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Data Article

Shotgun metagenomic data on the human stool samples to characterize shifts of the gut microbial profile after the *Helicobacter pylori* eradication therapy

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ARTICLE INFO

Article history:

Received 20 June 2017

Received in revised form

27 June 2017

Accepted 25 July 2017

Available online 28 July 2017

Keywords:

Human gut microbiota

Helicobacter pylori

Eradication

Antibiotics

ABSTRACT

The shotgun sequencing data presented in this report are related to the research article named “Gut microbiome shotgun sequencing in assessment of microbial community changes associated with *H. pylori* eradication therapy” (Khusnutdinova et al., 2016) [1]. Typically, the *H. pylori* eradication protocol includes a prolonged two-week use of the broad-spectrum antibiotics. The presented data on the whole-genome sequencing of the total DNA from stool samples of patients before the start of the eradication, immediately after eradication and several weeks after the end of treatment could help to profile the gut microbiota both taxonomically and functionally. The presented data together with those described in Glushchenko et al. (2017) [2] allow researchers to characterize the metagenomic profiles in which the use of antibiotics could result in dramatic changes in the intestinal microbiota composition. We perform 15 gut metagenomes from 5 patients with *H. pylori*

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<http://dx.doi.org/10.1016/j.dib.2017.07.070>

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