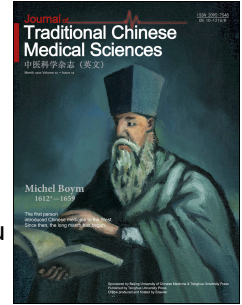


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## Composition of intestinal microflora associated with Yang-deficiency

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### Abstract

*Objective:* In this study, we investigated the composition of the intestinal microflora associated with Yang-deficiency and the function-specific members of this microflora.

*Method:* Subjects with normal and Yang-deficient constitutions were recruited in Beijing, with 30 subjects in each group. Illumina high-throughput sequencing was used to sequence the DNA of their fecal bacteria in the 16S rRNA V3–V4 region. The species abundance and distribution of the intestinal microflora in each specimen were determined with a statistical analysis of these sequences. We identified an underlying taxonomic trend with nonparametric PCoA and other statistical techniques.

*Results:* (1) Subjects with Yang-deficiency displayed more uneven abundances of the taxa in

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