis (PD) patients.

We hypothesized that the intestinal microbiota such as Lactobacillus species and

Bifidobacterium species differed between PD patients and healthy controls. The aim of the

study was to investigate these differences by real-time polymerase chain reaction (PCR)

analysis of fecal samples. From August 1, 2009 to March 31, 2010, a total of 29 nondiabetic

PD patients and 41 healthy controls from China Medical University Hospital were recruited

after giving their informed consent. Fecal samples were collected from the PD patients and

their age-matched counterparts in the morning using a standardized procedure. DNA

extracted from these samples was analyzed by real-time PCR. All Bifidobacteria,

Bifidobacterium catenulatum, B. longum, B. bifidum, Lactobacillus plantarum, L. paracasei

and *Klebsiella pneumoniae* were less frequently detected in the patient samples.

Dysbiosis (microbial imbalance) may impair intestinal barrier function and increase host

vulnerability to pathogen invasion. Further studies are necessary to confirm our findings

before clinical trials with probiotics supplementation in PD patients.

**Key Words:** End stage renal disease, dialysis, *Bifidobacterium*, *Lactobacilli*.

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