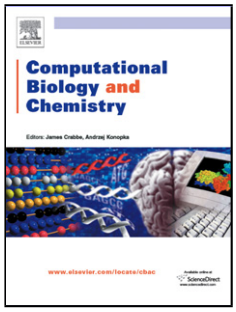

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Dynamics of the human gut phageome during antibiotic treatment

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Abstract

Bacterial viruses contribute to the dynamics of the microbiome communities, as they are involved in the horizontal gene transfer. Previously we studied changes in the gut microbiome of the two healthy individuals over the course of a 6-days antibiotics treatment and subsequent 28 days recovery time [1]. Now, from the same samples, the virus-like particles were isolated and sequenced. As the phage sequences are currently poorly represented in reference databases, the reads had to be assembled, annotated and their abundance had to be evaluated via reads mapping. We analyzed and compared patterns of changes in abundance of the phage scaffolds and scaffolds with antibiotics resistant genes, in both phage and whole-genome metagenomic sets. We observed an increase in abundance of scaffolds carrying antibiotic-resistant genes in response to the treatment.

Keywords: metagenomics, assembly, phages, phageome, bacteriophages

1. Introduction

Research into the human gut microbiome suggests that the microbiome is a complex dynamic network of mutually dependent actors from all of the branches of the Tree of Life [2]. Bacterial viruses (phages) strongly contribute to the structure and behavior of the network, as they are extremely abundant in the human gut, and provide a mechanism of horizontal gene transfer [3]. Therefore, the inner-workings of the human gut microbiome community cannot be fully explained without an understanding of the phage contribution.

A *healthy* gut microbial community is defined by the ability to restore its structure after a disturbance, such as an antibiotics treatment [4, 5]. We observed this resilience in our previous study when the microbiome of the two healthy participants was analyzed over the course of an antibiotics treatment and subsequent 28 days recovery time [1]. That study focused on characterization of the behavior of the bacterial part of the human gut microbiome in response to the antibiotics treatment.

Similarly to the microbiome, each person has their own unique phageome [6, 7], susceptible to diet interventions [8], diseases [9, 10] and antibiotics. As the gut phages were reported to be important for human health [3, 11], and to carry antibiotics resistant genes [12], now we will focus on describing the phage portion of the microbiome, their abundance and dynamics in response to the antibiotics treatment. This is a pilot study, aimed at developing methods for phage analysis

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