Data in Brief 11 (2017) 68–71

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

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

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ARTICLE INFO

Article history:
Received 10 December 2016
Received in revised form
29 December 2016
Accepted 11 January 2017
Available online 17 January 2017

Keywords:
Gut microbiota
Metagenome
Antibiotic therapy
Helicobacter pylori

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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http://dx.doi.org/10.1016/j.dib.2017.01.007