

Curr Microbiol. 2014 Nov;69(5):675-80. doi: 10.1007/s00284-014-0640-6. Epub 2014 Jun 27.

Gut microbe analysis between hyperthyroid and healthy individuals.

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Abstract

Clinicians have long recognized that thyroid hormones have some effects on the gastrointestinal tract. This study aimed to investigate the gut microbiota in hyperthyroid and assess whether there are alterations in the diversity and similarity of gut microbiota in the hyperthyroid when compared with healthy individuals. PCR-denaturing gradient gel electrophoresis (DGGE) with universal primers targeting V3 region of the 16S rRNA gene was employed to characterize the overall intestinal microbiota composition, and some excised gel bands were cloned for sequencing. Enterobacteriaceae, Enterococcus, Bifidobacterium, Clostridium, and Lactobacillus genus were also enumerated by quantitative real-time PCR. A significant difference between hyperthyroid and healthy groups ($(*) P < 0.05$) was shown in DGGE profiles. And real-time PCR showed obvious decrease of Bifidobacterium and Lactobacillus ($(*) P < 0.05$), and increase of Enterococcus ($(*) P < 0.05$) in the hyperthyroid group. This study shows the characterization of gut microbiota in hyperthyroid.

PMID: 24969306 [PubMed - indexed for MEDLINE]

