

Gut Microbiome Shotgun Sequencing in Assessment of Microbial Community Changes Associated with *H. pylori* Eradication Therapy

Khusnutdinova D., Grigoryeva T., Abdulkhakov S., Safina D., Siniagina M., Markelova M., Boulygina E., Malanin S., Tyakht A., Kovarsky B., Ismagilova R., Abdulkhakov R., Chernov V.
Kazan Federal University, 420008, Kremlevskaya 18, Kazan, Russia

Abstract

© 2016, Springer Science+Business Media New York. Disturbance of intestinal microbiota content and functions often results in different pathological conditions. Pharmacotherapy including antibiotics use is one of the factors leading to dysbiosis. To evaluate the influence of antibiotics use on intestinal microbiota metagenomic profiles of stool, samples of 74 patients before and after *Helicobacter pylori*—eradication therapy—were analyzed. Evaluation of taxonomic diversity changes based on Shannon index and Bray-Curtis metrics allows to range patients according to mild, moderate, and severe risk of disturbance of intestinal microbiota pathological conditions.

<http://dx.doi.org/10.1007/s12668-016-0285-y>

Keywords

Eradication therapy, *Helicobacter pylori*, Intestinal microbiota, Whole genome sequencing