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## Data Article

# Data on gut metagenomes of the patients with *Helicobacter pylori* infection before and after the antibiotic therapy



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## ABSTRACT

Antibiotic therapy can lead to the disruption of gut microbiota community with possible negative outcomes for human health. One of the diseases for which the treatment scheme commonly included antibiotic intake is *Helicobacter pylori* infection. The changes in taxonomic and functional composition of microbiota in patients can be assessed using “shotgun” metagenomic sequencing. Ten stool samples were collected from 4 patients with *Helicobacter pylori* infection before and directly after the *H. pylori* eradication course. Additionally, for two of the subjects, the samples were collected 1 month after the end of the treatment. The samples were subject to “shotgun” (whole-genome) metagenomic sequencing using Illumina HiSeq platform. The reads are deposited in the ENA (project ID: PRJEB18265).

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## Specifications Table

Subject area	Biology
More specific subject area	Bacterial metagenomics
Type of data	Text files: sequences
How data was acquired	DNA sequencing using Illumina HiSeq 2500 platform
Data format	Raw
Experimental factors	DNA extracted from stool samples
Experimental features	Two micrograms of total DNA per sample were used to create barcoded paired-end sequencing libraries. “Shotgun” sequencing was performed using Illumina HiSeq 2500 platform according to the recommendations of the manufacturer.
Data source location	Kazan, Russian Federation
Data accessibility	The data is deposited in the European Nucleotide Archive (project ID: PRJEB18265, URL: <a href="http://www.ebi.ac.uk/ena/data/view/PRJEB18265">http://www.ebi.ac.uk/ena/data/view/PRJEB18265</a> ).

## Value of the data

- The data can be used to assess the antibiotic-induced gut dysbiosis in a cultivation-independent manner via the changes in the relative abundance of microbial taxa and genes.
- Using the metagenomic datasets corresponding to three consequent time points - before, immediately after and 1 month after the end of the treatment - it is possible to analyze the temporal dynamics and resilience of gut microbial ecosystem.
- By calculating the relative abundance of the genes conferring antibiotic resistance from the data, researchers can evaluate the resistome of gut microbiota and its changes during and after the antibiotic intake.
- Identification of specific changes in gut microbiota composition as the result of *H. pylori* eradication using the presented data opens the way to designing new approaches to the alleviation of the side effects of the treatment.

## 1. Data

The presented dataset contains 10 “shotgun” human gut metagenomes assessed from stool samples from the patients with *Helicobacter pylori* infection. The total read length for the dataset is 87.6 Gbp (the metagenomes contain  $34.1 \pm 13.6$  mln of reads per sample, mean  $\pm$  s.d.). Details about the dataset are shown in [Table 1](#).

## 2. Experimental design, materials and methods

### 2.1. Cohorts assembly

The study was approved by the Local ethics committee of the Kazan (Volga region) Federal University. Each patient signed an informed consent before the start of the study. The patients were enrolled in University Hospital of Kazan Federal University (former Republican Clinical Hospital #2 of the Ministry of Healthcare of Republic of Tatarstan).

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